MOLECULAR EVOLUTION AND PHYLOGEOGRAPHY OF THE EASTERN MEDITERRANEAN WATER FROG (*PELOPHYLAX*) COMPLEX

A THESIS SUBMITTED TO
THE GRADUATE SCHOOL OF NATURAL AND APPLIED SCIENCES
OF
MIDDLE EAST TECHNICAL UNIVERSITY

BY

ÇİĞDEM AKIN PEKŞEN

IN PARTIAL FULFILLMENT OF THE REQUIREMENTS
FOR
THE DEGREE OF DOCTOR OF PHILOSOPHY
IN
BIOLOGY

JANUARY 2015

Approval of the thesis:

MOLECULAR EVOLUTION AND PHYLOGEOGRAPHY OF THE EASTERN MEDITERRANEAN WATER FROG (*PELOPHYLAX*) COMPLEX

submitted by **ÇİĞDEM AKIN PEKŞEN** in partial fulfillment of the requirements for the degree of **Doctor of Philosophy in Biology Department, Middle East Technical University** by,

Prof. Dr. Gülbin Dural Ünver _______________
Dean, Graduate School of **Natural and Applied Sciences**

Prof. Dr. Orhan Adalı _______________
Head of Department, **Biology**

Assoc. Prof. Dr. C. Can Bilgin _______________
Supervisor, **Biology Dept., METU**

Assoc. Prof. Dr. Jörg Plötner _______________
Co-Supervisor, **Molecular Lab, MfN, Berlin, DE**

Examining Committee Members:

Prof. Dr. Ahmet Murat Aytekin _______________
Biology Dept., Hacettepe University

Assoc. Prof. Dr. C. Can Bilgin _______________
Biology Dept., METU

Assoc. Prof. Dr. A. Elif Erson Bensan _______________
Biology Dept., METU

Assist. Prof. Dr. Ayşegül Birand _______________
Biology Dept., METU

Assist. Prof. Dr. Mehmet Somel _______________
Biology Dept., METU

Date: 22.01.2015

I hereby declare that all information in this document has been obtained and presented in accordance with academic rules and ethical conduct. I also declare that, as required by these rules and conduct, I have fully cited and referenced all material and results that are not original to this work.

Name, Last name: Çiğdem Akın Pekşen

Signature :

ABSTRACT

MOLECULAR EVOLUTION AND PHYLOGEOGRAPHY OF THE EASTERN MEDITERRANEAN WATER FROG *(PELOPHYLAX)* COMPLEX

Akın Pekşen, Çiğdem

Ph. D., Department of Biology
Supervisor: Assoc. Prof. Dr. C. Can Bilgin
Co-supervisor: Assoc. Prof. Dr. Jörg Plötner

January 2015, 342 pages

Water frogs (genus *Pelophylax*) in the eastern Mediterranean region represent a genetically and phylogenetically diverse group. Their dependence on freshwater habitats makes them highly sensitive to geological and climatic changes. Thus they are an ideal group to study the effect of past geological processes on molecular evolution of protein-coding and non-coding genes on the genome and on patterns of phylogeography in the eastern Mediterranean region.

In the first study, the complete sequence of water frog *Pelophylax lessonae*' serum albumin (SA) gene including all exons, all introns, upstream sequence of the 5' UTR and downstream sequence of the 3' UTR were reported. By aligning *P. lessonae'* albumin gene with albumin genes of closely and distantly related amphibian species, potential regulatory elements and functional motifs in the 5' UTR (TATA box, HP element, ADEI, ADEII) and 3' UTR (PLE, USE1 and 2, PAS, DSE), and in the exon-intron junctions were documented. Comparison of exon and intron lengths of the water frog with other vertebrate species revealed a strong length conservation in protein coding albumin exons among distinct vertebrate species, but high variation in intron lenghts. Moreover, the search of the entire scaffold for retroelements indicated several distinct classes of truncated retroelement families upstream of the 5' UTR, downstream of the 3' UTR and within individual albumin introns could be one of the important drivers of the albumin gene evolution. Finally, phylogenetic analysis based on nucleotide sequences of protein-coding albumin exons supported previous mitochondrial DNA (mtDNA) and the first intron of the SA gene findings which were the sister group relationship of *P. lessonae* and *P. bergeri,* a close relationships of *P. ridibundus* and *P. cf. bedriagae* from Anatolia. Moreover, *P. epeiroticus* is closely related to *P. ridibundus/P. cf. bedriagae.* In contrast to former mtDNA findings, the SA exon data revealed that *P. shqipericus* represent a distinct lineage, which was supported by previous protein electrophoretic investigations.

In the second study, phylogeographic patterns between mitochondrial (ND2 and ND3) and nuclear markers (SAI-1+*Rana*CR1) for water frog complex of the eastern Mediterranean region were compared. On the basis of analysis using extensive data set from mtDNA and nuDNA markers, these markers revealed discordances in the tree topology, the number of genetic stocks, the level of genetic differentiation, the times of divergence and the patterns of geographic distribution among distinct water frog lineages. These discordances between two markers were discussed by distinct processes such as incomplete lineage sorting, retention of ancestral polymorphism, introgression after secondary contact reacting with sex-biased or adaptive processes, and distinct selective constraints on genes. The major water frog lineages in the eastern Mediterranean region, *P. cretensis, P. cypriensis,* the Levant (*P. bedriagae*), Cilician groups, Central Asia groups, and Anatolian main allele groups (MAGs) could be affected in distinct ways from these processes that were discussed in this study.

Keywords: molecular evolution, the serum albumin gene, *Pelophylax lessonae,* retroelements, discordant phylogeography, eastern Mediterranean, water frog *(Pelophylax),* mtDNA, ND2, ND3, nuDNA, *SAI-1+RanaCR1*.

ÖZ

DOĞU AKDENİZ SU KURBAĞALARI *(PELOPYLAX)* KOMPLEKSİNİN MOLEKÜLER EVRİMİ VE FİLOCOĞRAFYASI

Akın Pekşen, Çiğdem

Doktora, Biyoloji Bölümü
Tez Yöneticisi: Doç. Dr. C. Can Bilgin
Ortak Tez Yöneticisi: Doç. Dr. Jörg Plötner

Ocak 2015, 342 sayfa

Doğu Akdeniz'deki su kurbağaları (genus *Pelophylax*) hem genetik hemde filogenetik olarak çeşitlilik gösteren bir grubu oluşturmaktadır. Bu hayvanların tatlı su ortamlarına olan bağımlılıkları onları hem jeolojik hem de iklim değişikliklerinin etkisine oldukça hassas duruma bir getirmektedir. Bu sebeplerden dolayı bu grup geçmişteki jeolojik olayların genomdaki protein kodlayan ve kodlamayan genlerin moleküler evrimine ve Doğu Akdeniz'deki filocoğrafik oluşumlarına olan etkileri çalışmak için ideal bir gruptur.

İlk çalışmada su kurbağası *Pelophylax lessonae* türünün serum albumin (SA) geninin tüm exonları, intronları, 5' UTR'ın yukarı, ve 3' UTR'ın aşağı kısmı olmak

üzere tüm gen sekansı bildirilmiştir. P. lessoanae albumin geni hem yakın hemde uzak diğer amfibi türleri ile hizalanarak genin 5' UTR (TATA box, HP element, CAT box ADEI, ADEII) ve 3' UTR (PLE, USE1 ve 2, PAS, DSE) bölgeleri ve exon-intronların birleşme noktalarındaki muhtemel düzenleyici ve fonksiyonel motifler belirlenmiştir. Su kurbağasının exon ve intron uzunluklarının diğer omurgalı türleri ile karşılaştırılması protein kodlayan albumin geninin exon uzunluklarının oldukça güçlü şekilde korunduğu buna karşın intron uzunluklarının oldukça değişkenlik gösterdiğini ortaya koymuştur. Bundan başka tüm scaffoltun retroelementler için taranması sonucu albumin geninin 5' UTR'ın yukarısında, 3' UTR'ın aşağısında ve intronların içinde çok sayıda farklı ailelere ait parçalanmış retroelementler olduğunu göstermiş ve bunların albumin geninin evrimindeki önemli faktörlerden biri olduğunu göstermektedir. Son olarak serum albuminin protein kodlayan exonlarının nükleotid sekansına dayalı olarak oluşturulan filogenetik analiz sonuçları daha önceki mitokondriyal DNA (mtDNA) ve SA'nin birinci intron sonuçları ile desteklenmektedir, buna göre bir tarafta *P. lessonae* ve *P. bergeri* kardeş grup oluştururken, diğer tarafta *P. ridibundus* ve Anadolu'dan *P. cf. bedriagae* ise diğer yakın grubu oluşturmakta ve *P. epeiroticus*'un son gruba yakın olduğu görülmektedir. Daha önceki mtDNA bulgularına karşın, SA exon verileri *P. shqipericus*'un farklı bir soyu gösterdiği ve bu bulgunun daha önceki protein elekroforetik araştırmaları tarafından desteklenmektedir.

İkinci çalışmada, Doğu Akdeniz Bölgesi'ndeki su kurbağalarının mitokondriyal (ND2 ve ND3) ve nükleer marker (SAI-1+RanaCR1)larının filocoğrafik oluşumları karşılaştırılmıştır. Mitokondriyal ve nuklear DNA markerlarının yoğun verilerinin analizlerine dayalı olarak elde edilen sonuçlar bu iki marker arasında ağaç topolojisinde, genetik stokların sayısında, genetik faklılaşmanın düzeyinde, ayrılma zamanlarında ve farklı su kurbağası soylarının coğrafik dağılımlarında uyumsuzluklar olduğunu göstermiştir. Bu iki marker arasındaki uyumsuzluklar farklı süreçler ile açıklanabilir ki bunlar genlerin soylardaki dağılımının eşit olmaması, atasal polimorfizmin tutulması, ikinci bağlantıdan sonra meydana gelen gen akışı ve bunun eşeye bağlı ve adaptive süreçler ile birlikte hareket etmesi ve

genler üzerindeki farklı selektif baskılar olabilir. Doğu Akdeniz'deki başlıca su kurbağası soyları olan *P. cretensis, P. cypriensis,* the Levant (*P. bedriagae*), Kilikya grupları, Orta Asya grupları, ve Anadolu MAGs bu süreçlerden farklı şekilde etkilendiği düşünülmekte olup bu çalışmada bunlar tartışılmıştır.

Anahtar kelimeler: moleküler evrim, serum albumin geni, *Pelophylax lessonae,* retroelements, uyumsuz filocoğrafya, Doğu Akdeniz, su kurbağası *(Pelophylax),* mtDNA, ND2, ND3, nuDNA, SAI-1+*Rana*CR1

To My Wonderful Family and My Partner, Ozan

ACKNOWLEDGEMENTS

I would like to express my deepest gratitude and sincerest appreciation to my supervisor Assoc. Prof. Dr. C. Can Bilgin for his guidance, continuous encouragement, invaluable help and great support throughout this study as well as my graduate education. I would like to also express my sincerest appreciation to my co-supervisor Assoc. Prof. Dr. Jörg Plötner for his invaluable help, continuous encouragement, advise and constructive criticism during PhD thesis.

I would like to thank to Dr. Thomas Uzzell for corrections, advise and valuable ideas during thesis writing process. I would like to thank to Dr. Peter Beerli for his guidance during phylogenetic analysis. I would like to thank to Dr. Rob Westaway for providing geological information. I would like to thank to Jose Grau for bioinformatic analysis. Lastly, I am also grateful to Robert Schreiber for his support during experiments.

I am grateful to my labmates Banu Kaya, Emel Çakmak, Semra Yalçın, Gözde Çilingir, Mustafa Durmuş, and Mert Elverici for their great friendship, encouragement, and cooperation. I would like to thank to Semra Yalçın, Banu Kaya and Mustafa Durmuş for production of geographic maps.

My special thanks also go to people involved in the my field teams: Ahmet Ekşioğlu, Emel and Yavuz Çakmak, Aysun Öz and Ali Kılıç. By helps of them, we have performed a wonderful sampling in Turkey and we have overcome several difficulties.

I would like to thank to several people from Ministry of Food, Agriculture and Livestock for providing vehicle, driver, personel and accommodation during field trips: Vahdettin Kürüm (Ankara), and agriculture managers of many provinces in Turkey, Ali Lek (Erzincan), Hamit Aygül (Malatya), Ali Kılıç (Elazığ), Namet Sevinç (Bingöl), Murat Yıldız (Muş), Kasım Piral (Bitlis), Mehmet İncir (Van), Yılmaz Zeren (Ağrı), Osman Çakır (Iğdır), Yusuf Yurdalan (Kars), Fevzi Karakoç (Ardahan), Mustafa Altun (Erzurum), Artvin (Mustafa Duman), Abdullah Ertuğrul (Bayburt), Bektaş Erdoğan (Trabzon), Hasan Irkın (Gümüşhane), Yaşar Kavak (Tokat), Ahmet Millici (Amasya), Kadir İspirli (Samsun), Mücait Yeşil (Sinop), İhsan Emiralioğlu (Kastamonu), Murat Akbay (Karabük), Yusuf Alagöz (Bartın), Metin Karaoğlanoğlu (Çankırı), Abdulbaki Şahin (Çorum), Mehmet Beykaya (Sivas), Adnan Akay (Kayseri), Ahmet Şahin (Nevşehir), Cemil Usanmaz (Niğde), Recep Öztorun (Aksaray), Harun Toker (Kırşehir), Ünal Koçak (Yozgat), Süleyman Yıldız (Kırıkkale), Mehmet Gündoğdu (Kahramanmaraş), Ahmet Avcı (Gaziantep), Erdal Özer (Adıyaman), Mehmet Altun (Bolu), Ayhan Ünal (Düzce), Yusuf Yıldırım (Sakarya), Abdullah Öztürk (Kocaeli), Selim Karahan (Yalova), İlkay Uçar (Çanakkale), Engin Sancı (Balıkesir), Mevlüt Gümüş (Eskişehir), Altuğ Atalay (Kütahya), Zekeriya Durmuş (Afyonkarahisar), Atilla Arslan (Uşak), Ömer Çelik (Manisa), Ahmet Güldal (İzmir), Muhsin Temel (Aydın), Yusuf Gülsever (Denizli), Ahmet Dallı (Muğla), Bedrullah Erçin (Antalya), Orhan Ekici (Burdur), Isparta (Sıddık İpek), Fikret Coşkun (Adana), Bestami Zabun (Antakya), İbrahim Sağlam (Osmaniye), Hasan Çebi (Kırklareli), Erdem Karadağ (Tekirdağ), Hikmet Doğru (Karaman), Orhan Soylu (Konya-Ereğli) and engineers of fisheries and aquaculture: Seyf Ali Ağatepe, Mustafa Balcı, Eda Uçar, Zeki Kurt, Sadık Doğan, Neşat Ulutaş, Özcan Aydın, Turgut Ertümen, Berika Erdem, Derya Salcı, İbrahim Pınar, Akgül Balcı, Durdu Ağdağı, Mustafa Durna, Ekrem Sam, Hilati Karaköy, Orhan Bülbül, Birol Yılmazer, Barış Aşık, Erkan Güneş, Hakan Eryıldırım, Özgür Öztek, Murat Aktaş, Bülent Yaşar, Hayati Güre, Sabri Erol, Abdurrahman Çetinkurşun, Ferrahi Saraçoğlu, Elif Öztürk, Akife Tarin, Yasemin Ezer, Tekin Yıldız, Selami Okka, Osman Kurt, Ahmet Özaydın, Hilmi Öter, Metin Polat, Mahmut Kurt. Many other people involved in this field trips: Ali Şenol, Onur Sarı, Ethem Elvan, Serdar Büyük, Selami Okka, Cansu Atalay, Ahmet Barutoğlu, Yüksel Güneş, Ahmet Akın, İhsan Kaçar, İlhami Uzun, Koray Sivrikaya, Cemal Çağlayan, Berke Kırlangıç, Murat Aksu, İsmail Sever, Yusuf Kuşoğlu, Nizamettin Özaslan, Mehmet Başhan.

I would like to express my heartful gratitude to my worderful family members; my mothers Radife and Fatma, my fathers Ahmet and Deniz, my brother, Mehmet, and my sisters Gülden and Gizem, and junior Yunus Kerim for their support and encouragement.

Last but not least I would like to express my deepest appreciation to my friend, my love and husband, Ozan for his endless love, support, patience, motivation, understanding. Without him, I could not overcome challenging times during this period. Of course I cannot forget our sweet buddgies Gypsy and Toto.

This work was supported by Swiss National Fund (grants 31-37579.93, 31-59144.99, 31-103903/1 and 31-64004.00), Deutsche Forschungsgemeinschaft (grants PL 213/9-1 and PO 1431/1-1), TUBITAK TBAG 111T584, TUBITAK TBAG 112T913.

TABLE OF CONTENTS

CHAPTERS

LIST OF TABLES

TABLES

LIST OF FIGURES

FIGURES

LIST OF ABBREVIATIONS

WGD	Whole genome duplication
SD	Segmental duplication
TE	Transposable elements
HGT	Horizontal gene transfer
MHG	Main haplogroups
UTR	Untranslated terminal repeats
mtDNA	Mitochondrial DNA
nuDNA	Nuclear DNA
aa	Amino acids
kd	Kilodalton
bp	Base pairs
SA	Serum albumin
PL	*Pelophylax lessonae*
ORF	Open reading frame
ITR	Inverted terminal repeat
HP	Hepatocyte-specific promoter element
ADE	Amphibian downstream element
PLE	Poly(A)-limiting element
USE	U-rich upstream element
PAS	Polyadenylation site
DSE	Downstream element
CPSF	Cleavage and polyadenylation specifity factor
CstF	Cleavage stimulatory factor
IRE	Iron responsive element
LTR	Long terminal repeat

TLE	Tc1-like elements
NLS	Nuclear localization signal
DR	Direct repeat
HLE	hAT-like element
MSC	Messinian salinity crisis
SAI	Serum albumin intron
Myr	Million years
Ma	Million years ago
MAG	Main allele group
MPR	Mid-Pleistocene revolution

CHAPTER 1

GENERAL INTRODUCTION

1.1. Analysis of Molecular Evolution

Molecular evolutionary research covers a broad range of topics starting from gene and genome evolution to molecular phylogenetics (Li, 1997; Page and Holmes, 1998; Graur and Li, 2000; Nei and Kumar, 2000; Yang, 2006). Based on genetic information stored in molecules (DNA, RNA, proteins), evolutionary patterns can be analyzed and phylogenetic relationships among species and supraspecific taxa can be inferred. As can be demonstrated by an ever-growing amount of molecular data, molecular approaches which supplement traditional non-molecular methods are a pivotal part of the toolkit of evolutionary biologists and systematists. For Amphibia, internet sequence databases (GenBank, EMBL) currently contain about 3.326.318 entries of DNA and RNA sequences. DNA sequences in particular, because they bear the code of life, provide the most detailed information possible for any organism - the instructions for how each working part should be assembled and operate (Page and Holmes 1998). Progress in technological development, in particular the simplification of molecular techniques and the reduction in expense, will almost certainly lead to a further increase of molecular studies. Thus, molecular evolution is a constantly changing and evolving field because of the steadily growing number of sequenced genomes, both prokaryotic and eukaryotic, available to the scientific community and the public at large.

1.2. Mechanisms of Genome Evolution

1.2.1. Gene and Genome Duplications

Genome evolution occurs at distinct levels; beside small scale changes such as single base substitutions, insertions and deletions, gene and whole genome duplications (WGD) are possible. All of these mutation events provide raw genetic material on which natural selection can act upon.

Genome duplications have been playing an important role in the vertebrate genome evolution since it was suggested (Ohno, 1970) that the early vertebrates have undergone two rounds of whole genome duplication (2 R WGD) about 600 Ma which was later documented by analysis of *Hox* genes and *Hox* gene clusters (Holland et al., 1994; 1997). 3R of WGDs were proposed to occur in the stem lineage of ray-finned fish (Meyer and Van de Peer, 2005). These global events could extremely increase the number of gene copies and produce several distinct paralogs which provide novel raw material for evolutionary processes leading to genomic innovations (Zhang 2003); the globin gene family is an impressive example (reviewed by Storz et al. 2013).

These gene copies could remain or be lost differently according to their functions throughout evolution of vertebrate lineages (Blomme et al., 2006). Therefore the fate of paralogs can be different: i) both gene copies can remain and obtain new functions, (neofunctionalization); ii) they can acquire degenerative complementary mutations thus both are necessary to perform the original function of the ancestral gene (subfunctionalization) (Force et al., 1999); iii) they can maintain the same function by gene conservation through concerted evolution (Li, 1997); iv) they can evolve to pseudogenes, mostly functionless, which are not deleterious and not eliminated by selection (Zhang, 2003), and provide the organism genetic diversity (Gu, 2003). In the last case, it increases tolerance to changing environmental conditions decreasing the probability of extinction (Crow and Wagner, 2006).

Rather than WGD, gene duplications can also arise from segmental duplications (SDs), unequal crossing over and transpositions events. SDs are characterized by low copy number and can change from few base pairs to many megabases. They have played an important role in the evolution of the human and primate genomes, for example many rapidly evolving exons are found within SDs (Lorente-Gardos et al., 2013). SDs can be arranged as adjacent duplications, interspersed intrachromosomally or interchromosomally (Ramos and Ferrier, 2012). It was suggested that distinct DNA-based mechanisms are responsible for these arrangements. For instance, non-homologous end-joining (NHEJ) more likely results in adjacent duplications (Meisel, 2009) while non-allelic homologous recombination (NAHR) between repetitive elements on the genome accounts for interspersed duplications (Fiston-Lavier et al., 2007). In the second mechanism, unequal crossing over produces linked duplicated genes in the chromosome which can include many genes, a single gene or the part of a gene. Retrotransposition mechanism, in contrast, generates gene copies randomly inserted into the genome and not linked to the original copy. Because mRNA is reverse transcribed into cDNA which is inserted into the genome, many regulatory elements such as promoter are not transcribed during this process. Thus, new gene copies generally become pseudogenes which do not contain regulatory sequences necessary for transcription (Zhang, 2003).

1.2.2. Transposable Elements

Transposable elements (TEs) are important drivers of genome evolution and are intrinsic components of regulatory networks (Feschotte 2008). TE-derived sequences such as promoters (Van de Lagemaat et al., 2003; Marino-Ramirez et al., 2005; Cohen et al., 2009; Conley et al., 2008; Jern and Coffin, 2008), polyadenylation signals and termination sites (Roy-Engel et al., 2005; Lee et al., 2008; Conley and Jordan, 2012), and smRNAs (Smalheiser and Torvik, 2005) are involved in regulation of gene expression at both the transcriptional and post-transcriptional level (Feschotte, 2008; Medstrand et al., 2005; Rebollo et al., 2012).

Transposable elements are classified into two groups according to their structure and mode of transposition: i) Retrotransposons (class I elements) which mobilize via reverse-transcription using an RNA intermediate, and ii) DNA transposons (class II elements) which replicate without an RNA intermediate, either by a cut-and-paste mechanism (DNA transposons), by rolling circle DNA replication (helitrons), or by so far unknown mechanisms (politrons/mavericks) (e.g. Levin and Moran 2011; Rebollo et al., 2012). Among the Class I elements two major subclasses are recognized: (1) retroelements (REs) with long terminal repeats (LTRs) and (2) elements without LTRs (non-LTR REs) (Rebollo et al., 2012; Deininger and Batzer, 2002).

The copy number of TEs is significantly related with the genome size (Kidwell, 2002). For instance, TEs make up only small parts of the fruit fly (*Drosophila melanogaster*) and the worm (*Caenorhabditis elegans*) genomes (15-22% and 12%, respectively). In contrast, half or even more than half of the vertebrate genomes is dominated by distinct classes of TEs. For example, 47% of the genome of giant salamander, the largest genome in vertebrates (14 Gb to 74 Gb), is dominated by TEs, particulary by LTR retrotransposons (Sun et al., 2011). In human, 45% of the genome contains TEs (Chenais et al., 2012).

In addition to their impact on genome size variation, TEs can influence the dynamics of the genome in different ways. Activity of TEs may result in both destructive and constructive alterations (Kidwell and Lisch, 2000). Deleterious effects occur if TEs insert into coding sequences which can lead to premature termination of the peptide sequence and thus, disrupt gene function (Chenais et al., 2012). Many TE derived sequences, however, can act as cis-regulatory elements at promoter and enhancer regions (Jordan et al., 2003; Cohen et al., 2009; Teng et al., 2011); they can also function as an antisense promoter for genes that are located at 5' of the complete element (Kazazian, 2004). Moreover, TEs may evolve to new protein coding genes in a process called exonization (Sela et al., 2010). Alzohairy et al. (2013) reviewed how TEs became parts of functional genes in eukaryotic genomes in the process of “molecular domestication”. As a result of a fusion between TEs and host genes chimeric proteins can originate as demonstrated for the SETMAR gene (Roman et al., 2007). Recently, the availability of transcriptome data from the European water frog species *P. lessonae* and its comparison to transcriptome data obtained from *Silurana* revealed that TEs, particularly LTR retroelements, may play important roles during embryogenesis (Grau et al., 2014).

Moreover, TEs can carry an intragenic poly(A) signal such as human L1 and Alu elements (Roy-Engel et al., 2005) which results in premature cleavage of the transcripts. Besides their promoter and intragenic poly(A) functions, these elements can cause 5' and 3' transduction during insertion because they can carry sequences from a promoter upstream of the complete element and downstream of the poly(A) signal (Kazazian, 2004). Lastly, they can contain some characteristics which may result in microRNAs, as known from miniature inverted repeat transposable elements (MITEs) (Feschotte, 2008). It was also suggested that precursor of mammalian microRNAs are ancient MIR (SINE) and L2 (LINE) elements (Smalheiser and Torvik, 2005). At chromosomal level, TEs are potential sources for several types of chromosomal rearrangements. For example, the human genome is rich in L1 and Alu elements which make quite likely non-allelic homologous recombination; mispairing between these non-LTR elements can result in deletions, segmental duplications, inversions or translocations (Konkel and Batzer, 2010).

1.2.3. Exon Shuffling

Exon shuffling is an important molecular mechanism for the formation of new genes and also for genome and proteome evolution (Liu and Grigoriev, 2004) in complex eukaryotic genomes because increase in genome size is correlated with increase in intron length and the number of repetitive elements which make more likely potential of exon shuffling by intronic recombination (Keren et al., 2010). Exon shuffling gives rise to a new exon combination produced by recombination between intronic sequences of unrelated genes, which assorts exonic sequences randomly (Gilbert, 1978) or exon duplication occurs within the same gene (Kondrashov and Koonin, 2001; Long et al., 2003).

Non-coding intronic sequences are long and harbour many types of repetitive elements which make them recombination hotspot regions via mismatch or nonhomologous recombination (Patthy, 1999; Kolkman and Stemmer, 2001). Exon shuffling can be symmetric and asymmetric according to intron phase, which indicate the position of a given intron within a codon. Phase 0 introns are located between two codons, phase 1 introns lie between the first and second nucleotide of the codon, and phase 2 intron is found between the second and third nucleotide of the codon (França et al., 2012). Thus, symmetric exons have the same phase in their flanking introns including three groups 0-0, 1-1, 2-2 while asymmetric exons are 0-1, 0-2, 1-0, 1-2, 2-0 and 2-1. It was suggested that only symmetric exons can be subjected to exon shuffling, tandemly duplicated or deleted with preserving the reading frame (Kolkman and Stemmer, 2001; França et al., 2012).

Exon shuffling significantly contributed to metazoan evolution and to the development of multidomain proteins. These proteins function in tissue remodelling processes, cell-to-cell and cell-to-matrix interactions, cell-to-cell communication, that is, are mainly essential for multicellularity of metazoa (Patthy, 1999). It was documented that ancient domains are flanked by phase 0 introns and they have a tendency of distribution to take place in the central part of proteins. In contrast, modern domains are frequently flanked by phase 1 introns, and they are mainly found in their carboxyl and amino ends (Vibranovski et al., 2005; 2006; França et al., 2012). In addition, genes reflecting high degree exon shuffling events could provide novel sources for protein-protein interactions; both interactions among multiple types of other domains and interactions with other copies of themselves during metazoan evolution (Cancherini et al., 2010).

1.2.4. Horizontal Gene Transfer

Horizontal gene transfer (HGT), also referred as lateral gene transfer, is a non-sexual movement of genetic material between closely or distantly related genomes in contrast to vertical transmission of genetic information from parents to offspring (Keeling and Palmer, 2008). The transfer of genes can occur via distinct ways such as bacteria, viruses, transposons, other vectors and direct contacts or initial hybridization (Syvanen, 2012). Particularly, early developmental stages in multicellular eukaryotes provide a weak link for entry of foreign genes into new genomes (Huang, 2013). HGT is important in bacterial genome evolution (Frost et al., 2005) while its role in eukaryotes is greatly variable because several types of transfers are possible. In the simple transfer, genes from bacteria to eukaryotes move and duplicate or replace the homologous copies. In the serial transfer, transfer from bacteria to eukaryotes follows the second eukaryotic lineage which results in complex relationships. In the novel gene transfer, a new function is provided to the eukaryotic lineage (Keeling and Palmer, 2008; Rajarapu, 2014). It can show a patchy distribution among eukaryotic lineages because of differential loss or gain. Therefore, its role in genome evolution is variable. HGT of transposable elements among eukaryotic lineages is one of the best example how they impact on genome evolution from a neutral variation to genome-wide innovation which can result in speciation or adaptation (Schaack et al., 2010). Moreover, transferred genes in distinct eukaryote species take part in parasitism, disease resistance, new metabolic pathways, nutrient and energy metabolism, and many other new functions, supporting evidence in the adaptative evolution of eukaryotes (Haegeman et al., 2011; Fitzpatrick, 2012; Zhu et al., 2011).

There are three main approaches to predict HGT in eukaryotes. Initially, codon-based approach is based on comparison of G+C content and codon usage of recipient with donor organism after HGT because organisms have specific base frequency and codon usage characteristics (Becq et al., 2010; Azad and Lawrence, 2011). This approach is suitable for recent HGT rather than ancient one (Lawrence and Ohman, 1997). Secondly, the BLAST-based approach is to use database search to find out the most similar sequence to a query sequence of a gene (Keeling and Palmer, 2008; Whitaker et al., 2009). Lastly, phylogenetic approach is based on conflict between a gene tree and species phylogeny. Any incongruence between two phylogenetic trees is an indicator of HGT, which requires well sampling of homologous sequences, their multiple alignment, phylogenetic tree construction and topology comparison. Each approach has distinct drawbacks (Keeling and Palmer, 2008; Whitaker et al., 2009; Schönknecht et al., 2013, Rajarapu, 2014)

1.3. Molecular Phylogeography

Phylogeography studies how historical processes shaped the current distribution of species by utilizing phylogenetic analysis of genetic data and their geographic distribution (Avise et al., 1987, reviewed later by Hickerson et al., 2010). It answers questions about a single species such as species delimitation (Knowles and Carstens, 2007), past hybridization, introgression, hybrid zones (Hewitt, 2001) and multiple species named as comparative phylogeography which studies how past common geological and climatic events have affected the contemporary species diversity by looking at overlapping historical patterns of genetic divergence and gene flow in time and space (Hickerson et al., 2010). Many early phylogenetic studies were based on mainly mitochondrial DNA (mtDNA), while recently there is a considerable transition to multilocus markers. Although distinct genes have distinct evolutionary rates which could give rise to distinct phylogenetic signals, application of data partition methods on concatenated datasets can help to resolve the problem (Nylander et al., 2004). Brito and Edwards (2009) suggested a large number of multiple and independent loci can overcome the effect of coalescent variation and HGT events and resolve incongrunce between the gene tree and the species tree.

1.3.1. Phylogenetics and Phylogeography of the Eastern Mediterranean Water Frogs (genus *Pelophylax*)

The discovery of the hybrid nature of the common European edible frog, *Pelophylax esculentus*, and its taxonomic separation from one of its parental species, the pool frog, *P. lessonae* (Berger, 1967; 1968) has intensified the research on western Palearctic water frogs resulting in acquisition of large genetic data sets on the basis of which diverse questions on the evolutionary genetics, systematics, and ecology of western Palearctic water frogs (reviewed by Graf & Polls Pelaz 1989; Plötner 2005).

Water frogs in the Eastern Mediterranean area present a huge genetic, organismal, phylogenetic, and ecological diversity. Despite their high similarity in morphology, they show considerable genetic divergence, indicating the existence of several cryptic species. Distinct levels of genetic divergence are present, some lineages are considered to represent distinct evolutionary species (Beerli et al., 1996; Plötner et al., 2010, Akın et al., 2010b). Water frogs are found in all types of freshwater habitats, and because of their sensitive skin structure they are easily affected from environmental changes. All make them hence as a candidate group to study the impact of past historical geological and climatic events on contemporary phylogeography and molecular evolution (Beerli et al, 1996, Plötner et al. 2010, Akın et al., 2010b).

The first phylogenetic study of water frogs from eastern Mediterranean region (although samples are only from the Aegean region) based on 31 protein electrophoretic loci indicated four main groups which are (1) *P. cretensis* and *P. epeiroticus* group, close to (2) *P. perezi* and *P. saharicus* outgroup and (3) *P. lessonae* and *P. shqipericus* group close to (4) a diverse group comprising of *P. cerigensis, P. cf.bedriagae* and *P. ridibundus.* The relationships within the last group could not be resolved (Beerli et al., 1996).

A more comprehensive study based on mtDNA (12 rDNA and ND3), including water frogs from Anatolia, Syria, Jordan, and Central Asia, indicated that water frogs from Cyprus and Central Asia represent distinct species. Moreover, Anatolian frogs did not belong to either *P. ridibundus* from Europe or *P. bedriagae* from Syria; the Anatolian clade comprised several subclades (one of them represented the *caralitanus* lineage) and the so-called Ceyhan lineage from the Çukurova plain. All Anatolian lineages formed a single huge clade together with *P. cretensis* and *P. epeiroticus*. In addition to this clade, two additional clades are present: one clade consists of *P. lessonae, P. bergeri* and *P. shqipericus*; the other includes *P. saharicus* and *P. perezi* (Plötner and Ohst, 2001; Plötner et al., 2001). The following study (Lymberakis et al., 2007) based on distinct mtDNA genes (16S rRNA and cytochrome b) verified the previous results and revealed new finding about *P. cerigensis* and *P. kurtmuelleri,* however, their phylogenetic relationships with respect to *P. bedriagae* and P. *ridibundus* remained unresolved in this research.

Certainly the most detailed studies from eastern Mediterranean region using an intensive data set (612 samples) on the basis of mtDNA (ND3 and ND2) documented an extreme genetic diversity which was represented by six main haplogroups (MHGs) (Plötner et al., 2010; Akın et al., 2010b) (Fig 1). MHG1 includes *P. ridibundus* and *P. kurtmuelleri* from European and Balkan populations, respectively. MHG2 indicates the Levant populations (*P. bedriagae*). MHG3 is unique for Cyprus water frogs, described as a new species *P. cypriensis*

(Plötner et al., 2012). MHG4 and 5 are distributed around the Çukurova plain in Anatolia. MHG6 is the greatest group inhabiting an area from western Anatolia to the Caspian Sea. It is subdivided into four subgroups (MHG6a-d). MHG6a is found in the southwestern Anatolia, representing *P*. cf. *caralitanus*. MHG6b only occurs in western Antalya, and on the islands Rhodos and Karpathos. It was described as a distinct species, *P*. cf. *cerigensis* (Beerli et al., 1994), its systematic status, however, is not yet clear. MHG6c is distributed from western Anatolia to the Caspian Sea. MHG6d was found in the river systems Euphrates and Tigris (Plötner et al., 2010; Akın et al., 2010b). As for *P*. cf. *cerigensis*, the systematic status of these two MHGs still remains unclear (Fig 1.1).

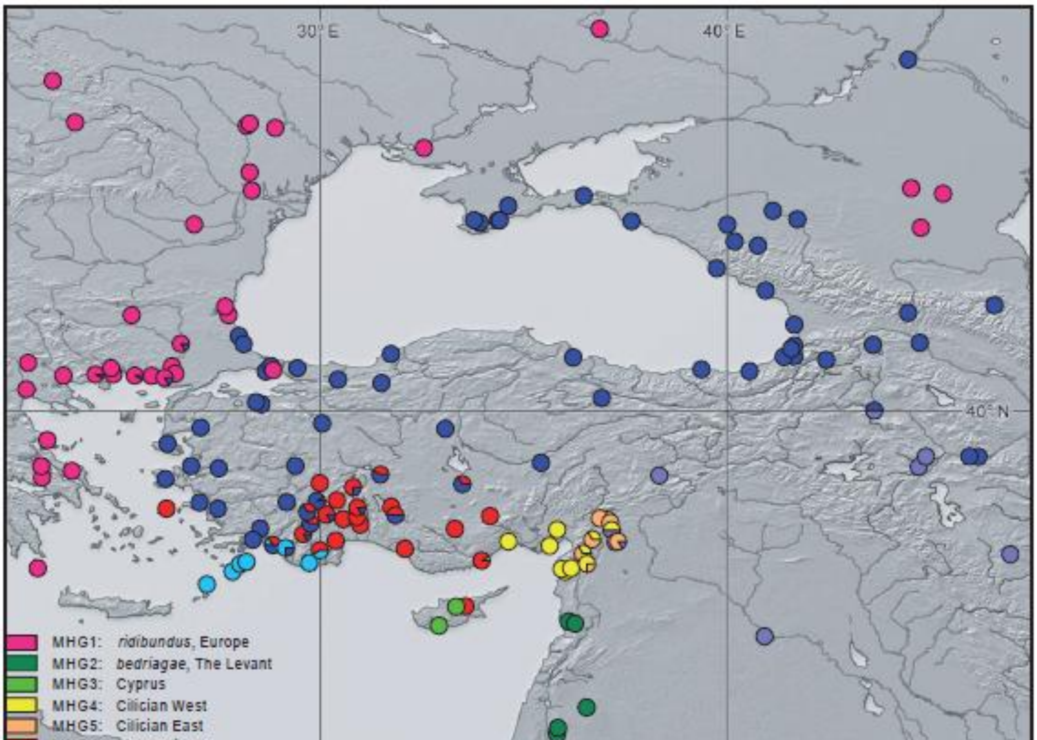


Figure 1.1. Geographic distribution of water frogs' main haplogroups (MHGs) and subgroups (a-d) of water frogs in Anatolia and neighbouring regions.

1.4. The Present Study

As indicated above water, the frog complex presents a biologically fascinating array of questions; my theses is focused on molecular evolution and phylogeography of eastern Mediterranean region water frog complex. The main aim was to evaluate phylogenetic and phylogeographic hypotheses formulated on the basis of mtDNA (e.g. Plötner et al., 2010; Akın et al., 2010a;b) and intron 1 of the serum albumin gene (Plötner et al. 2009; 2012).

The goal of the first manuscript was to analyze the structure and molecular evolution of the serum albumin gene of the pool frog *P. lessonae*. The complete sequence of the albumin gene including all exons and introns, upstream sequence of the 5' UTR and downstream sequence of the 3' UTR were presented. Potential regulatory elements and functionally important motifs in the 5' and 3' UTR, and in the exon-intron junctions were documented by aligning sequences from closely and distantly related amphibian species. A comparison of exon and intron lengths of the pool frogs with other vertebrate species provided insight about molecular evolution of the albumin gene. Moreover, the entire scaffold of *P. lessonae* was scanned for retroelements which were described and systematized. Finally, phylogenetic relationships between selected water frog species were tested using both nucleotide and amino acid sequences of the albumin exons.

The task of second manuscript was to study phylogeographic patterns of mitochondrial genes (ND2 and ND3) and the nuclear marker serum albumin intron 1 (SAI-1) in water frog complex of the eastern Mediterranean region. These results revealed discordances in the tree topology, the number of genetic stocks, the level of genetic differentiation, the times of divergence and the patterns of geographic distribution. These discordances between two markers are discussed in the light of distinct processes that are incomplete lineage sorting, retention of ancestral polymorphism, introgression after secondary contact in concert with sex-biased or adaptive processes.

1.5. References

Akın, Ç., Bilgin, M., Bilgin, C.C. (2010a) Discordance between ventral colour and mtDNA haplotype in the water frog *Rana (ridibunda) caralitana*, 1988 Arıkan. *Amphibia-Reptilia* 31: 9–20.

Akın, Ç., Bilgin, C.C., Beerli, P., Westaway, R., Ohst, T., Litvinchuk, S.N., et al. (2010b) Phylogeographic patterns of genetic diversity in eastern Mediterranean water frogs were determined by geological processes and climate change in the Late Cenozoic. *J Biogeogr* 37: 211–2124.

Alzohairy, A.M., Gyulai, G., Jansen, R.K., Bahieldin, A. (2013) Transposable elements domesticated and neofunctionalized by eukaryotic genomes. *Plasmid* 69: 1-15.

Avise, J.C., Arnold, J., Ball, R.M., Bermingham, E., Lamb, T., Neigel, J.E., Reeb, C.A., Saunders, N.C. (1987) Intraspecific phylogeography: the mitochondrial DNA bridge between population genetics and systematics. *Annu Rev Ecol Syst* 18: 489-522.

Azad, R.K. and Lawrence J.G. (2011) Towards more robust methods of alien gene detection. *Nucleic Acids Res* 39: e36.

Becq, J., Churlaud, C. Deschavanne, P. (2010) A benchmark of parametric methods for horizontal transfer detection. *PLoS One* 5: e9989.

Beerli, P., Hotz, H., Tunner, H., Heppich, S., Uzzell, T. (1994) Two new water frog species from the Aegean islands Crete and Karpathos (Amphibia, Salientia, Ranidae). *Notulae Naturae, Academy of Natural Sciences of Philadelphia* 470:1-9.

Beerli, P., Hotz, H. & Uzzell, T. (1996) Geological dated sea barriers calibrate protein clock for Aegean water frogs. *Evolution* 50**:** 1676-1687.

Berger, L. (1967) Embryonal and larval development of F1 generation of green frogs different combinations. *Acta Zool Cracov* 12(7): 123-160.

Berger, L. (1968) Morphology of the F1 generation of various crosses within *Rana esculenta*-complex. *Acta Zool Cracov* 13: 301-324.

Blomme, T., Vandepoele, K., Bodt, S., Simillion, C., Maere, S., Peer, Y.V. (2006) The gain and loss of genes during 600 million years of vertebrate evolution. *Genome Biol* 7(5): R43, doi:10.1186.

Brito, P.H. and Edwards, S.V. (2009) Multilocus phylogeography and phylogenetics using sequence-based markers. *Genetica* 135: 439-455.

Cancherini, D.V., França, G.S., de Souza, S.J. (2010) The role of exon shuffling in shaping protein-protein interaction networks. *BMC Genomics* 11(Suppl 5): 1-13.

Chenais, B., Caruso, A., Hiard, S., Casse, N. (2012) The impact of transposable elements on eukaryotic genomes: from genome size increase to genetic adaptation to stressful environments. *Gene* 509: 7-15.

Cohen, C.J., Lock, W.M., Mager, D.L. (2009) Endogenous retroviral LTRs as promoters for human genes: a critical assesment. *Gene* 448: 105-114.

Conley, A.B., Piriyapongsa, J., Jordan, I.K. (2008) Retroviral promoters in the human genome. *Bioinforma Oxf Engl* 24: 1563-1567.

Conley, A.B., Jordan, I.K. (2012) Cell type-specific termination of transcription by transposable element sequences. *Mob DNA* 3: 15.

Crow, K.D. and Wagner, G.P. (2006) What is the role of genome duplication in the evolution of complexity and diversity? *Mol Biol Evol* 23(5): 887-892.

Deininger, P.L., Batzer, M.A. (2002) Mammalian retroelements. *Genome Res* 12: 1455-1465.

Feschotte, C. (2008) Transposable elements and the evolution of regulatory networks. *Nat Rev Genet* 9: 397-405.

Fiston-Lavier, A.S., Anxolabehere, D., Quesneville, H. (2007) A model of segmental duplication formation in Drosophila melanogaster. *Genome Res* 17: 1458-1470.

Fitzpatrick, D.A. (2012) Horizontal gene transfer in fungi. *FEMS Microbiol Lett* 329: 1-8.

Force, A., Lynch, M., Picket, F.B., Amores, A., Yan, Y.L., Postlethwait, J. (1999) Preservation od duplicate genes by complementary, degenerative mutations. *Genetics* 151: 1531-1545.

França, G.S., Cancherini, D.V., de Souza, S.J. (2012) Evoloutionary history of exon shuffling. *Genetica* 140: 249-257.

Frost, L.S. et al., (2005) Mobile genetic elements: the agents of open source evolution. *Nat Rev Microbiol* 3: 722-732.

Gilbert, W. (1978) Why genes in pieces? *Nature* 271: 501.

Graf, J.D., Polls-Pelaz, M. (1989) Evolutionary genetics of the *Rana esculenta* complex. In: *Evolution and ecology of unisexual vertebrates* p. 289-302. Dawley, R.M., Bogart, J.P., Eds, Albany.

Grau, J.H., Poustka, A.J., Meixner, M., Plötner, J. (2014) LTR retrolements are intrinsic components of transcriptional networks in frogs. *BMC Genomics* 15 (626): 1-16.

Graur, D. and Li, W.-H. (2000) Fundamentals of molecular evolution. Sinauer Associates, Sunderland, Massachusetts.

Gu, X. (2003) Functional divergence in protein (family) sequence evolution. *Genetica* 118: 133-141.

Haegeman, A., Jones, J.T., Danchin, E.G.J. (2011) Horizontal gene transfer in nematodes: a catalyst for plant parasitism? *Mol Plant Microbe Interact* 24: 879-887.

Hewitt, G.M. (2001) Speciation, hybrid zones and phylogeography or seeing genes in space and time. *Mol Ecol* 10: 537-549.

Hickerson, M.J., Cartens, B.C. et al. (2010) Phylogeography's past, present, and future: 10 years after Avise, 2000. *Molecular Phylogenet Evol* 54: 291-301.

Holland, P.W., Garcia-Fernandez, J., Williams, N.A., Sidow, A. (1994) Gene duplications and the origins of vertebrate development. *Dev Suppl* 125-133.

Holland, P.W. (1997) Vertebrate evolution: something fishy about Hox genes. *Curr Biol* 7: 570-572.

Huang, J. (2013) Horizontal gene transfer in eukaryotes: the weak-link model. *Bioessays* 863-875.

Jern, P., Coffin, J.M. (2008) Effects of retroviruses on host genome function. *Annu Rev Genet* 42: 709-732.

Jordan, I.K., Rogozin, I.B., Glazko, G.V., Koonin, E.V. (2003) Origin of a substantial fraction of human regulatory sequences from transposable elements. *Trends Genet* 19: 68-72.

Kazazian, H.H. (2003) Mobile elements: drivers of genome evolution. *Science* 303: 1626-1632.

Keeling, P.J. and Palmer, J.D. (2008) Horizontal gene transfer in eukaryotic evolution. *Nat Rev Genet* 9: 605-618.

Keren, H., Lev-Maor, G., Ast, G. (2010) Alternative splicing and evolution: diversification, exon definition and function. *Nat Rev Genet* 1-11.

Kidwell, M.G. (2002) Transposable elements and the evolution of genome size in eukaryotes. *Genetica* 115: 49-63.

Kidwell, M.G., and Lisch, D.R. (2000) Transposable elements and host genome evolution. *TREE* 15(3): 95-99.

Knowles, L.L., Carstens, B.C. (2007) Delimiting species without monophyletic gene trees. *Sys Biol* 56: 887-895.

Kolkman, J.A. and Stemmer, W.P.C. (2001) Directed evolution of proteins by exon shuffling. *Nat Biotechnol* 19: 423-428.

Kondrashow, F.A. and Koonin, E.V. (2001) Origin of alternative splicing by tandem exon duplication. *Hum Mol Genet* 10: 2661-2669.

Konkel, M.K., Batzer, M.A. (2010) A mobile threat to genomic stability: the impact of non-LTR retrotransposons upon the human genome. *Semin Cancer Biol* 20: 211-221.

Lawrence, J.G. and Ohman, H. (1997) Amelioration of bacterial genomes: rates of change and exhange. *J Mol Evol* 44: 383-397.

Lee, J.Y., Ji, Z., Tian, B. (2008) Phylogenetic analysis of mRNA polyadenylation sites reveals a role of transposable elements in evolution of the 3'-end of genes. *Nucleic Acids Res* 36: 5581-5590.

Levin, H.L., Moran, J.V. (2011) Dynamic interactions between transposable elements and their hosts. *Nat Rev Genet* 12: 615-627.

Li, W.-H. (1997) Molecular Evolution. Sinauer Associates, Sunderland, Massachusetts.

Liu, M., Grigoriev, A. (2004) Protein domains correlate strongly with exons in multiple eukaryotic genomes - evidence of exon shuffling? *Trends Genet* 20: 399-403.

Long, M., Betran, E., Thornton, K., Wang, W. (2003) The origin of new genes: glimpses from the young and old. Nat Rev Genet, 4(11): 865-875.

Lorente-Galdos, B., Bleyhl, J., Santpere, G., Vives, L., Ramirez, O., Hernandez, J., Anglada, R., Cooper, G.M., Navarro, A., Eichler, E.E., Marques-Bonet, T. (2013) Accelerated exon evolution within primate segmental duplications. *Genome Biol* 14(R9): 1-12.

Lymberakis, P., Poulakakis, N., Manthalou, G., Tsigenopoulos, C.S., Magoulas, A., Mylonas, A. (2007) Mitochondrial phylogeography of Rana (Pelophylax) populations in the eastern Mediterranean region. *Mol Phylogenet Evol* 44: 115-125.

Mariño-Ramírez, L., Lewis, K.C., Landsman, D., Jordan, I.K. (2005) Transposable elements donate lineage-specific regulatory sequences to host genomes. *Cytogenet Genome Res* 110: 333-341.

Meisel, R.P. (2009) Repeat mediated gene duplication in the *Drosophila pseudoobscura* genome. *Gene* 438: 1-7.

Medstrand, P., van de Lagemaat, L.N., Dunn, C.A., Landry, J.-R., Svenback, D., Mager, D.L. (2005) Impact of transposable elements on the evolution of mammalian gene regulation. *Cytogenet Genome Res* 110**:** 342-352.

Meyer, A., Van de Peer, Y. (2005) From 2R to 3R: evidence for a fish-specific genome duplication (FSGD). *Bioessays* 27: 937-945.

Nei, M., Kumar, S. (2000) Molecular Evolution and Phylogenetics. Oxford University Press, New York.

Nylander, J.A.A., Ronquist, F., Huelsenbeck, J.P., Nieves-Aldrey, J.L. (2004) Bayesian phylogenetic analysis of combined data. *Syst Biol* 53: 47-67.

Ohno, S. (1970) Evolution by gene duplication. New York: Springer-Verlag.

Page, R.D.M., and Holmes, E.C. (1998) Molecular evolution: a phylogenetic approach. Blackwell, Osney Mead, Oxford, U.K.

Patthy, L. (1999) Genome evolution and the evolution of exon-shuffling - a review. *Gene* 238: 103-114.

Plötner, J. (2005) *Die westpaläarktischen Wasserfrösche.* Von Märtyrern der Wissenschaft zur biologischen Sensation. Z f Feldherpetologie, Beiheft 9, Laurenti, Bielefeld.

Plötner, J., Ohst, T., Böhme, W., Schreiber, R. (2001) Divergence in mitochondrial DNA of Near Eastern water frogs with special reference to the systematic status of Cypriot and Anatolian populations *(Anura, Ranidae). Amphibia – Reptilia* 22: 397-412.

Plötner, J., Ohst. T. (2001) New hypothesis of the western Palearctic water frog complex (Anura: Ranidae). *Mitt Mus Nat kd Zool Reihe* 77: 5-21.

Plötner, J., Köhler, F., Uzzell, T., Beerli, P., Schreiber, R., Guex, G.-D. & Hotz, H. (2009) Evolution of serum albumin intron-1 is shaped by a 5' truncated non-long terminal repeat retrotransposon in western Palearctic water frogs (Neobatrachia). *Mol Phylogenet Evol* 53: 784–791.

Plötner, J., Uzzell, T., Beerli, P., Akın, Ç., Bilgin, C. C., Haefeli, C., Ohst, T., Köhler, F., Schreiber, R., Guex, G.-D., Litvinchuk, A. N., Westaway, R., Reyer, H.-U., Hotz, H., (2010) Genetic divergence and evolution of reproductive isolation in eastern Mediterranean water frogs. In: Glaubrecht, M., Schneider, H. (Eds.), Evolution in action. *Case studies in adaptive radiation and the origin of biodiversity. Special volume from the SPP 1127 "Radiations – Genesis of Biological diversity" of the DFG.* Springer, Heidelberg, Berlin.

Plötner, J., Baier, F., Akın, Ç., Mazepa, G., Schreiber, R., Beerli, P., Litvinchuk, S.N., Bilgin, C.C., Borkin, L., Uzzell, T. (2012) Genetic data reveal that water frogs of Cyprus (genus Pelophylax) are an endemic species of Messinian origin. *Zoosyst Evol* 88: 261-283.

Rajarapu, G. (2014) Horizontal gene transfer. *Phylogenetics and Evolutionary Biology* 2(2):1-3.

Ramos, O.M., Ferrier, D.E.K. (2012) Mechanisms of gene duplication and translocation and progress towards understanding their relative contributions to animal genome evolution. *International Journal of Evolutionary Biology* 1-10, doi:10.1155/2012/846421.

Rebollo, R., Romanish, M.T., Mager, D.L. (2012) Transposable elements: an abundant and natural source of regulatory sequences for host genes. *Annu Rev Genet* 46: 21-42.

Roman, Y., et al., (2007) Biochemical characterization of a SET and transposase fusion protein. Metnase: its DNA binding and DNA cleavage activity. *Biochemistry* 46: 11369-11376.

Roy-Engel, A.M., et al. (2005) Human retroelements may introduce intragenic polyadenylation signals. *Cytogenet Genome Res* 110: 365-371.

Schaack, S., Gilbert, C., Feschotte, C. (2010) Promiscuous DNA: horizontal transfer of transposable elements and why it matters for eukaryotic evolution. *Trends Ecol Evol* 25: 537-546.

Schönknect, G., Weber, A.P.M., Lercher, M.J. (2013) Horizontal gene acquisitions by eukaryotes as drivers of adaptive evolution. *Bioessays* 36: 9-20.

Sela, N., Mersch, B., Hotz-Wagenblatt, A., Ast, G. (2010) Characteristics of transposable elements exonizationnwithin human and mouse. *PLoS One* 5: e10907.

Smalheiser, N.R., Torvik, V.I. (2005) Mammalian microRNAs derived from genomic repeats. *Trends Genet* 21: 322-326.

Storz, J.F., Opazo, J.O., Hoffman, F.G. (2013) Gene duplication, gene duplication, and the functional diversification of vertebrate globins. *Mol Phylogenet Evol* 66(2): 469-478.

Sun, C., et al., (2011) LTR retrotransposons contribute to genomic gigantism in plethodontid salamanders. *Genome Biol Evol* 4: 168-183.

Syvanen, M. (2012) Evolutionary implications of horizontal gene transfer. *Ann Rev Genet* 46: 341-358.

Tang, H. (2007) Genome assembly, rearrangement, and repeats. *Chem Rev* 107: 3391-3406.

Teng, L., Firpi, H.A., Tan, K. (2011) Enhancers in embriyonic stem cells are enriched for transposable elements and genetic variations associated with cancers. *Nucleic Acids Res* 39: 7371-7379.

Van de Lagemaat, L.N., Landry, J.-R., Mager, D.L., Medstrand, P. (2003) Transposable elements in mammals promote regulatory variation and diversification of genes with specialized functions. *Trends Genet TIG* 19:530-536.

Vibranovski, M.D., Sakabe, N.J., de Oliveira, R.S., de Souza, S.J. (2005) Signs of ancient and modern exon-shuffling are correlated to the distribution of ancient and modern domains along proteins. *J Mol Evol* 61: 341-350.

Vibranovski, M.D., Sakabe, N.J., de Souza, S.J. (2006) A possible role of exon-shuffling in the evolution of signal peptides of human proteins. *FEBS Letters* 580: 1621-1624.

Whitaker, J.W., McConkey, G.A., Westhead, D.R. (2009) Prediction of horizontal gene transfers in eukaryotes: approaches and challenges. *Biochemical Soc T* 37: 792-795.

Yang, Z. (2006) Computational molecular evolution. Oxford University Press.

Zhang, J.Z. (2003) Evolution by gene duplication: an updatae. *Trends Ecol Evol* 18: 292-298.

Zhu, B., Lou, M-M., Xie, G-L., Zhang, G-Q. et al., (2011) Horizontal gene transfer in silkworm Bombyx mori. *BMC Genomics* 12: 248.

CHAPTER 2

MANUSCRIPT 1: MOLECULAR EVOLUTION AND CHARACTERIZATION OF THE SERUM ALBUMIN GENE OF THE POOL FROG, *PELOPHYLAX LESSONAE*

Çiğdem Akın Pekşen, Jose Grau, Albert J. Poustka, Thomas Uzzell, C. Can Bilgin, Jörg Plötner

2.1. Introduction

Serum albumin (SA) is a globular monomeric protein containing only one polypeptide chain of 605-610 amino acid residues. As the most abundant component of the plasma protein system SA is essential for maintaining the colloid osmotic (oncotic) pressure, allowing a proper distribution of body fluids between intravascular compartments and body tissues. It also serves as a transport protein for numerous endogenous and exogenous compounds, for example hormones, metals, fatty acids, and diverse metabolites (reviewed by Rothschild et al 1988; Fanali et al., 2012). In mammals and other vertebrates SA is synthesized in the liver (Peters and Anfinsen 1950, Miller et al. 1951, 1954); in frogs albumin is also expressed in skin (Zhang et al. 2005).

SA is encoded by a single gene except for the tetraploid frog species *Xenopus laevis* which possesses, as a result of genome duplication, two SA genes and the dodecaploid *X. ruwenzoriensis* which even has three albumin encoding genes (Westley et al. 1981). All vertebrate SA genes so far analysed were composed of 15 exons and 14 intervening sequences (Sargent et al. 1981, Minghetti et al. 1986).

We here reported the complete SA gene sequence of the pool frog species *Pelophylax lessonae*. Based on comparisons with homologous sequences of other frog species, putative regulatory elements and functional motifs have been identified. Moreover, we compared exon and intron lengths of the water frog with other vertebrate species to get insight about molecular evolution of the albumin gene. We also described retroelements inserted in the entire scaffold of *P. lessonae.* As a highly polymorphic protein SA was often used as a genetic marker for systematic, phylogenetic, and population genetic studies in WPWFs (e.g. Tunner 1979, Uzzell and Hotz 1979, Uzzell 1979). Based on exon sequences we re-analyzed the phylogenetic relationships of selected species and compared our results with those obtained from studies on other mitochondrial and nuclear DNA markers (Plötner, 1998; Plötner & Ohst, 2001; Plötner, 2005; Plötner et al., 2007; 2009; 2010; 2012; Akın et al., 2010b).

2.2. Material and Methods

2.2.1. Sources of Albumin Sequences

The SA genes of the *Silurana tropicalis* (release v7.1) and *Xenopus laevis* genomes (release v7.2) were downloaded from Xenbase.org (Bowes et al., 2008). Albumin data of *Gallus gallus* (NC_006091, Hillier et al., 2004), *Rattus norvegicus* (NC_005113, Gibbs et al., 2004*), M. musculus* (NC_000071, Church et al., 2009) and *Homo sapiens* (NC_000004, Hillier et al., 2005) were obtained from GenBank. The *P. lessonae* SA gene was obtained from a genome assembly with an N50 of 21kb constructed from several next generation sequence libraries of different lengths using SOAPdenovo genome assembler (Poustka, Grau and Plötner, unpublished). The SA gene was identified with BlAST searches using default parameters and the *Silurana* sequence as a query; it was included in a scaffold of ca. 64kb.

2.2.2. Alignment and Motif Searches

The alignment of the serum albumin exon sequences of *P. lessonae* with the coding sequence of *P. shqipericus*, the alignment of the 5' and 3' regions of the *P. lessonae* serum albumin gene with those of other amphibian species, and alignments of exonic and intronic sequences of the *P. lessonae* albumin gene with those of other vertebrate species were conducted in MEGA 6.06 (Tamura et al., 2013) using the ClustalW (Thompson et al., 1994) and Muscle algorithms (Edgar, 2004). Alignments were manually improved.

2.2.3. Search For Transposable Elements and Repetitive Sequences

To search for available interspersed repeats and low complexity DNA elements in the *P. lessonae* scaffold (64.077 bp), which included the complete albumin gene, the program Repeat Masker (Smit, Hubley and Green unpublished; RepeatMasker at http://repeatmasker.org) and the program TRF (http://tandem.bu.edu/trf/trf.html) (Benson, 1999) were used. Options used in the Repeat Masker were search include search engine=cross match; speed/sensitivity=slow; DNA source=vertebrate.

As a result of Repeatmasker searches, truncated transposable elements (TEs) were found in the *P. lessonae* scaffold which matched with complete TEs of vertebrate genomes stored in the Repbase repeat database (Jurka et al., 2005). These reference sequences were used as queries in BLAST searches against the *P. lessonae* genome to find copies of these elements specific to *P. lessonae*, termed as PL elements.

Because most of the PL elements are truncated, consensus sequences were reconstructed by aligning several hundred of these copies in the *P. lessonae* genome. Alignments of several copies of the complete elements were performed in MEGA 6.06 (Tamura et al., 2013) using ClustalW algorithm (Thompson et al., 1994) and Muscle algorithm (Edgar, 2004).

Each consensus element was screened for target site duplications, repeats, and transposase domains. Inverted terminal repeats of the derived consensus elements were found using the EMBOSS explorer einverted repeat (http://emboss.bioinformatics.nl/cgi-bin/emboss/einverted). ORF Finder (http://www.ncbi.nlm.nih.gov/gorf/gorf.html) was used to identify putative open reading frames from deduced nucleotide sequences and the types of proteins encoded by autonomous elements. Derived consensus elements and their translated proteins were blasted against nucleotide sequence and protein databases such as NCBI (http://www.ncbi.nlm.nih.gov/), UCSC genome browser (http://genome.ucsc.edu/), and EMBL (http://www.embl.de/) to identify and annotate element specific genes.

2.2.4. Phylogenetic Analyses Based on Protein Coding Exon Sequences

To reveal phylogenetic relationships among western Palearctic water frogs on the basis of albumin gene, nucleotide sequences of protein coding exons (up to the first stop codon) were used. Sequences of *Rana chensinensis, Rana kukunoris, X. laevis,* and *S. tropicalis* were included for outgroup comparisons. Sequence alignment based on the amino acid sequences was performed with MAFFT (http://mafft.cbrc.jp/alignment/server/) using the L-INS-i algorithm (Katoh et al., 2005).

In order to test whether positive selection is operating on the gene, a codon-based z-test was performed for all sequences (scope=overall average) on the basis of the modified Nei-Gojobori method (Nei and Kumar, 2000) as implicated in MEGA6.0 under the alternative hypothesis $d_N > d_S$ (positive selection) where d_N

is the number of non-synonymous substitutions per non-synonymous site and d_S is the number of synonymous substitutions per synonymous site (d_S), and the null hypothesis ($d_N = d_S$) where sequence evolution of protein coding exons is follow a neutral model of sequence evolution.

Genealogical relationships of SA sequences were reconstructed with maximum likelihood (ML) as implemented in MEGA 6.06 (Tamura et al., 2013) using the option 'partial deletion' for gaps/missing data treatment and 'Nearest-Neighbor-Interchange' as the heuristic search method. Nodal support was evaluated by bootstrapping (Felsenstein, 1985) with 1,000 replicates. The model that best describe the patterns of sequences of sequence evolution was selected on the basis of the Bayesian Information Criterion (BIC, Schwarz, 1978) and ML as implemented in MEGA. As a result the General Time Reversible (GTR) model (Tavare, 1986) with gamma-shaped rate variation (G=2.58) was chosen. (BIC=12505.7). Genetic distances were calculated on the basis of uncorrected p distance and the number of nucleotide and aa differences among distinct water frog species.

2.3. Results and Discussion

2.3.1. Structure of the Albumin Gene

The SA gene of the pool frog covers 32,460 bp starting from the putative cap site to the first poly(A) addition site. It consists of 15 exons, interrupted by 14 introns as in mammals and other frog species (Fig. 2.1, Appendices 2.1 and 2.2) (Sargent et al., 1981a,b; Minghetti et al., 1986; Schorpp et al., 1988). As in human, pool frog' introns are located within polypeptide chain between codon 3 and 1 and between 2 and 3 alternately. It is found in all three domains of SA protein, which supports the idea that albumin gene arose from a single primordial domain as a result of triplication (Sargent et al., 1981). In contrast to the SA gene lengths of

Xenopus laevis (11868 bp) and *Silurana. tropicalis* (12465 bp), the SA gene of pool frogs is significantly longer caused by much longer intronic sequences (Appendix 2.1) which are inserted by many retroelements (REs) (Table 2.1).

Figure 2.1. Schematic structure of pool frog'serum albumin gene from the Cap site of the first exon to the first polyadenylation site of the last exon. Translated exons are red marked; the partially translated exon 1 and exon 14 and the completely untranslated exon15 are yellow coloured. Introns are indicated by dark grey boxes.

2.3.1.1. The 5' Region of the Water Frog Albumin Gene

In their 5' region of the SA gene, from the cap site at position +1 to position -330, water frogs revealed considerable homology to *Rana chensinensis*, *R. kukunoris*, *X. laevis* and *S. tropicalis* (Fig. 2.2). Several conserved motifs are seen which may play functional roles for gene regulation in frogs and other vertebrates. The consensus sequence of the initiator element (Inr) (PyPyA$_{+1}$NT/APyPy) of the water frog SA gene is identical to that of mammals (Bucher, 1990). The TATA box (TATAAATGT) located from -32 to -24 (Goldberg, 1979) is conserved in all six species. Only two base subtitutions are seen in *X. laevis* and *S. tropicalis.* A 13 bp hepatocyte-specific promoter element (HP1), with a consensus sequence GNTANTNNTNNNC (Schorpp, et al., 1988b), is located at positions -65 to -53. Except for three base changes in two positions, this element is extremely conserved, not only in the SA gene of the amphibians used in this study, but also in the promoters of the albumin and alpha-fetoprotein genes of chicken and mammals; this indicates an important function for hepatocyte specific expression for these genes and as a regulatory element during vertebrate evolution (Kugler et al., 1988; Schorpp, et al., 1988). Presence of a TATA box within a distance of 70 bp is required for the function of the HP element (Ryffel et al., 1989). A putative CAT box sequence, CCAAT was found at position -178; it is conserved among *S. tropicalis, X. laevis, P. ridibundus* and *P. lessonae.* The presence of a CAT box in the SA gene coincides with findings of Mantovani' (1998) who surveyed 96 unrelated SA promoters, including that of the *X. laevis*, but contradicts the statement of Schorpp et al. (1988a) who postulated the absence of a CAT box in the 68 kd and 74 kd albumin genes of *X. laevis*. Downstream from the CAT box, two conserved motifs were found. The first 10 bp motif with the consensus sequence AATYACCMAA, named amphibian downstream element I (ADE I), is located between positions -255 and -264. The second element (ADE II) is 37 bp long, located between positions -282 and -318, is highly conserved (81%) among *X. laevis, S. tropicalis, P. ridibundus,* and *P. lessonae*. It is partially overlapped by downstream element III (DE III) found in promoters of the albumin genes of rat, human, and mouse (Cereghini et al., 1987;1988), with which exhibits 59% of homology. Similar to amphibians, several regulatory elements were identified within a 150 bp region of human, rat and mouse SA promoters, including a TATA box, a so called proximal element (PE), a CAT box, DE I, II and III. These elements are thought to be involved in tissue-specific expression of the albumin gene (Cereghini et al., 1987). The specific functions of these elements, however, are not yet clear and have to be analysed experimentally.

```
                -340                  -318                                -281            -264     -255
                                                         ADE II                                ADE I
P.lessonae       TTTCAGACGCAGACTGGGATACTGTCATAATCAAGGATCACTTTGCTTAACCTTTTGTTCGTAGTTTCACAGCCTAATCACCAAACGCTTACATTAGTA
P.ridibundus     TTTCAGACGCAGACTGGGATACTGTCATAATCAAGGATCACTTTGCTTAACCTTTTGTTCGTAGTTTCACAGCCTAATCACCAAACGCTTACATTAGTA
R.chensinensis   ---------------------------------------------------------------------------------------------------
R.kukunoris      ---------------------------------------------------------------------------------------------------
X.laevis         ATTTGGGCACATACCAATACACTAGTATACACAAAGATCAGTTTGCTTAACCTTTTGTTC----------AGC--AATTACCAAAGACGTTGACTAGCC
S.tropicalis     TTTGGGGCACAGACCAGTACA-TAGTATACACAAAGATCAGTTTGCTTAACCTTTTGTTC--AGT----------AATTACCCAAGACTTTGCCTTGCC

               -241                                                           -178                              -143
                                                                              CAT BOX
P.lessonae       AAATTATAACTGATCTACAAGGTCTTT-----CAA---AAAATGTGTTG--------------CCAATCCAAGCCCACTTTACAACTGATTCAGTATTG
P.ridibundus     AAATTATAACTGATCTACAAGGTCTTT-----CAA---AAAATGTGTTG--------------CCAATCCAAGCCCACTTTACAACTGATTCAGTATTG
R.chensinensis   -------------------------------------------------------------------------------------------CAGTATTG
R.kukunoris      -------------------------------------------------------------------TGCAAGCCCACTTAACAATTGATTCAGTATTG
X.laevis         CA--------TGCT-----AGGTTTTTTTTCACAATTTAAAAGGTTTTTCAAAATTCAGAAAACCAATATA-GAGCAACAG-CAATACGTT----ATT-
S.tropicalis     CA--------TGAT-----AGTTTTTTTCCTTTAATTTACAAGGTCTTTCAAAGAGCAGCA-TCCAATATA-CAGCAACAG-CAATACATT----ATT-
```

Figure 2.2. 5' regions of the serum albumin gene P. *lessonae, P. ridibundus*, *P. chensinensis*, *P. kukunoris*, *X. laevis*, and *S. tropicalis*, starting with the translation initiation codon (Met) up to position -340, the start site transcription (+1). Dashes indicate gaps introduced to optimize in the alignment. Conserved regulatory motifs are red colour and underlined.

-65 -53

HP ELEMENT

P.lessonae TGTTTTGTCATTCTTTGT-G-TT---TCTAGAAA-CGAGCCAAA----TTGTAATTAATTATAAAGCCA---GTCTG**GTTAATCATTT-C**CAAATAGGA
P.ridibundus TGTTTTGTCATTC-TTGT-G-TT---TCTGGAAA-CGAGCCAAA----TTGTAATTAATTATAAAGCCA---GTCTG**GTTAATTATTT-C**CAAATAGGA
R.chensinensis TGTTTTGCCATTCTTTGT-G-TT---TCTAGAGA-CGAGCCAAAA--TTTGTA-TTAATTATAAAGCCA---GTCTG**GTTAATTATTT-C**TGAATAGGA
R.kukunoris TGTTTTGGCATTCTTTGT-G-TT---TTTAGAGA-CGAGCCAAAA--TTTGTA-TTAATTATAAAGCCA---GTCTG**GTTAATTATTT-C**TGAATAGGA
X.laevis TGACCTTAAAAGTT-----GATTGACATTAGGAAATTCCACAAAGCTAAAACAACTGCAAACAGAACAATTTGATAG**GTTAATAATTTTC**CAGATCTCT
S.tropicalis TGACT----- ----------------TTAGGAAACTCCACAAAGCTTAAAAAACTGCAA-CAGAACAATTTGATAG**GTTAATAATTTTC**CAGATCTCT

-32 +1 Met

TATA BOX CAP SITE

P.lessonae TGCAAAAATGG**TATAAATGT**CTGCCTTTCCCTTAGCTGAT-**TTAGGCT**TCTAAGAGAACCTC-CAAAAAACATTTGCCACC**ATG**
P.ridibundus TGCAAAAATGG**TATAAATGT**CTGCCTTTCCCTTAGCTGAT-**TTAGGCT**TCTAAGAGAACCTC-CAAAAAACATTTGCCACC**ATG**
R.chensinensis TGCAAAAATTG**TATAAATGT**CTGCCTTTCCTTTAGCTGAT-**TTAGGCT**TCCAAGAGATCCTC-CTAAAAACATTTGCAACC**ATG**
R.kukunoris TGCAAAAATTG**TATAAATGT**CTGCCTTTCCTTTAGCTGAT-**TTAGGCT**TCCAAGAGATCCTC-CTAAAAACATTTGCAACC**ATG**
X.laevis CTGAGCAATAG**TATAAAACA**AGAGGTATCACTCATTTCAGA**TCAGGCT**TCTCAGAGGTCCCCACCCAATACATCTCCAGTC**ATG**
S.tropicalis CTTAGGAATAG**TATAAAGCA**AGAGGTATCACTCATTTCAGA**TCAGGCT**TCTATGAGGTCCCCACCCAATACACCTCCAGTC**ATG**

Figure 2.2. (continued).

2.3.1.2. The 3' Region of the Water Frog Albumin Gene

The 3' UTR region extends from the stop codon following exon 14 to the end of exon 15. It contains several conserved cis-regulatory elements (Fig. 2.3); 5' to 3', these are poly(A)-limiting elements a and b (PLEa, PLEb), U-rich upstream element 1 (USE1), poly(A) signal (PAS), U-rich upstream element 2 (USE2), polyadenylation site (PAS), and GU-rich downstream element (GU-rich DSE). PAS is the essential motif for 3' terminal cleavage and efficient polyadenylation, AAUAAA (Conway and Wickens, 1985). It is completely conserved among these species except that its position in *R. chensinensis* and *R.kukunoris* is shifted nine bases downstream; (the positions of these PAS were obtained from UTRscan (UTRdb and UTRsite, 2010). USE1 and USE2 are conserved U-rich upstream elements. They were found within 20 nt of both the 5' and 3' ends of PAS in all of these species. In *P. lessonae* conserved GU-rich downstream element (GU-rich DSE) was identified just of the poly(A) site (0). Although PAS is certainly needed for mRNA 3' end polyadenylation, the presence of these conserved USEs in all of these species (and of GU-rich DSE in *P. lessonae*) support their functional roles in efficient cleavage and polyadenylation. PAS and GU-rich DSE are known binding sites for cleavage and polyadenylation specificity factor (CPSF) and cleavage stimulatory factor (CstF), promoting enzymatic reactions of the 3'end processing (MacDonald et al., 1994; Murthy and Manley, 1995). Similarly, USE1, core upstream element (Hu et al., 2005) is a target site for specific protein complex that enhances element 3' end formation (Danckwardt et al., 2007). Graber et al. (1999) suggested that all yeast and plant 3'UTR have USE2 between the PAS and poly(A) site, indicating that it is evolutionary conserved element (Hu et al., 2005). Most of eukaryotes have this conserved pattern of USE1-PAS-DSE in their 3' UTR (Proudfoot, 2011). poly(A)-limiting elements (PLE_A and PLE_B) are two cis-acting elements, firstly identified in *X. laevis* albumin pre-mRNA have also been found ($PLE_{A,}$ between -176 and -159; and $PLE_{B,}$ between -131 and -108). These elements in the last exon are independently involved in regulating of the length poly(A) tail on albumin pre-mRNA, and may cause its short (17-residue). Such nuclear control of poly(A)-tail length is common among vertebrates (Gupta et al., 1998; Gu et al., 1999). In the alignment, they showed nearly 70% homology with the elements found in *X. laevis*. Finally, in *S. tropicalis* iron responsive element (IRE) was found between -146 and -10 as a result of UTRscan (UTRdb and UTRsite, 2010). IRE are perhaps involved in mRNA stability: a low iron concentration may enhance the binding affinity of the IRE binding protein to the IREs, which may in turn inhibit attack by the nuclease on the cleavage site; when iron concentration increases, the IRE-binding protein is released and nucleolytic cleavage takes place (Binder et al., 1994). Functional roles of PLE_A and PLE_B in the poly(A) length control, in *P. lessonae, P. ridibundus* and in other species and IRE in albumin pre-mRNA in *S. tropicalis* should be also tested experimentally.

```
              Stop Codon                             PLE_A                                          PLE_B
                                             -176            -159                        -131                  -108
P.lessonae       UGA-----CAU-GGA--ACAGGCCA-----AAAGCUGAUAGAACAAGA-----CUGUGUUGAGCCACUAGGUU--AAACCAUCAUCAACUGGUCACUGA
P.ridibundus     UAA-----CAU-GGA--ACAGGCCA-----AAAGCUGAUAGAACAAGA-----CUGUGUUGAGCCACUGGGUU--AAACCAUCAUCAACUGGUCACUGA
R.catesbeiana    UAA-----CAU-GGA--ACAGGCCA-----CAAGCUAAUAUAACAAGA-----CAGCCUUGAGCCACUAGGUU--AAAUCAUCAUCAACUGGUCACUGA
R.chensinensis   UGA-----CAU-GGA--ACAGGCCA-----CAAGCUGAUAGAACAAGA-----CAGCCAUGAGCCACUAGGUU--AAAUCAUCAUUAACUGGUCAUUAA
R.kukunoris      UGA-----CAU-GGA--ACAGGCCA-----CAAGCUGAUAGAACAAGA-----CAGCCAUGAGCCACUAGGUU--AAAUCAUCAUUAACUGGUCAUUAA
X.laevis         UAAGAGUCCAUAAGAGCAAAGACCAGCCUUCAAACUCACUGAGGAACACCUUCCAUCUCUCAAACACAAGAAAAAAAAGUUCCUUCAGCUGAAAA--GA
S.tropicalis     UAA----------GAGCAAAGGCCAGCCUUCAAACUGACCAAGGAAGAUCUUCCAUCUCUCAAACAC-AG-AAAAAAGUUUUCUUCAGCUGAAAAU-GA

                                                                         USE1         PAS            USE2
                -107                                                 -52    -46    -38   -33      -23   -18
P.lessonae       -UACAUGU-------------CUCUGAAGACUCAAGUAGAAAAAAACAAUCA---UUUUACUGCAAA--AAUAAA--AAAUAAAUUCUUU-------AU
P.ridibundus     -UACAUGU-------------CUCUGAAGACUCAAGUAGAAAAAAACAAUCA---UUUUACUGCAAA--AAUAAA--AAAUAAAUUCUUU-------AU
R.catesbeiana    AUACAUGUUGCUGAUACAUGUCUCUGAAGACUCAAGUAGAAAAAAACUACCAUCGUUUUACUGCAAAAUAAUAAA-AAAAUAAAUUCUUU-------AU
R.chensinensis   AUACAUGUUGCUGAUACAUGUCUCUGAAGACUCAAGUAGAAAAAAACUACCAUCGUUUUACUGCAAAAUAAUAAGAAAAAUAAAUUCUUC-------A-
R.kukunoris      AUACAUGUCGCUGAUACAUGUCUCUGAAGACUCAAGUAGAAAAAAACUACCAUCGUUUUACUGCAAAAUAAUAAGAAAAAUAAAUUCUUC-------A-
X.laevis         G--CAU-UUG-----------CUCAGACCAUUCAACU-----------------GUGUG-UUGC-----AAUAAA-----UAAAGCAUUUAAAAAAA-U
S.tropicalis     A--CAU-UUG-----------CUCAGAGCAUUCAUCU-----------------GUUUG-UUGC-----AAUAAA-----UAAAGCGUUUAAAAAAAAU
```

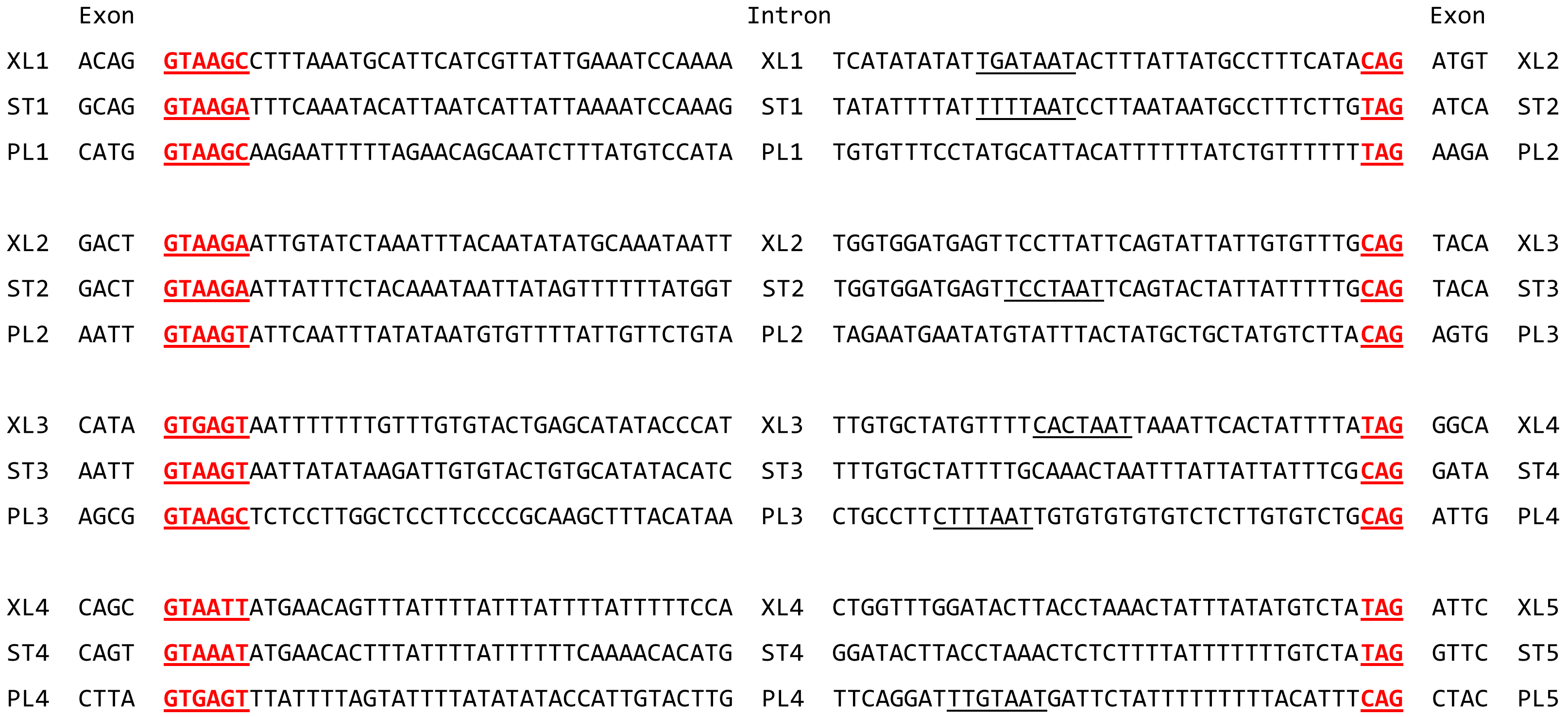
Figure 2.3. Sequence alignment of the 3' UTR of *P. lessonae*, *P. ridibundus*, *R. catesbeiana*, *R.chensinensis*, *R. kukunoris*, *X. laevis* and *S. tropicalis* albumin genes. Poly(A) site is accepted as position 0. Regulatory motifs both in the upstream and downstream of the poly(A) site are shown in underlined red colour.

```
                      Poly(A)
                       Site  DSE (GU rich)
                       -1+1          +14
P.lessonae       GA-C-UGGAUGUUCUUGGUGUCUGUUUUUAUG
P.ridibundus     GA-C-UGG------------------------
R.catesbeiana    GA-C-CAG------------------------
R.chensinensis   GAAC-UGG------------------------
R.kukunoris      GAAC-UGG------------------------
X.laevis         ATATAGAG------------------------
S.tropicalis     AUAUAGC-------------------------
```

Figure 2.3. (continued).

2.3.1.3. 5' and 3' Splice Junctions of the Water Frog's Albumin Gene

To identify consensus sequences at 5' and 3' splice junctions, all fourteen splice sites were aligned among *P. lessonae, S. tropicalis* and *X. laevis.* The consensus sequence of the first six nucleotide at 5' splice site is GTAAGT as indicated by Mount (1982). Upstream of the 3' splice site, the branch point sequence, the pyrimidine rich tract, and at the intron-exon junction C/T,AG are found and their consensus sequences are concordant with Mount (1982)'s findings. A putative branch point consensus sequences (T/CNT/CTA/GAT/C) including the reactive adenosine involve in the lariat formation during pre-mRNA splicing (Ruskin et al., 1984; Reed and Maniatis, 1985) is found in different positions in all species (Fig 2.4).



```
     Exon                                                         Intron                                                    Exon
XL1  ACAG  GTAAGCCTTTAAATGCATTCATCGTTATTGAAATCCAAAA  XL1  TCATATATATTGATAATACTTTATTATGCCTTTCATACAG  ATGT  XL2
ST1  GCAG  GTAAGATTTCAAATACATTAATCATTATTAAAATCCAAAG  ST1  TATATTTTATTTTTAATCCTTAATAATGCCTTTCTTGTAG  ATCA  ST2
PL1  CATG  GTAAGCAAGAATTTTTAGAACAGCAATCTTTATGTCCATA  PL1  TGTGTTTCCTATGCATTACATTTTTTATCTGTTTTTTTAG  AAGA  PL2

XL2  GACT  GTAAGAATTGTATCTAAATTTACAATATATGCAAATAATT  XL2  TGGTGGATGAGTTCCTTATTCAGTATTATTGTGTTTGCAG  TACA  XL3
ST2  GACT  GTAAGAATTATTTCTACAAATAATTATAGTTTTTTATGGT  ST2  TGGTGGATGAGTTCCTAATTCAGTACTATTATTTTTGCAG  TACA  ST3
PL2  AATT  GTAAGTATTCAATTTATATAATGTGTTTTATTGTTCTGTA  PL2  TAGAATGAATATGTATTTACTATGCTGCTATGTCTTACAG  AGTG  PL3

XL3  CATA  GTGAGTAATTTTTTTGTTTGTGTACTGAGCATATACCCAT  XL3  TTGTGCTATGTTTTCACTAATTAAATTCACTATTTTATAG  GGCA  XL4
ST3  AATT  GTAAGTAATTATATAAGATTGTGTACTGTGCATATACATC  ST3  TTTGTGCTATTTTGCAAACTAATTTATTATTATTTCGCAG  GATA  ST4
PL3  AGCG  GTAAGCTCTCCTTGGCTCCTTCCCCGCAAGCTTTACATAA  PL3  CTGCCTTCTTTAATTGTGTGTGTGTCTCTTGTGTCTGCAG  ATTG  PL4

XL4  CAGC  GTAATTATGAACAGTTTATTTTATTTATTTTATTTTTCCA  XL4  CTGGTTTGGATACTTACCTAAACTATTTATATGTCTATAG  ATTC  XL5
ST4  CAGT  GTAAATATGAACACTTTATTTTATTTTTTCAAAACACATG  ST4  GGATACTTACCTAAACTCTCTTTTATTTTTTTGTCTATAG  GTTC  ST5
PL4  CTTA  GTGAGTTTATTTTAGTATTTTATATATACCATTGTACTTG  PL4  TTCAGGATTTGTAATGATTCTATTTTTTTTTACATTTCAG  CTAC  PL5
```

Figure 2.4. Comparison of 5' and 3' splice positions among *P. lessonae*, *S. tropicalis* and *X. laevis*. Numbers of exons and introns are given next to species (XL, ST, and PL). Conserved elements at 5' and 3' splice sites are shown as underlined and red colour, and putative branch point positions are underlined.

	Exon		Intron			Exon	
XL5	AAAG	**GTATAG**TGTGCAGAAAAAGTAGTTTACCTATTCCATTTTA	XL5	GTCTTACTATGATGCCTTTTTTTTTAAATTTCCTTTA**TAG**	ATGA	XL6
ST5	AAAG	**GTATAG**TGTTCAGAAATCCAGTAATTTCACATTTCCCAGT	ST5	ATTTCTAATCATGTTGTTAATTTTTTTATTAACCTTA**TAG**	ATTA	ST6
PL5	ACGG	**GTATGC**CATTAAACTTCTTGAAATTAAACAATGTTATTGC	PL5	TTTTTTTTTTTTATGTTTGAAACAATACTTTCTTTTG**CAG**	ATGC	PL6
XL6	CACT	**GTAAGT**GGTTCTCTATACTGATGTGATTTGTAGCATGAAA	XL6	GTGTGTCTCTGCTCTTTTCTTTCAATATATCGTATTT**CAG**	AAAT	XL7
ST6	CAAT	**GTAAGT**TGCTATCTATACTGTCTAAAATGTGTACATTTGT	ST6	GTATGTATCTGTTTCTTAATTTCTATATATTGTATTC**CAG**	AAAT	ST7
PL6	CACT	**GTAAGT**ATCTATTCCCAATCCAGGAAATATATGTAGGGGA	PL6	TTTTTTTCGATGCGGTAACTGCTTCTTTCTCATTTAT**CAG**	AACA	PL7
XL7	GAGG	**GTAAGC**AATTCTGGACAATAACAACCTGATAGAACACATC	XL7	TGATTTTTTTTTTCTGTGAAACTTTCTCTCACTCTGA**TAG**	CTGG	XL8
ST7	GAGG	**GTAAGC**AATTTTGATTAAGAGACCTGATGTATCACACCAG	ST7	GGTTGAACAACCCCTTTAATAATCTTTTCCATTCTGA**TAG**	ATGG	ST8
PL7	AAGG	**GTAAGC**CTGTGCACCAAACATTTTAATATCTCCTTCATCA	PL7	TACGATGTTATCATGCATATGTATTTTATATCTTTGA**CAG**	ATGG	PL8
XL8	GAAG	**GTAAAA**ATATGTTTTACATGTATTACACATTATCATATAT	XL8	TAATTTAATGCATGTAATTAATTATGCATGTGTTTTA**TAG**	ATAC	XL9
ST8	GCAG	**GTAAAG**ATAATACGTTATATATGTGTTACACATTGTAATA	ST8	AGTTACATTATTATTATGAATTGTGCCTGTTTTTTTA**TAG**	ATAT	ST9
PL8	CCCA	**GTAAGT**ATACCTTTTAATGTTTATACAATTGCCATCAAGT	PL8	TTATGTCACTTTAAACAGTCATTTGCATTTGTTTCTC**CAG**	CTTT	PL9
XL9	TGGA	**GTATGT**TTATTTTACACTTTAAAGCCCTGTATGTACTTAA	XL9	GGAATTCTTGATTTACATCTATTAACTCCTGTCATAT**TAG**	CCTG	XL10
ST9	TGCA	**GTAGGT**TTTTTTTTTAACTCTTTAAAACCAAGTGTGTACT	ST9	GGCCTCATTACTAATTAGAATTCTTATCCTTTTTTAT**TAG**	GCTA	ST10
PL9	TGCC	**GTATGT**ATATGAATGTTACTGTTACAGTCCAAATAGTAAA	PL9	TTTTTTTTCATTTAAAGTATTTATTTTATTTTCATTT**CAG**	CCTA	PL10

Figure 2.4. (continued).

	Exon	Intron			Exon	
XL10	ATGA	**GTAAGT**TTTACAGATACTGATAAACAGTTGGACAGTTGGA	XL10	TACATTTACTACATAAACATTAAGTATTTTTTGGTTT**CAG**	CGCT	XL11
ST10	ATGA	**GTAAGT**TTCACAGATATAGATATCCTATTTCTTTGTTTAT	ST10	TAGTAAATCTGCCCCTAAGTTTTTTCTTCTTTTGTTT**TAG**	GCTG	ST11
PL10	TTCA	**GTAAGT**TAAGCGTGTAGCATTTACAATTTTGAACATTTTA	PL10	CATTAACACTTTGCTAAGAACCGGTTTTCCTTTTTTC**CAG**	GCTG	PL11
XL11	AGAC	**GTATGT**ATATATTGTTTATGTTTTGCTTAGATTACTGCAT	XL11	GTGTTTATATTGAAGTTATATTTTTTTCTTCCTTTTA**AAG**	CTCA	XL12
ST11	AGAC	**GTATGT**ATATATTGTTTGTTATGTTTTGCTTGGGTTTATG	ST11	TTGTTGATATTGATGTCCTGTTTTTCACTTCCCTTTA**AAG**	CTTA	ST12
PL11	AAAG	**GTAAGC**TCTTCTTGTTTTCTATCCTTTCAATAGATTTTTA	PL11	CACTAAACCTCTCAATGTTTTCTAATATTTTACATCA**CAG**	CTGG	PL12
XL12	AGAA	**GTAAAT**ATCTATAATTTCCCATTTTTTGTCATTATTTTTT	XL12	ATAATTATTTTCATATATATTTTTTTATTATTTGTTTA**CAG**	ATTC	XL13
ST12	AGAC	**GTAAAT**ATTTTTGCCATTATTGTTTGATGTAATTCTTTGA	ST12	TGAAATAACTTAATATATATGTATTTTTCTTTGGTTA**TAG**	ATTC	ST13
PL12	TGGT	**GTAAGT**TTTGGAAAAACAGCCATGAGAGGCTTTAAAGATT	PL12	TTTCTTAACATTGTTTAAAATTATATAATTTTCTTTA**CAG**	GTTG	PL13
XL13	AGAG	**GTATGG**CAACACTCTTGTGTTTTTTGTATTATGAAAACAA	XL13	TTTATGTCTAATCTCATGTTTTATCTTATTTATCCCA**CAG**	AAAC	XL14
ST13	AGAG	**GTATGG**CAACACTCTTGTCCTTTTTGTATCATGAAAACAA	ST13	CCTACTTACTGTCTTACTTCTTATCTTATTTACCTTG**CAG**	AAAA	ST14
PL13	GAAG	**GTATGT**AATGTGACTGCTGTGCAATGTGTATAATGCCAAC	PL13	TTTAATAATAAATGAATTCTGTTATTTGTGTATATTT**TAG**	AAAG	PL14
XL14	**CCAG**	**GTAAGA**TTAGATGCCTAAAATCTACAACTTTATGCAAGTG	XL14	ACATTTGTCTTAGTTTAACACATTCTCTTTTGTTTTG**CAG**	CCTT	XL15
ST14	CCAG	**GTAAGG**TCAAATGCCTTAAACAGATGTGTACAACATTGTA	ST14	TGCAACAACTTCTAAATTCACAATTTCTTTTGTTGTG**CAG**	CCTT	ST15
PL14	ACAG	**GTAAGT**CTTGCAGTGTGCATGAATGGTATATGTATTTGTA	PL14	TTTGCAGTGTATAAACCAGAACTTTCCTTTCTTCAAA**CAG**	GCCA	PL15

Figure 2.4. (continued).

2.3.1.4. Exons and Introns of the Pool Frog's Albumin Gene

Exons of pool frog's albumin gene are very short and their lengths are nearly equal to those in *S. tropicalis*, *X. leavis*, *G. gallus*, *R. norvegicus*, *M. musculus* and human albumin genes except partially translated exon1, exon14 and untranslated exon15. Their average length in water frog' s gene is approximately 133 bp, and ranging from 46 bp to 224 bp. (Fig. 2.5; Appendix 2.1).

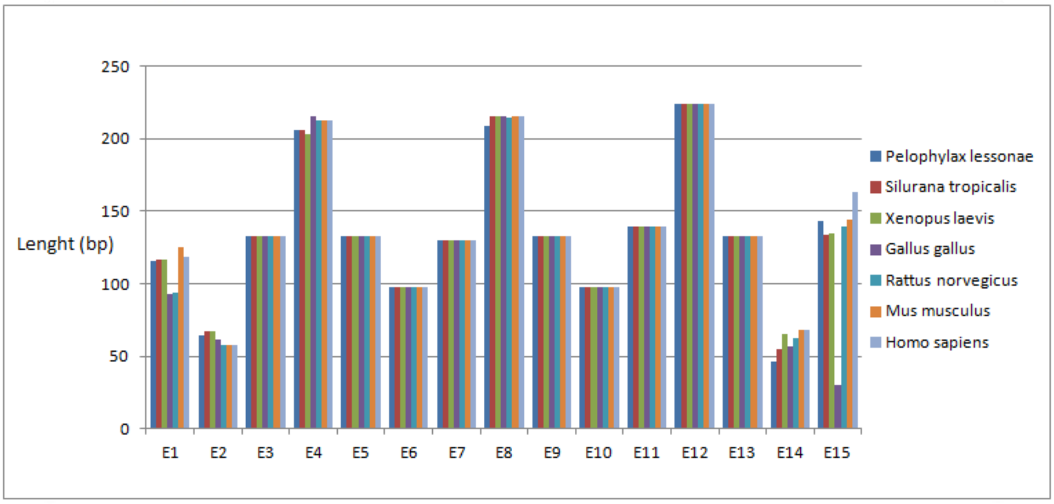


Figure 2.5. Comparison of serum albumin exon lengths among *P. lessonae, S. tropicalis, X. laevis, G. gallus, R. norvegicus, M. musculus* and human.

In contrast to this length conservation in protein coding albumin exons among distinct vertebrate species, intron lenghts are highly variable. Remarkably, in comparison with *S. tropicalis*, *X. leavis*, and other vertebrate species, introns of *P. lessonae* are extremely long. Their mean length is 2175 bp and ranging from 95 bp to 4748 bp. In contrast, the mean lengths of introns for *S. tropicalis* and *X. laevis* are 734 bp and 703 bp respectively (Fig. 2.6; Appendix 2.1). Particularly, lengths of intron 3, 4, 5, 8, 10, 11 and 13 are more than three-fold comparing with *S. tropicalis*, X. *laevis* and other vertebrate species. In this study, we documented that these introns have many truncated copies of several distinct types of DNA transposons and retrotransposons and simple repeats. Thus, these long intronic sequences of pool frog serum albumin gene indicate that the gene is potential target of several retroelement families.

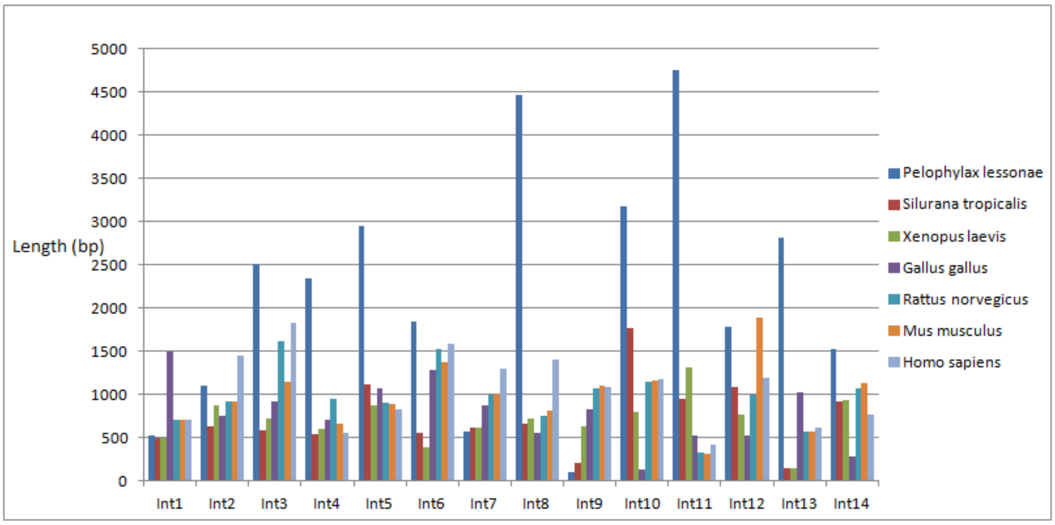


Figure 2.6. Comparison of serum albumin intron lengths among *P. lessonae, S. tropicalis, X. laevis, G. gallus, R. norvegicus, M. musculus* and human.

2.3.2. Drivers of Serum Albumin Gene Evolution

Eukaryotic genomes, which are usually larger than prokaryotic genomes, contain distinct types of repeat families. These are considered an important sources of genomic rearrangements. Repeats include interspersed repeats (transposable elements, segmental duplications, and processed pseudogenes) and tandem repeats (microsatellites and minisatellites) (Tang, 2007). Transposable elements particulary have a considerable impact on genome size, genomic variation in both non-coding and coding parts, adaptation, and shaping the eukaryotic genome. These mobile repetitive elements form two classes: i) LTR (long terminal repeat) or retrovirus and Non-LTR retroelements, both mobilized by RNA intermediates

ii) DNA transposons, mobilized by DNA intermediates. Both groups have autonomous and nonautonomous elements (Kazazian, 2004; Chenais et al., 2012; Rebollo et al., 2012).

The current study showed that repetitive elements are also important drivers of the evolution of the serum albumin gene because truncated elements of several distinct families of DNA transposons, non-LTR and LTR retroelements, and tandem repeats and simple repeats were found upstream of the 5' UTR, downstream of the 3' UTR and within individual albumin introns (Table 2.1). Truncated DNA transposons come from the Tc1Mar-Tc1, hAT-Charlie, RC/Helitron, hAT-Tip100 families, and truncated non-LTR elements are grouped within the LINE/CR1, LINE/L1-Tx1 and LINE/Penelope families. A single truncated LTR element, belonging to the Gypsy family was found. The prominent characteristics of these truncated elements and their corresponding families are explained in detail below and in Table 2.1.

Table 2.1. Classification of truncated repetetive elements obtained from Repeat Masker (RM) and TRF programs' searches and length and insertion sites of these elements within the albumin gene starting from the upstream 5' UTR to downstream of the 3' UTR according to start point (+1)

Class	Family	Element	Program	Start	Stop	Length (bp)	Insertion Site
DNA transposons	**TcMar-Tc1**	Tc1-10_Xt-1	RM	7444	7233	212	upstream of the 5'UTR
		Tc1-10_Xt-2	RM	6878	6477	402	upstream of the 5'UTR
		TC1_RT-3	RM	2851	2667	185	upstream of the 5'UTR
		TC1_PP-4	RM	2683	2549	135	upstream of the 5'UTR
		Tc1-1Ory-5	RM	2423	817	1607	upstream of the 5'UTR
		TC1_FR3-6	RM	5555	5922	368	intron 4
		TC1_FR3-7	RM	5907	6293	387	intron 4
		TC1DR1-8	RM	15364	16365	1002	intron 8
		TC1-13_Xt-9	RM	21772	21958	187	intron 11
		TC1-13_Xt-10	RM	24984	25579	596	intron 11
		TC1DR1-11	RM	47511	48454	944	downstream of the 3'UTR
	hAT-Charlie	hAT-2_TS-1	RM	2417	2497	81	intron 3
		hAT-2_ET-2	RM	17880	17965	86	intron 10
		hAT-2_ET-3	RM	18007	18167	161	intron 10
		hAT-2_TS-4	RM	18724	18821	98	intron 10
		hAT-2_OG-5	RM	18818	18892	75	intron 10
		hAT-2_TS-6	RM	18882	18988	107	intron 10
	RC/Helitron	Helitron-1_DR-1	RM	15120	15223	104	intron 8
		Helitron-1_DR-2	RM	16581	16668	88	intron 8
		Helitron-1_DR-3	RM	47172	47262	91	downstream of the 3'UTR
		Helitron-1_DR-4	RM	48617	48706	90	downstream of the 3'UTR

Table 2.1 (continued).

Class	Family	Element	Program	Start	Stop	Length (bp)	Insertion Site
DNA transposons	**hAT-Tip100**	hAT-32_CPB	RM	2710	2778	69	intron 3
		hAT-N33_CPB	RM	54341	54387	47	downstream of the 3'UTR
		hAT-N33_CPB	RM	55040	55078	39	downstream of the 3'UTR
LTR retroelements	**Gypsy**	Gypsy-24-l_XT	RM	36356	36646	291	downstream of the 3'UTR
Non-LTR retrolements	**LINE/CR1**	CR1_1a_Xt-1	RM	281	346	66	intron 1
		CR1-2_XT-2	RM	4879	5006	128	intron 4
		CR1_1a_Xt-3	RM	43276	43336	61	downstream of the 3'UTR
		CR1-2_XT-2-4	RM	43376	45276	1901	downstream of the 3'UTR
		CR1-2_XT-7	RM	45464	46171	708	downstream of the 3'UTR
	LINE/L1-Tx1	KibiDR1	RM	14122	14219	98	intron 8
	LINE/Penelope	Penelope-5_XT	RM	50802	50951	150	downstream of the 3'UTR
Others	**Simple repeat**	(GTTCTGTCACACT)n	TRF	7465	7441	25	upstream of the 5'UTR
		(AATA)n	RM	5877	5849	29	upstream of the 5'UTR
		(TATTT)n	RM	5347	5321	27	upstream of the 5'UTR
		(ATCAGTGCCCATCAGGTCAGCCTC)n	TRF	2438	2499	62	intron 3
		(ATCAT)n	RM	2499	2525	27	intron 3
		(CTCCCCCCCAGTACAGACCTCT)n	TRF	2889	2971	83	intron 3
		(T)n	RM	9214	9235	22	intron 5
		(GGGCAAGTGGGCCCCCC)n	TRF	11144	11184	41	intron 6
		(A)n	RM	12455	12475	21	intron 7

Table 2.1. (continued)

Class	Family	Element	Program	Start	Stop	Length (bp)	Insertion Site
Others	**Simple repeat**	(TATT)n	TRF	13262	13289	28	intron 8
		(AGATAA)n	RM	13446	13487	42	intron 8
		(AGTTATTTTGAGG)n	TRF	16491	16518	28	intron 8
		(TGATGGGCACTGATAGGCTGCAC)n	TRF	18722	18985	264	intron 10
		(CAAGTATAACCC)n	TRF	21657	21681	25	intron 11
		(AT)n	RM	22452	22497	46	intron 11
		(AAATAT)n	RM	23904	23937	34	intron 11
		(T)n	RM	26656	26681	26	intron 12
		(CAGTG)n	RM	27415	27440	26	intron 12
		(CATTG)n	RM	36237	36264	28	downstream of the 3'UTR
		(A)n (TRF)	TRF	39061	39089	29	downstream of the 3'UTR
		(AT)n (TRF)	TRF	40804	40907	104	downstream of the 3'UTR
		(ATATACA)n	RM	46412	46458	47	downstream of the 3'UTR
		(TATATTA)n	RM	46790	46871	82	downstream of the 3'UTR
		(CTGGTCACTCTGCATTGAAGGGGGCACG)n	TRF	49137	49226	90	downstream of the 3'UTR
	Low complexity	GA-rich	RM	17014	17076	63	intron 8
		A-rich	RM	18644	18690	47	intron 10
		A-rich	RM	32729	32770	42	downstream of the 3'UTR
		A-rich	RM	46503	46540	38	downstream of the 3'UTR
		A-rich	RM	52475	52506	32	downstream of the 3'UTR

2.3.2.1. DNA Transposons

2.3.2.1.1. Tc1Mar-Tc1 Family

This family is widespread in both plants and animals including, invertebrates and vertebrates (Plasterk et al., 1999). The length of complete Tc1-like elements (TLE) ranges between 1 and 5 kb. They have a single transposase-encoding gene (282-345 aa), are flanked by two inverted terminal repeats (ITR), variable in their lengths (Plasterk et al., 1999). Transposase proteins usually have two main domains: a DNA-binding domain in the N-terminal region and a catalytic domain in the carboxy-terminal region region; these are separated by a nuclear localization signal (NLS). The DNA binding domain contains one or two helix-turn-helix motif, which are responsible for recognition and binding of ITRs; the catalytic domain includes DDD or DDE motifs, which carry out DNA cleavege and joining reactions during transposition (Benjamin et al., 2007; Muńoz-Lopez and Garcia-Pérez, 2010). ITRs contains three functional motifs: the cleavage site, a DNA transposon binding site, and an enhancer (Benjamin et al., 2007). In the *P. lessonae* scaffold containing the albumin gene, 11 truncated Tc1-like elements (TLE) were found. As a result of search using the program Repeatmasker in the Repbase repeat database (Jurka et al., 2005), these were found to represent seven distinct intact TLE.

2.3.2.1.1.1. PL Tc1-1Ory Element

The single copy of Tc1-1Ory is the longest (1607 bp) Tc1-like element (TLE) found in the albumin gene. To obtain a consensus sequence for this elements, the reference sequence of Tc1-1Ory (Pocwierz-Kotus et al., 2007) from the Repbase database was blasted against the *P. lessonae* genome; 1366 hits were returned. 230 of these hits longer than 600 bp were aligned to derive a consensus sequence named as PL Tc1-1Ory. The overall structure of the element resembles Tc1-like elements in fish and amphibians (Leaver, 2001): it has an open reading frame

(ORF) encoding an intact transposase with 339 aa, which is flanked by nearly identical inverted terminal repeats of 219 bp. Each ITR contains 22 bp direct repeats. PL Tc1-1Ory thus belongs to the inverted repeat/direct repeat (IR/DR) group of Tc1-like elements described by Izswak et al. (1995). In the region between the left ITR and the transposase initiation codon, two eukaryotic promoter motifs, a CCAAT box (binds to the transcription factor NFY) (Mantovani, 1998) and a TATAA box (Bucher, 1990) are recognized. In the right ITR region, a putative poly(A) signal (PAS) and iron responsive element (IRE) were found as a UTR scan (Fig 2.7). Both the nucleotide sequence and the aa sequence of the transposase aa are nearly identical (99% identity) to the element in Atlantic salmon (*Salmo salar;* positions 120142 to 121747 in GenBank GQ505859.1; Lukacs et al., 2010) with 14 nucleotides and 4 aa changes in ITR regions and ORF. Moreover, presence of several other active elements in *P. lessonae* genome indicates very recent horizontal transmission of this element from salmon to pool frog *P. lessonae*. The copy of the element found in the upstream of the 5' UTR of the albumin gene is also nearly identical to the consensus sequence of the element only with very small insertions or deletions in ITRs and only two aa changes, which is predicted that it is also naturally functional element. This element is also very similar to passport, a native Tc1 transposon in flattfish (Clark et al., 2009), a preference for insertion into genes, can be useful tool for the manipulation of vertebrate genome.

A

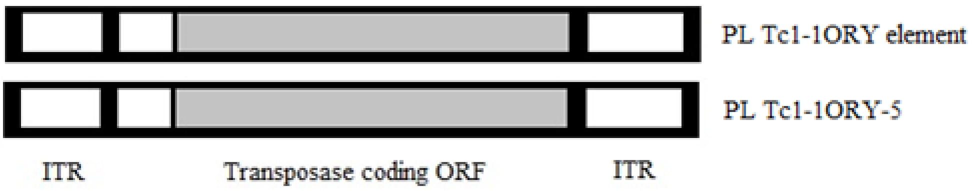


Figure 2.7. Structure of the PL Tc1-1ORY element and its consensus sequence. A) Structure of PL Tc1-1ORY and of its copy in the serum albumin gene. The white coloured rectangular boxes represent inverted terminal repeats; the gray coloured rectangle represents the transposase encoding region. B) The consensus sequence of the 1634 bp PL Tc1-1ORY element. The translated transposase is indicated below the ORF. The putative CAT box, TATA box and poly(A) signal are underlined and shown by bold letters, and the region indicating a putative IRE is marked by blue arrows. At the beginning and end of the sequence, ta repeat is duplicated genomic target site, which is used by Tc1-like transposons. Regions of the sequence representing ITRs are underlined with a black colour and DRs within them are shown by red colour letters.

B

taCAGTGCCT**TGCGAAAGTATTCGGCCCCCTT**GAACTTTTCGACCTTTTGCCACATTTCAGGCTTCAAACAT

AAAGATATAAAACTGTAATTTTTTGTGAAGAATCAACAACAAGTGGGACACAATCATGAAGTGGAACGAAAT

TTATTGGATATTTCAAACTTTTTTAACAAATAAAAAACTGAAAAATTGGGCG**TGCAAAATTATTCAGCCCCT**

CAT box

TTACTTTCAGTGCAGCAAACTCTCTCCAGAAGTTCAGTGAGGATCTCTGAATGAT**CCAAT**GTTGACCTAAAT

TATA box

GACTAATGATGATAAATAGAATCCACCTGTGTGTAATCAAGTCTCCG**TATAAAT**GCACCTGCACTGTGATAG

TCTCAGAGGTCCGTTTAAAGCGCAGAGAGCATCatgaagaacaaggaacacaccaggcaggtccgagatact

M K N K E H T R Q V R D T

gttgtggagaagtttaaagccggatttggatacaaaaagatttcccaagctttaaacatcccaaggagcact

V V E K F K A G F G Y K K I S Q A L N I P R S T

gtgcaagcgataatattgaaatggaaggagtatcagaccactgcaaatctacgaagacctggccgtccctct

V Q A I I L K W K E Y Q T T A N L R R P G R P S

aaactttcagctcatacaaggagaagactgatcagagatgcagccaagaggcccatgatcactctggatgaa

K L S A H T R R R L I R D A A K R P M I T L D E

ctgcagagatctacagctgaggtgggagactctgtccataggacaacaatcagtcgtatactgcacaaatct

L Q R S T A E V G D S V H R T T I S R I L H K S

ggcctttatggaagagtggcaagaagaaagccatttcttaaagatatccataaaaagtgttgtttaaagttt

```
G  L  Y  G  R  V  A  R  R  K  P  F  L  K  D  I  H  K  K  C  C  L  K  F
gccacaagccacctgggagacacaccaaacatgtggaagaaggtgctctggtcagatgaaaccaaaatcgaa
A  T  S  H  L  G  D  T  P  N  M  W  K  K  V  L  W  S  D  E  T  K  I  E
ctttttggcaacaatgcaaaacgttatgtttggcgtaaaagcaacacagctcatcaccctgaacacaccatc
L  F  G  N  N  A  K  R  Y  V  W  R  K  S  N  T  A  H  H  P  E  H  T  I
cccactgtcaaacatggtggtggcagcatcatggtttgggcctgcttttcttcagcagggacagggaagatg
P  T  V  K  H  G  G  G  S  I  M  V  W  A  C  F  S  S  A  G  T  G  K  M
gttaaaattgatgggaagatggatggagccaaatacaggaccattctggaagaaaacctgatggagtctgca
V  K  I  D  G  K  M  D  G  A  K  Y  R  T  I  L  E  E  N  L  M  E  S  A
aaagacctgagactgggacggagatttgtcttccaacaagacaatgatccaaaacataaagcaaaatctaca
K  D  L  R  L  G  R  R  F  V  F  Q  Q  D  N  D  P  K  H  K  A  K  S  T
atggaatggttcacaaataaacatatccaggtgttagaatggccaagtcaaagtccagacctgaatccaatc
M  E  W  F  T  N  K  H  I  Q  V  L  E  W  P  S  Q  S  P  D  L  N  P  I
gagaatctgtggaaagaactgaaaactgctgttcacaaacgctctccatccaacctcactgagctcgagctg
E  N  L  W  K  E  L  K  T  A  V  H  K  R  S  P  S  N  L  T  E  L  E  L
ttttgcaaggaggaatgggcaaaaatttcagtctctcgatgtgcaaaactgatagagacataccccaagcga
F  C  K  E  E  W  A  K  I  S  V  S  R  C  A  K  L  I  E  T  Y  P  K  R
cttacagctgtaatcgcagcaaaaggtggcgctacaaagtattaaCTTAAGGGGGCTGAATAATTTTGCACG
L  T  A  V  I  A  A  K  G  G  A  T  K  Y  *
                                           Poly(A) Signal
CCCAATTTTTCAGTTTTTTATTTGTTAAAAAAGTTTGAAATATCCAATAAATTTCGTTCCACTTCATGATTG
                                  ↓                 IRE
TGTCCCACTTGTTGTTGATTCTTCACAAAAAATTACAGTTTTATATCTTTATGTTTGAAGCCTGAAATGTGG
                                               ↓
CAAAAGGTCGAAAAGTTCAAGGGGGCCGAATACTTTCGCAAGGCACTGta     1634 bp
```

Figure 2.7. (continued).

2.3.2.1.1.2. PL Tc1-10Xt Element

This element has two truncated copies (212 and 402 bp) upstream of the 5' UTR of the albumin gene. To obtain a consensus sequence of this element, the reference sequence of the Tc1-10Xt (Eagle) was blasted against the *P. lessonae* genome; the search returned 628 hits. Because the consensus element is very short, particulary at the 5' region, all copies of the element from 50 bp to 1346 bp were used to derive a consensus sequence of the element, named as PL Tc1-10Xt. Although it has an intact transposase open reading frame (339 aa), both the left ITR and the transcriptional regulator region (between the left ITR and the transposase initiation codon) contain deletions more than 50 bp. No copy of a PL Tc1-10Xt element intact for these regions was found in the *P. lessonae* genome. Thus, the length of the left ITR is 125 bp. In contrast, the ORF flanking the right ITR is 216 bp in long, with 12 bp imperfect DRs. In the transcriptional regulatory region, only the TATA box is identified; and in the 3' UTR, only the IRE (Fig 2.8). Both complete consensus nucleotide sequence of the element and its transposase coding ORF and regions show the highest similarity to Tc1-10Xt (Eagle) element (*Silurana tropicalis* - consensus sequence from Repbase, Pocwierz-Kotus et al. 2007). Similarity between the aa sequences of the transposases is 91% (309/339). This low similarity even in transposase coding ORFs and many in frame shifts and stop codons in ORFs in several copies of the element in *P. lessonae* genome, and a great deletion in 5' UTR and many small insertions and deletions in both the 5' and 3' UTR indicate ancient transmission of these elements from *S. tropicalis* to *P. lessonae* or they have inherited from the common ancestor. Accumulations of mutations through time could make it as an inactive element in *P. lessonae* genome. Two truncated copies of the element were found upstream of the 5' UTR of the albumin gene. The longer copy extends from the end of the ORF to the 3' end of the right ITR whereas short copy covers a very small region within the ORF.

A

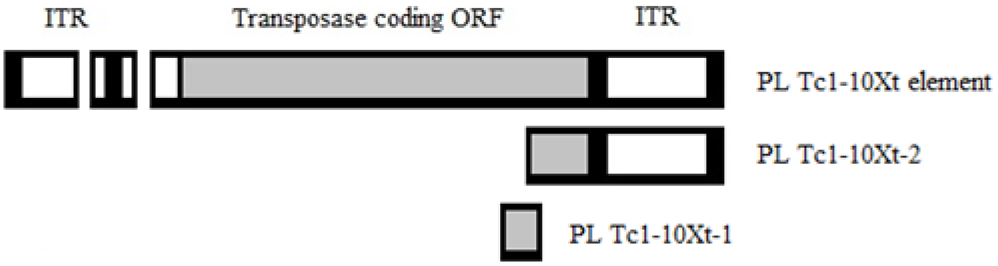


Figure 2.8. Structure of PL Tc1-10Xt element and its consensus sequence. A) Structure of the PL Tc1-10Xt element and its two copies in the serum albumin gene. White coloured rectangles indicate inverted terminal repeats; and gray coloured rectangles represent transposase encoding region. B) The consensus sequence of the 1612 bp PL Tc1-10Xt element. The transposase translation is indicated below the ORF. The putative TATA box is underlined and shown by bold letters, and the region of the putative IRE is marked by blue arrows. At the beginning and end of the sequence, ta repeat is duplicated genomic target site, which is used by Tc1-like transposons. Regions of the sequence representing ITRs are underlined with a black colour and DRs within them are shown by red coloured letters.

B

taCAGTGCCTTGAAAAAGTATTCATACCCCTTGAAATTTTCCACATTTTGTCATGTTACAACCAAAAACGTA

AATGTATTTTATTGGGATTTTATGTGATAGACCAACACAAAGTGG---------------------------

-------------------------ACAAATAAATAACTGAAAAGTGGGGTGTGCATAATTATTCAGCCCCC

TTT--TAAATAGAGTCCACCTG

TATA box

TGTGTAATTTAATCTCAG**TATAAAT**ACAGCTGTTCTGTGAAGCCCTCAGAGGTTTGTTAGAGAACCTTAGTG

AACAAACAGCATCatgaaggccaaggaacacaccagacaggtcagggataaagttgtggagaagtttaaagca

M K A K E H T R Q V R D K V V E K F K A

gggttaggttataaaaaaatatcccaagctttgaacatctcacggagcactgttcaatccatcatccaaaaa

G L G Y K K I S Q A L N I S R S T V Q S I I Q K

tggaaagagtatggcacaactgcaaacctaccaagacatggccgtccacctaaactgacaggccgggcaagg

W K E Y G T T A N L P R H G R P P K L T G R A R

agagcattaatcagagaagcagccaagaggcccatggtaactctggaggagctgcagagatccacagctcag

R A L I R E A A K R P M V T L E E L Q R S T A Q

gtgggagaatctgtccacaggacaactattagtcgtgcactccacaaatctggcctttatggaagagtggca

V G E S V H R T T I S R A L H K S G L Y G R V A

agaagaaagccattgttgaaagaaagccataagaagtcccgtttgcagtttgcgagaagccatgtgggggac

```
R  R  K  P  L  L  K  E  S  H  K  K  S  R  L  Q  F  A  R  S  H  V  G  D
acagcaaacatgtggaagaaggtgctctggtcagatgagaccaaaattgaactttttggcctaaaagcaaaa
T  A  N  M  W  K  K  V  L  W  S  D  E  T  K  I  E  L  F  G  L  K  A  K
cgctatgtgtggcggaaaactaacactgcacatcaccctgaacacaccatccccaccgtgaaacatggtggt
R  Y  V  W  R  K  T  N  T  A  H  H  P  E  H  T  I  P  T  V  K  H  G  G
ggcagcatcatgttgtggggatgcttttcttcagcagggacagggaagctggtcagagttgatgggaagatg
G  S  I  M  L  W  G  C  F  S  S  A  G  T  G  K  L  V  R  V  D  G  K  M
gatggagccaaatacagggcaatcttagaagaaaacctgttagagtctgcaaaagacttgagactggggcgg
D  G  A  K  Y  R  A  I  L  E  E  N  L  L  E  S  A  K  D  L  R  L  G  R
aggttcaccttccagcaggacaacgaccctaaacatacagccagagctacaatggaatggtttagatcaaag
R  F  T  F  Q  Q  D  N  D  P  K  H  T  A  R  A  T  M  E  W  F  R  S  K
catattcatgtgttagaatggcccagtcaaagtccagacctaaatccaattgagaatctgtggcaagacttg
H  I  H  V  L  E  W  P  S  Q  S  P  D  L  N  P  I  E  N  L  W  Q  D  L
aaaattgctgttcacagacgctctccatccaatctgacagagcttgagctattttgcaaagaagaatgggca
K  I  A  V  H  R  R  S  P  S  N  L  T  E  L  E  L  F  C  K  E  E  W  A
aaaatgtcactctctagatgtgcaaagctggtagagacatccccaaaaagacttgcagctgtaattgcagcg
K  M  S  L  S  R  C  A  K  L  V  E  T  S  P  K  R  L  A  A  V  I  A  A
aaaggtggttctacaaagtattgaCTCAGGGGGCTGAATACAAATGCACGCCACACTTTTCACATATTTATT
K  G  G  S  T  K  Y  *
TGTAAAAAATGTTGAAAACCATTTATCATTTTCCTTCCACTTCACAATTATGTGCCACTTTGTGTTGGTCTA
    ↓                             IRE
TCACATAAAATCCCAATAAAATACATTTACGTTTTTGGTTGTAACATGACAAAATGTGGAAAATTTCAAGGG
                    ↓
GTATGAATACTTTTTCAAGGCACTGta     1612 bp
```

Figure 2.8. (continued).

2.3.2.1.1.3. PL Tc1-RT Element

This element has one very short truncated copy (185 bp) upstream of the 5' UTR of the albumin gene, which overlaps a very short region in the ORF (Fig 2.9). To obtain consensus sequence of this element, the Repbase reference sequence of Tc1-RT was blasted against the *P. lessonae* genome. The search returned 695 hits.

Because the element is considerably truncated particularly at the 5' region, all copies of the element from 100 bp to 1473 bp were used to derive a consensus sequence, named as PL Tc1-RT. Although it contains an intact transposase open reading frame (339 aa), all copies of it in the *P. lessonae* genome have a deletion about of 50 bp in their left ITRs. An internal DR 16 bp long follows this deletion. The predicted length of left ITR is thus about 210-220 bp. In contrast, the right ITR carries an imperfect 19 bp DRs; and the predicted length is about 210-220 bp. This uncertainity in lengths of both DRs and ITRs can be explained by accumulation of mutations through time after the insertion of original element. This element, like PL Tc1-1Ory element, belong to the inverted repeat/ direct repeat (IR/DR) group of Tc1-like elements described by Izswak et al. (1995). In the transcriptional regulatory region, only the CAT box is identified, probably because of accumulation of mutations through time (Fig 2.9). Both the complete consensus nucleotide sequence of the element and its transposase coding ORF show the greatest similarity to Tc1-RT element (*Rana temporaria* - consensus sequence from Repbase; Leaver, 2001). Similarity between the aa sequences of the transposases is 98% (339/333), even though the consensus sequence of PL Tc1-RT has an intact transposase ORF while the ORF of Tc1-RT has a stop codon and is thus not complete. None of copies of PL Tc1-RT in the *P. lessonae* genome has an intact ORF. Moreover, the long deletion in the left ITR, and several types of mutations (insertions and deletions) in both ITRs and the transcriptional regulatory region again could indicate an ancient transmission of this element from *Rana temporaria* to the *P. lessonae* genome. Or the direction of transmission not clear, probably both *R. temporaria* and *P. lessonae* have inherited this from the same common ancestor.

A

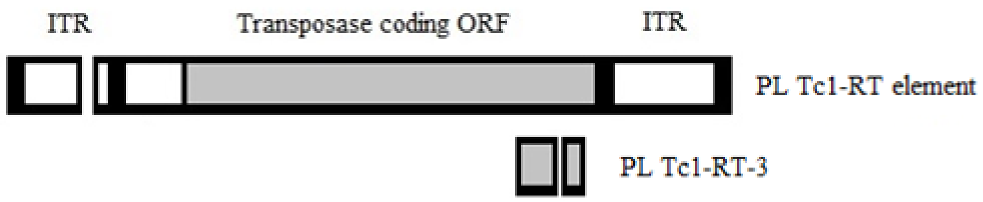


Figure 2.9. Structure of PL Tc1-RT element and its consensus sequence. A) Structure of type PL Tc1-RT element and its copy in the serum albumin gene. The white coloured rectangles indicate inverted terminal repeats; and gray coloured rectangles represents the transposase encoding region. B) The consensus sequence of the 1646 bp PL Tc1-RT element and positions where nucleotide sequences are translated indicated below the ORF. The putative CAT box is underlined and shown by bold letters. At the beginning and end of the sequence, ta repeat is duplicated genomic target site, which is used by Tc1-like transposons. Regions of the sequence representing ITRs are underlined with a black colour and DRs within them are shown by red colour letters.

B

```
taCAGTGCCTTGCAAAAGTATTCACCCCCTTGACTTTTTACCTATTTTGTTACATTACAGCCTTAAGTTCAA

TGTTTTGTTAATCTGAATTTTATGTGATGGATCAGAACACAATAGTCTAAGTTGGTGAAGT-----------

----------------------------------------CTGAAAATTGGCATGTGCGTATGTATTCACCC

                                    CAT box

CCTTTGTTATGAAGCCCATAAAAAGCTCTGGTGCAACCAATTACCTTCAGAAGTCACATAATTAGTGAAATG

ATGTCCACCTGTGTGCAATCTAAGTGTCACATGATCTGTCATTACATATACACACCTTTTTTGAAAGGCCCC

AGAGGCTGCAACACCTAAGCAAGAGGCACCACTAACCAAACACTGCCatgaagaccaaggaactctccaaa

                                               M  K  T  K  E  L  S  K

caagtaagggacaatgttgttgagaagtacaagtcagggttaggttataaaaaaatatccaaatctttgatg

Q  V  R  D  N  V  V  E  K  Y  K  S  G  L  G  Y  K  K  I  S  K  S  L  M

atccccaggagcaccatcaaatctatcataaccaaatggaaagaacatggcacaacagcaaacctgccaaga

I  P  R  S  T  I  K  S  I  I  T  K  W  K  E  H  G  T  T  A  N  L  P  R

gacggccgcccaccaaaactcacggaccgggcaaggagggcattaatcagagaggcagcacagagacctaag

D  G  R  P  P  K  L  T  D  R  A  R  R  A  L  I  R  E  A  A  Q  R  P  K

gtaaccctggaggagctgcagagttccacagcagagactggagtatctgtacataggacgacaataagccgt

V  T  L  E  E  L  Q  S  S  T  A  E  T  G  V  S  V  H  R  T  T  I  S  R

acgctccatagagttgggctttatggcagagtggccagaagaaagccattactttcagcaaaaacaaaatg
```

T L H R V G L Y G R V A R R K P L L S A K N K M

gcacgttttgagtttgcgaaaaggcatgtgggagactcccaaaatgtatggaggaaggtgctctggtctgat

A R F E F A K R H V G D S Q N V W R K V L W S D

gagactaaaattgaacttttcggccatcaaagaaaacgctatgtctggcgcaaacccaacacatcacatcac

E T K I E L F G H Q R K R Y V W R K P N T S H H

ccaaagaacaccatccccacagtgaaacatggtggtggcagcatcatgctgtggggatgtttttcagcagcc

P K N T I P T V K H G G G S I M L W G C F S A A

gggactgggaaactggtcagagttgagggaaagatggatggtgctaaatacagggatattcttgagcaaaac

G T G K L V R V E G K M D G A K Y R D I L E Q N

ctgtaccactctgtgcgtgatttgaggctaggacggaggttcaccttccagcaggacaatgaccccaaacac

L Y H S V R D L R L G R R F T F Q Q D N D P K H

actgctaaagcaacacttgagtggtttaaggggaaacatgtaaatgtgttggaatggcctagtcaaagccca

T A K A T L E W F K G K H V N V L E W P S Q S P

gacctcaatccaatagaaaatctgtggtcagacttaaagattgctgttcacaagcgcaaaccatccaacttg

D L N P I E N L W S D L K I A V H K R K P S N L

aaggagctggagcagttttgcaaggaggaatgggcaaaaatcccagtggtaagatgtggcaagctcatagag

K E L E Q F C K E E W A K I P V V R C G K L I E

acttatccaaagcgacttggagctgtgattgccgcaaaaggtggctctacaaagtattgaCTTTAG**GGGGGT**

T Y P K R L G A V I A A K G G S T K Y *

GAATAGTTATGCACATTGACTTTTTCTGTTATTTTGTCCTATTTGTTGTTTGCTTCACAATAAAAAAAAAAA

AACATCTTCAAAGTTGTGGGCATGTTCTGTAAATTAAATGATGCAAATCCTCAAACAATCCATGTTAATTCC

AGGTTGTGAGGCAACAAAACACGAAAAATGCCAA**GGGGGTGAATACTTTTGCAAGGCA**CTGta **1646bp**

Figure 2.9. (continued).

2.3.2.1.1.4. PL Tc1-PP Element

This element has one very short truncated copy (135 bp) upstream of the 5' UTR of the albumin gene; it overlaps a very short region in the ORF and the right ITR (Fig 2.10). To obtain a consensus sequence of this element, the reference sequence of Tc1-PP was blasted against the *P. lessonae* genome; the search returned 547 hits. Because the element is truncated at both the 5' and 3' regions, all copies of the element from 100 bp to 1283 bp were used to derive a complete consensus sequence, named as PL Tc1-PP element. It has an intact transposase open reading frame (339 aa), but both its the left and particularly right ITRs (27 bp are present) are extremely truncated. Therefore, none of DRs is found. In the transcriptional regulatory region, two eukaryotic promoter motifs, a CCAAT box and a TATAA box are recognized (Fig 2.10). Both the consensus nucleotide sequence of the element and its transposase coding ORF and regions show the greatest similarity to the Tc1-PP element (*Pleuronectes platessa* - consensus sequence from Repbase database, Leaver 2007). Similarity between the aa sequences of the transposases is 87% (296/339). Extreme truncations in both ITRs and several mutations (indels) in the transposase encoding ORF indicate ancient transmission of this element from a marine flatfish species *(Pleuronectes platessa)* to *P. lessonae*. Because all copies of this element in the *P. lessonoae* genome contain extremely truncated ITRs, it seems possible that the original element inherited by *P. lessonae* already had very short ITRs or they could considerably accumulate mutations through time, and remain as fossil elements that it cannot be possible to recognize them.

A

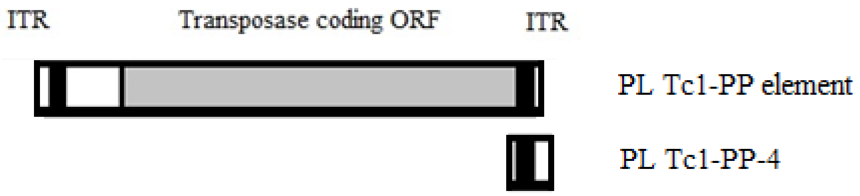


Figure 2.10. Structure of PL Tc1-PP element and its consensus sequence. A) Structure of the PL Tc1-PP element and its copy in the serum albumin gene. White coloured rectangles indicate inverted terminal repeats; and gray coloured rectangle represents transposase encoding region. B) The consensus sequence of the 1298 bp PL Tc1-PP element. Positions where nucleotide sequences are translated indicated below. The putative CAT box and TATA box are underlined and shown by bold letters. Regions of the sequence representing truncated ITRs are underlined with a black colour.

B

```
ATGGTTTTCAAAATTTTTTACAAATAAATATCTGAAAAGTGTGGCGTGCATTTGTATTCAGCCCCCTTTACT
                           Cat Box
CTGATACCCCTAACTAAAATCTAGTGGAACCAATTGCCTTCAG-------------AAGTCACCTAATTAGT
                                Tata Box
AAATAGAGTCCACCTGTGTGTAATTTAATCTCAGTATAAATACAGCTGTTCTGTGAAGCCCTCAGAGGTTTG
TTAGAGAACCTTAGTGAACAAACAGCATCatgaaggccaaggaacacaccagacaggtcagggataaagtt
                             M  K  A  K  E  H  T  R  Q  V  R  D  K  V
gtggagaagtttaaagcagggttaggttataaaaaaatatcccaagctttgaacatctcacggagcactgtt
V  E  K  F  K  A  G  L  G  Y  K  K  I  S  Q  A  L  N  I  S  R  S  T  V
caatccatcatccgaaaatggaaagagtatggcacaactgcaaacctaccaagacatggccgtccacctaaa
Q  S  I  I  R  K  W  K  E  Y  G  T  T  A  N  L  P  R  H  G  R  P  P  K
ctgacaggccgggcaaggagagcattaatcagagaagcagccaagaggcccatggtaactctggaggagctg
L  T  G  R  A  R  R  A  L  I  R  E  A  A  K  R  P  M  V  T  L  E  E  L
cagagatccacagctcaggtgggagaatctgtccacaggacaactattagtcgtgcactccacaaatctggc
Q  R  S  T  A  Q  V  G  E  S  V  H  R  T  T  I  S  R  A  L  H  K  S  G
ctttatggaagagtggcaagaagaaagccattgttgaaagaaagccataagaagtcccgtttgcagtttgcg
L  Y  G  R  V  A  R  R  K  P  L  L  K  E  S  H  K  K  S  R  L  Q  F  A
agaagccatgtgggggacacagcaaacatgtggaagaaggtgctctggtcagatgagaccaaaattgaactt
R  S  H  V  G  D  T  A  N  M  W  K  K  V  L  W  S  D  E  T  K  I  E  L
tttggcctaaaagcaaaacgctatgtgtggcggaaaactaacactgcacatcaccctgaacacaccatcccc
F  G  L  K  A  K  R  Y  V  W  R  K  T  N  T  A  H  H  P  E  H  T  I  P
accgtgaaacatggtggtggcagcatcatgttgtggggatgcttttcttcagcagggacagggaagctggtc
T  V  K  H  G  G  G  S  I  M  L  W  G  C  F  S  S  A  G  T  G  K  L  V
agagttgatgggaagatggatggagccaaatacagggcaatcttagaagaaaacctgttagagtctgcaaaa
R  V  D  G  K  M  D  G  A  K  Y  R  A  I  L  E  E  N  L  L  E  S  A  K
gacttgagactggggcggaggttcaccttccagcaggacaacgaccctaaacatacagccagagctacaatg
D  L  R  L  G  R  R  F  T  F  Q  Q  D  N  D  P  K  H  T  A  R  A  T  M
gaatggtttagatcaaagcatattcatgtgttagaatggcccagtcaaagtccagacctaaatccaattgag
E  W  F  R  S  K  H  I  H  V  L  E  W  P  S  Q  S  P  D  L  N  P  I  E
```

Figure 2.10. (continued).

aatctgtggcaagacttgaaaattgctgttcacagacgctctccatccaatctgacagagcttgagctattt
N L W Q D L K I A V H R R S P S N L T E L E L F
tgcaaagaagaatgggcaaaaatgtcactctctagatgtgcaaagctggtagagacatccccaaaaagactt
C K E E W A K M S L S R C A K L V E T S P K R L
gcagctgtaattgcagcgaaaggtggttctacaaagtattgaCACAGGGGGGTGAATACTAATGCACCC
A A V I A A K G G S T K Y * **1298bp**

Figure 2.10. (continued).

2.3.2.1.1.5. PL Tc1-DR1 Element

This element has two truncated copies, one in intron 8 (1002 bp) and one downstream of the 3' UTR (944 bp). Because the reference sequence of Tc1-DR1 obtained from Repbase contains only the ORF, this incomplete reference sequence was blasted against GenBank; the search yielded a signficant match to a longer element (1642 bp) found in Atlantic salmon (*Salmo salar* - EF467298, GenBank, from 34140 to 35412, complementary strand; Yazawa et al.,, 2008). This longer reference sequence was blasted against the *P. lessonae* genome. The search returned 2984 hits; 352 hit sequences longer than 1000 bp were used to derive a consensus sequence. The consensus sequence of the element (PL Tc1-DR1) has an intact transposase ORF (340 aa) flanked by identical ITRs about 221 bp each. The left ITR contains 20 bp and the rigth ITR contains 19 bp DRs respectively. The element thus belongs to the inverted repeat/ direct repeat (IR/DR) group of Tc1-like elements described by Izswak et al. (1995). In the region between the left ITR and the transposase initiation codon, only one eukaryotic promoter motif, a CCAAT box, is recognized (Fig 2.11). Both the complete consensus nucleotide sequence of the element and its transposase-encoding ORF show the greatest similarity to the element (EF467298.1) found in Salmo salar (Yazawa et al., 2008). Similarity between aa sequences of transposases is 97% (328/340). This high level of similarity together with the presence of several copies of the element in the *P. lessonae* genome indicates very recent horizontal transmission of this element from salmon to water frog, which is still mobilizing within *P. lessonae* genome. Both copies of the element in the serum albumin gene correspond to the transposase coding ORF containing insertions and deletions that result in frame shifts and stop codons (Fig 2.11A)

A

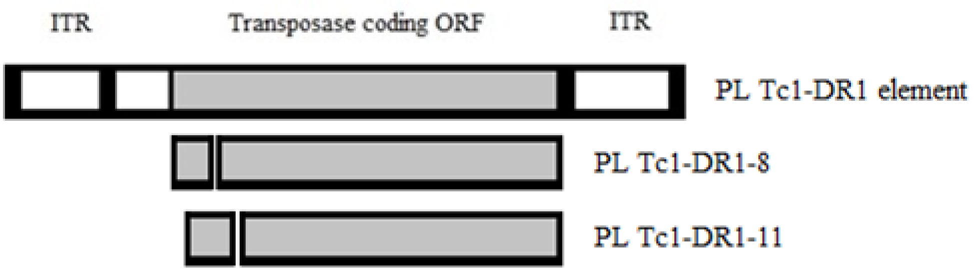


Figure 2.11. Structure of PL Tc1-DR1 element and its consensus sequence. A) Structure of PL Tc1-DR1 element and its copies in the serum albumin gene. The white coloured rectangles indicate inverted terminal repeats; gray coloured rectangle represents transposase encoding region. B) The consensus sequence of the 1650 bp PL Tc1-DR1 element. The transposase translation is indicated below the ORF. The putative CAT box is underlined and shown by bold letters. Regions of the sequence representing ITRs are underlined and DRs within them are shown by red colour letters.

B

ACATACAGTATCTC**ACAAAAGTGAGTACACCCCT**CACATTTTTGTAAATATTTTATTATATCTTTTCATGTG

ACAACACTGAAGAAATGACACTTTGCTACAATGTAAAGTAGTGAGTGTACAGCTTGTATAACAGTGTAAATT

TGCTGTCCCCTCAAAATAACTCAACACACAGCCATTAATGTCTAAACCGCTGGCA**ACAAAAGTGAGTACACC**

CAT Box

CCTAAGTGAAAATGTCCAAATTGGGC**CCAAT**TAGCCATTTTCCCTCCCCGGTGTCATGTGACTCGTTAGTGT

TACAAGGTCTCAGGTGTGAATGGGGAGCAGGTGTGTTAAATTTGGTGTTATCGCTCTCACTCTCTCATACTG

GTCACTGGAAGTTCAACatggcacctcatggcaaagaactctctgaggatgtgaaaaaaagaattgttgct

M A P H G K E L S E D V K K R I V A

ctacataaagatggcctaggctataagaagattgccaagaccctgaaactgagctgcagcacggtggccaag

L H K D G L G Y K K I A K T L K L S C S T V A K

accatacagcggtttaacaggacaggttccactcagaacaggcctcgccatggtcgaccaaagaagttgagt

T I Q R F N R T G S T Q N R P R H G R P K K L S gcacgtgctcagcgtcatatccagaggttgtctttgggaaatagacgtatgagtgctgccagcattgctgca

A R A Q R H I Q R L S L G N R R M S A A S I A A

gaggttgaaggggtgggggtcagcctgtcagtgctcagaccatacgccgcacactgcatcaaattggtctg

E V E G V G G Q P V S A Q T I R R T L H Q I G L

catggctgtcgtcccagaaggaagcctcttctaaagatgatgcacaagaaagcccgcaaacagtttgctgaa

H G C R P R R K P L L K M M H K K A R K Q F A E

gacaagcagactaaggacatggattactggaaccatgtcctgtggtctgatgagaccaagataaacttattt

D K Q T K D M D Y W N H V L W S D E T K I N L F

ggttcagatggtgtcaagcgtgtgtggcggcaaccaggtgaggagtacaaagacaagtgtgtcttgcctaca

G S D G V K R V W R Q P G E E Y K D K C V L P T

gtcaagcatggtggtgggagtgtcatggtctggggctgcatgagtgctgccggcactggggagctacagttc

V K H G G G S V M V W G C M S A A G T G E L Q F

attgagggaaccatgaatgccaacatgtactgtgacatactgaagcagagcatgatcccctcccttcggaga

I E G T M N A N M Y C D I L K Q S M I P S L R R

ctgggccgcagggcagtattccaacatgataacgaccccaaacacacctccaagacgaccactgccttgcta

L G R R A V F Q H D N D P K H T S K T T T A L L

aagaagctgagggtaaaggtgatggactggccaagcatgtctccagacctaaaccctattgagcatctgtgg

K K L R V K V M D W P S M S P D L N P I E H L W

ggcatcctcaaacggaaggtggaggagcgcaaggtctctaacatccaccagctccgtgatgtcgtcatggag

G I L K R K V E E R K V S N I H Q L R D V V M E

gagtggaagaggactccagtggcaacctgtgaagctctggtgaactccatgcccaagagggttaaggcagtg

E W K R T P V A T C E A L V N S M P K R V K A V

ctggaaaataatggtggccacacaaaatattgaCACTTTGGGCCCAATTTGGACATTTTCACTT**AGGGGTGT**

L E N N G G H T K Y *

ACTCACTTTTGTTGCCAGCGGTTTAGACATTAATGGCTGTGTGTTGAGTTATTTTGAGGGGACAGCAAATTT

ACACTGTTATACAAGCTGTACACTCACTACTTTACATTGTAGCAAAGTGTCATTTCTTCAGTGTTGTCACAT

GAAAAGATATAATAAAATATTTACAAAAATGTG**AGGGGTGTACTCACTTTTG**TGAGATACTGTATGT

1650 bp

Figure 2.11. (continued).

2.3.2.1.1.6. PL Tc1-FR3 Element

In the intron 4 of the serum albumin gene contains two truncated copies (368 and 387 bp) of this element. To obtain a consensus sequence of this element, the reference sequence of the Tc1-FR3 from Repbase database (Smith, 2002) were blasted against the *P. lessonae* genome; the search returned 1569 hits; 384 copies of the element larger than 400 were alinged to derive a consensus sequence. The consensus sequence of the element (PL Tc1-FR3) has an intact transposase ORF (343 aa), which is flanked by short imperfect ITRs (29 bp) that contain very short DRs (5 bp). In the transcriptional regulatory region, the CAT box and TATA box are identified (Fig 2.12). Both the complete consensus nucleotide sequence of the element and its transposase-encoding ORF show the greatest similarity to the element found in Takifugu ruripes (Fugu - assembly HE591539, from 5007707 to 5008942, complementary strand). Similarity between aa sequences of the transposases is 84 % (287/343). This low similarity in the entire element, many in frame shifts and stop codons in ORFs and long truncations both the 5' and 3' UTR in several copies of the element in the *P. lessonae* genome, indicate ancient transmission of this element from fish to water frog. Two truncated copies of the element found in the intron 4 of the albumin gene overlap with the last region of the ORF (Fig 2.12).

A

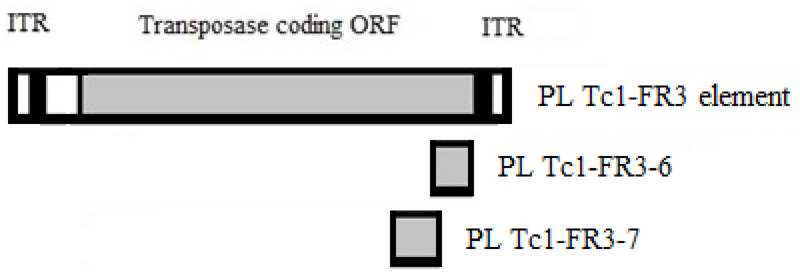


Figure 2.12. Structure of PL Tc1-FR3 element and its consensus sequence. A) Structure of PL Tc1-FR3 type element and its copies in the serum albumin gene. The white coloured rectangules indicate inverted terminal repeats and gray coloured rectangle represents the transposase encoding region. B) The consensus sequence of the 1248 bp PL Tc1-FR3. The transposase translation is indicated below the ORF. The putative CAT box and TATA box are underlined and shown by bold letters. Regions of the sequence representing ITRs are underlined and DRs within them are shown by red colour letters.

B

CAT Box

CACTATATTGCCAAAAGTATTGGGACACCCCTCCAAATCATTGGATTCAGGTGTT**CCAAT**CACTTCCACGGC

Tata Box

CACAGGTG**TATAAAA**TCAAGCACCTAGGCATGCAGACTGCTTCTACAAACATTTGTGAAAGAatgggtcgc

M G R

tctcaggagctcagtgaattcaagcatggtaccgtgataggttgccacctgtgcaataagtccatccgtgaa

S Q E L S E F K H G T V I G C H L C N K S I R E

atttccttgctactaaatattccacggtcaactgttagtggtattataacaaagtggaagcaactgggaaca

I S L L L N I P R S T V S G I I T K W K Q L G T

acagcaactcagccacgaagtggtaggccacgtaaaatgacagagcggggtcagcgcatgctgaagcgcaca

T A T Q P R S G R P R K M T E R G Q R M L K R T

gtgcgcagaagtcgccaactgtctgcagagtcaatagctacagacctccaaacttcgtgtggccttcagatt

V R R S R Q L S A E S I A T D L Q T S C G L Q I

agcacaacaacagtgcgtagagagcttcatggaatgggtttccatggccgagcagctgcatccaagccttac

S T T T V R R E L H G M G F H G R A A A S K P Y

atcaccaagtgcaatgcaaagcgtcggatgcagtggtgtaaagcacgccgccactggactctagagcagtgg

I T K C N A K R R M Q W C K A R R H W T L E Q W

agacgtgttctctggagtgacgaatcacgcttctctgtctggcaatctgatggacgtgtctgggtttggcgg

R R V L W S D E S R F S V W Q S D G R V W V W R

ttgccaggagaacggtacttgcctgactgcattgtgccaagtgtaaagtttggtggagggggattatggtg

```
L   P   G   E   R   Y   L   P   D   C   I   V   P   S   V   K   F   G   G   G   G   I   M   V
tggggttgtttttcaggggttgggcttggccccttagttccagtgaagggaactcttaaggcgtcagcatac
W   G   C   F   S   G   V   G   L   G   P   L   V   P   V   K   G   T   L   K   A   S   A   Y
caagacattttggacaatttcatgctcccaactttgtgggaacagtttggggatggccccttcctgttccaa
Q   D   I   L   D   N   F   M   L   P   T   L   W   E   Q   F   G   D   G   P   F   L   F   Q
catgactgcgcaccagtgcacaaagcaaggtccataaagacatggatgagcgagtttggggtggaggaactt
H   D   C   A   P   V   H   K   A   R   S   I   K   T   W   M   S   E   F   G   V   E   E   L
gactggcctgcacagagtcctgacctcaacccgatagaacacctttgggatgaattagagcggagactgcga
D   W   P   A   Q   S   P   D   L   N   P   I   E   H   L   W   D   E   L   E   R   R   L   R
gccaggccttctcgtccaacatcagtgcctgacctcacaaatgcgcttctggaagaatggtcaaacattccc
A   R   P   S   R   P   T   S   V   P   D   L   T   N   A   L   L   E   E   W   S   N   I   P
atagacacactcctaaaccttgtggacagccttcccagaagagttgaagctgttatagctgcaaagggtggg
I   D   T   L   L   N   L   V   D   S   L   P   R   R   V   E   A   V   I   A   A   K   G   G
ccaactcaatattgaACCCTACGGACTAAGACTGGGATGCCATTAAAGTTCATGTGTGTGTAAAGGCAGGTG
P   T   Q   Y   *
TCCCAATACTTTTGGCAATATAGTG          1248bp
```

Figure 2.12. (continued).

2.3.2.1.1.7 Structural Characteristics of ITR and Transposase Genes of P. lessonae consensus TLEs

The characteristic of *P. lessonae* ITRs and transposase genes are summarized in Table 2.2. All ITRs are well conserved (85-100% identity), varying from 29 bp (PL Tc1-FR3) to 221 bp (PL Tc1-DR1). Like other vertebrate TLEs such as PPTN, RTTN, SSTN (Leaver, 2001) and Frog Prince transposons (Miskey et al., 2003), they have DRs in the extremities of their ITRs, that act as binding site for the transposase. As comparing to PL Tc1-DR1 and PL Tc1-1Ory, PL Tc1-FR3 ITRs has very short DRs (5 bp). In addition, PL Tc1-1Ory, PL Tc1-Xt and PL Tc1-RT contain a highly conserved motif "CAGTG" at the 5' end, and "GTCAC" at the 3' end, of ITRs (Brezinsky et al., 1990). The size of 5' UTRs ranges from 72 bp (PL Tc1-FR3) to 187 bp (PL Tc1-RT). Except PL Tc1-DR1 and PL Tc1-FR3, they all have a TA duplication at the beginning and end of the element, a sign of a Tc1-mariner insertion event. In all PL elements, the transposase ORF, which range from 339aa to 343 aa and have a highly conserved [D,D(34)E] motif in the catalytic domain, is uninterrupted and intact.

Table 2.2. Main features of *P. lessonae* consensus TLEs.

Name			PL Tc1-1Ory	PL Tc1-10Xt	PL Tc1-RT	PL Tc1-PP	PL Tc1-DR1	PL Tc1-FR3
Size (bp)			1634	1612	1646	1298	1650	1248
ITR	ITR size (bp)	Left	219	125*	189*	67*	221	29
		Right	219	216	192*	27*	221	29
	% identity ITR		99	99	85	*	100	100
	DR size (bp)		22	12	16-19	*	19-20	5
	CAGTG motif		Yes	Yes	Yes	*	No	No
Transposase gene	ORF quality		intact 339 aa	intact 339 aa	intact 339 aa	intact 339 aa	intact 340 aa	intact 343 aa
	5' UTR size (bp)		174	144*	187	164	156	72
TA duplica.			Yes	Yes	Yes	*	No	No

2.3.2.1.2. hAT/Charlie Family

DNA transposons of the hAT superfamily are widespread in fungi, plants and animals (Calvi et al., 1991; Rubin et al., 2001), including such vertebrates such as frogs, lizards, snakes and mammalians (Pace et al., 2008; Novick et al., 2010). Recently, the group has been subdivided into two distinct subfamilies (Ac and

Buster; Arensburger et al., 2011). Elements are generally 2.5 to 5 kb long. An 8 bp target site duplication (TSD) is formed during transposition. The ORF encoding transposase is flanked by two short ITRs (5-27 bp), which share a low sequence similarity in their consensus sequence (Kempken and Windhofer, 2001; Rubin et al., 2001). According to Hickman et al. (2005) and Arensburger et al. (2011) hAT transposon families contain four domain in their transposase: an N-terminal domain carrying a BED zinc finger; a DNA-binding domain involved in oligomerization; a catalytic domain having the first two carboxylates of the catalytic triad (DD); and a long insertion with several α-helices that ends with a glutamate residue (E) in close proximity to the catalytic domain. Lastly, the catalytic triad (DDE) is completed (Hickman et al., 2005). In the *P. lessonae* scaffold, six truncated hAT-like elements (HLE), representing three distinct HLEs were identified.

2.3.2.1.2.1. PL hAT-2-TS Element

This element has three very short truncated copies (81, 98 and 107 bp) in introns 3 and 10 of the albumin gene; each overlaps a very short region in the transcriptional regulatory region (Fig 2.13). To obtain consensus sequence of this element, the reference sequence of the hAT-2-TS from the Repbase database (Novick et al., 2010) was blasted against the *P. lessonae* genome, which returned 943 hits. Because the consensus element is considerably truncated in both the UTR and ORF parts, particularly at the 5' end, all copies of the element from 56 bp to 1580 bp were used to derive a complete consensus sequence, named as PL hAT-2-TS element. Although an intact transposase coding ORF (601 aa) is present, there is very long deletion (469 bp) in the 5' UTR region; it is not found any copies of the element in the complete *P. lessonae's* genome. Perhaps this deletion was present at the first insertion into the *P. lessonae* genome. It contains very short ITRs about 16 bp long. In the transcriptional regulatory region, only the TATA box is identified as a result of online search for promoter and functional motifs using NsiteM (http://linux1.softberry.com/berry.phtml) (Solovyev et al., 2010). Both complete consensus nucleotide sequence of the element and its transposase coding ORF and regions show the highest similarity to element in the tarsier (*Tarsius syrichta* - consensus sequence from Repbase; Novick et al., 2010). Similarity between aa sequences of transposases is 95% (570/601). None of the copies of PL hAT-2-TS element in the *P. lessonae* genome has an intact ORF. Moreover, the long deletion in the 5' UTR, and several other insertions and deletions in both UTRs, the transcriptional regulatory region, and ORF indicate very ancient transmission of this element to *P. lessonae* genome. It is not clear how this element can invade from a mammalian species to amphibian, however, recently it was indicated that parallel transfer in tetrapod genomes are very common which could be explained through the way of prey to predator transmission (Novick et al., 2010). Or much more likely some form of this element was present in the very ancient common ancestor of tarsiers and frogs, and has been inherited by both (with changes, mostly deleterious).

A

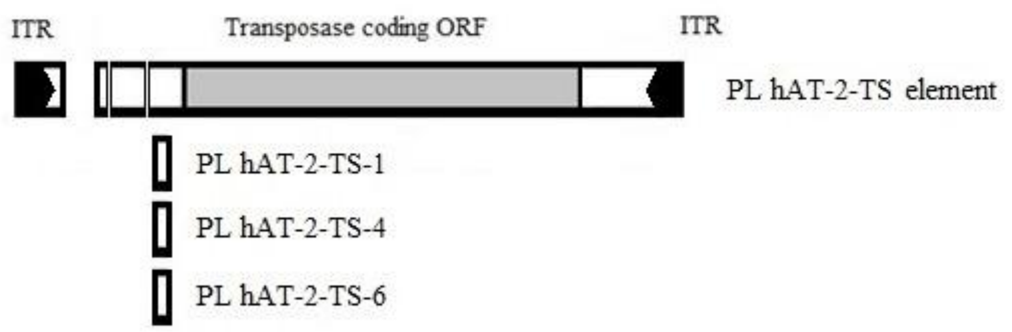


Figure 2.13. Structure of the PL hAT-2-TS element and its consensus sequence. A) Structure of PL hAT-2-TS element and its copies in the serum albumin gene with black coloured triangle indicating inverted terminal repeats and gray coloured rectangles representing the transposase encoding region. B) The consensus sequence of the 3538 bp PL hAT-2-TS element and with translations of the nucleotide sequences indicated below. The putative TATA box is underlined and shown by bold letters. Regions of the sequence representing ITRs are underlined with black.

B

```
CAGGGGTCCTCAAACTACGGCCCGCGGGCCACATGCGGCCCGCCAAGGACATTTATCCGGCCCGCCGGGTGT
TTTTGCCGCCGCTGCCTGTCC---------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
------------------------------------------------------------------------
--------------------------------------------------------AGTGCTCAGTGTTAAT
GCAAATGGTCAGCGCTCAGTATTAATGCAAATGGTCAGCGGTCAGTGTTAATGCAAATGGTCAGCGCTCAGT
GTTAATGCAAATGGTCAGCGGTCAGTATTAATGCAAATGGTCAGCGGTCAGTGTTAATGCAAATGGTCAGTG
GTCAGTATTAATGCTAATGGTCAGCGGTCAGTATTAATGCGAATGGTCAGCGGTCAGTGTTAATGCTAATGG
TCAGTGCTCAGTGTTATCGCATGGGGGCCCCAAACTGGTAATCTGCCTAGGGCCCCATGGGAACTTAA----
-------AGACAGCCGAGGAGTAGAAAACCCAATTTAATTGACAGTAAGTGCATTTATATTCTGATTGCTAT
TCAGTTGTATGATGTTGTATGTTGTGTGCTGTGTAAGCCCCGGTTCACACTGTTGCGATCTCTGAGCAGTGC
GAGTTCAGCCATATGCTTGTATGGCTGAACTTGCATTCGATTCGGAAGAAAAAAGGCACACGTGCCTTCTTT
TTTCCTGCAGTGGAATCGGATCGCATGGGTCTTCTCACCCATGCGATCAGATTCCTGTGCGAGTTCACA---
---------------ACAGGGCAGTGTGAACTGGAAATATGGTGCGGGAACCGGCACGATTACAGAGCCGGT
TCCTGCACCGCACCAGTGTGAGCCTGGGGTAAAAGCGGAGTTCCACCAACATGGGCACTGGTGAGGCTGAAA
TGATGTGGACTGGTAAGGCTACATTGATGGACACTGATCAGGCTGCATTGATGGGCACTGATGAGGCTGCAT
TGATGGGCAGTGCAGTCTGTATGTCTCTGTGTGGGCAAAGTTATTGCTGGTATATTGTTTTTGTAGCGCTGT
               Tata Box
GTGTGTGTATATATATTATATATATATATGTATATATATATGTATTTTACTAATAGCAATTTGGAATCCCTA
GGAAATCatgatgtcaaaaaaaagaaaaattgactctgagtgcagggtattcaaagaacagtggacttac
       M  M  S  K  K  R  K  I  D  S  E  C  R  V  F  K  E  Q  W  T  Y
gattactttttcacgcagtacaaagaaagagctgtttgtctgatatgccagaatatagtgtctgtgttcaag
D  Y  F  F  T  Q  Y  K  E  R  A  V  C  L  I  C  Q  N  I  V  S  V  F  K
gaatacaatttgcgtcgacactacaaaactcaacataaagataaatatgattgtttggtcggacaagtgaga
E  Y  N  L  R  R  H  Y  K  T  Q  H  K  D  K  Y  D  C  L  V  G  Q  V  R
```

Figure 2.13. (continued).

```
aaagaaaaaatattaaaactgaaaaatacattgacaactcagcaaaatacttttgtgaagcaaaagcagcta
K  E  K  I  L  K  L  K  N  T  L  T  T  Q  Q  N  T  F  V  K  Q  K  Q  L
aatatatcatcattgcgagcaagttttcaagttgccaagctcatagcgtgcactggcagaccattcgtagag
N  I  S  S  L  R  A  S  F  Q  V  A  K  L  I  A  C  T  G  R  P  F  V  E
ggagaatttgttaaagaatgccttctttctgttgccaaagagatgtgtccagagaaggctgatttatttagt
G  E  F  V  K  E  C  L  L  S  V  A  K  E  M  C  P  E  K  A  D  L  F  S
acagtgagtctttcaggacctacaattacacgaagaattgaagaaatgggagaaaatttgcatctgcatttg
T  V  S  L  S  G  P  T  I  T  R  R  I  E  E  M  G  E  N  L  H  L  H  L
caaaactcctcaaaaaaactatgctatttttcattggcactcgacgaaagcaatgatgttcgtgattctgca
Q  N  S  S  K  K  L  C  Y  F  S  L  A  L  D  E  S  N  D  V  R  D  S  A
caacttctaattttcattcgtgggacaaatgaatatttcgaagtcacagaggagcttgctgcactgaaaagc
Q  L  L  I  F  I  R  G  T  N  E  Y  F  E  V  T  E  E  L  A  A  L  K  S
atcaaaggaacaacaacaggagaggatatctatgaaaaagtttgccaaactatgaatgatttggagctggac
I  K  G  T  T  T  G  E  D  I  Y  E  K  V  C  Q  T  M  N  D  L  E  L  D
tgggctaaactagccagtgtgacaactgatggtgctcctagcatggtggggtctatgaaaggagtggttgca
W  A  K  L  A  S  V  T  T  D  G  A  P  S  M  V  G  S  M  K  G  V  V  A
cgcattaaaaaagagatggacaaacacaaccattcacatccaatagccatacactgcctcatccaccaacaa
R  I  K  K  E  M  D  K  H  N  H  S  H  P  I  A  I  H  C  L  I  H  Q  Q
gcactgtgttgtaaatcattgaagttggactctgtcatgaaaattgtggtatcttgtgttaacttcattaga
A  L  C  C  K  S  L  K  L  D  S  V  M  K  I  V  V  S  C  V  N  F  I  R
gctcatgcactaaaccacagacagtttcaggaatttctgtctgagctaaatgttgcctatgaagatattctg
A  H  A  L  N  H  R  Q  F  Q  E  F  L  S  E  L  N  V  A  Y  E  D  I  L
taccacacagaagtccgttggctgagtcgagggagagttttgaaacgtttttatgacttacttccacaggtt
Y  H  T  E  V  R  W  L  S  R  G  R  V  L  K  R  F  Y  D  L  L  P  Q  V
tctgcttttatgctttcgaaaaacaaagaagtaccagagctcaaagatgcagaatggaaatggcaccttgcc
S  A  F  M  L  S  K  N  K  E  V  P  E  L  K  D  A  E  W  K  W  H  L  A
tttctgacagatgtaacagagctactcaacagtttcaatgttcaacttcaaggaaaggggaagctcatctgt
F  L  T  D  V  T  E  L  L  N  S  F  N  V  Q  L  Q  G  K  G  K  L  I  C
gatatgcattcacatgtgaaagcatttcaagtaaaattagacctcctcattaaacaagtgaaggaggaaaac
D  M  H  S  H  V  K  A  F  Q  V  K  L  D  L  L  I  K  Q  V  K  E  E  N
ttctgccatctccccacgactcaaaaccttttggctgaaaaaccagcagttgcattcccaaacaaaacatgt
F  C  H  L  P  T  T  Q  N  L  L  A  E  K  P  A  V  A  F  P  N  K  T  C
```

Figure 2.13. (continued).

gtggatttactagaaattttgcaaaaggagtttcaatttagatttaaagagcttcatctccatgaacaggac

V D L L E I L Q K E F Q F R F K E L H L H E Q D

atacagcttttccggaacccattttctgttgacattgaaattgttgatccgatttaccaaatggaattggct

I Q L F R N P F S V D I E I V D P I Y Q M E L A

gaactacagaattgtgactctctgaaagacgcattcaaatcaagcagccttactaatttctatgcatctctc

E L Q N C D S L K D A F K S S S L T N F Y A S L

ccctctgagacatatcctaatctcaggaaccatgcactcaaaattgcaaccatctttggcagcacctatgtc

P S E T Y P N L R N H A L K I A T I F G S T Y V

tgtgaacagacttttcccgaatgaaacatctgaaatctccaaccagatccagactaactgatgaacacttg

C E Q T F S R M K H L K S P T R S R L T D E H L

catcacttgctacgactagcagtgacaaatatggaaccggatattgaccatctcattagccaaaagcaggcc

H H L L R L A V T N M E P D I D H L I S Q K Q A

catacttcccattgaAATACTGGTAAGTTTCTTTATTTAACTTTACTTGTTCTTCATTTTAAATATTGTATT

H T S H *

TGTTCCCGTTTTGTTTTTTTCACTTCAAAATAAGATATGTGCAGTGTGCATAGGAATTTGTTCACAGTTTTT

TTTTTTTTTAAACTATAGTCCGGCCCTCCAATGGTCTGAGGGACAGTGAACTGGCCCCCTGTTTAAAAA**GTT**

TGAGGACCCCTG **3538 bp**

Figure 2.13. (continued).

2.3.2.1.2.2. PL hAT-2-ET Element

This element has two very short truncated copies (86 and 161 bp long) in intron 10 of the serum albumin gene, which overlap a very short region in the transcriptional regulatory region (Fig 2.14). To obtain a consensus sequence of this element, the reference sequence of the hAT-2-ET from Repbase database (Novick et al., 2010) were blasted against the *P. lessonae* genome; the search returned 695 hits. Because the element is considerably truncated in both the UTRs and ORF parts, particularly at the 5' end, all copies of the element from 44 bp to 1797 bp were used to derive a complete consensus sequence (PL hAT-2-ET). Although an intact transposase coding ORF (601 aa) is present, there is very long deletion (about 188 bp)in the 5' UTR region, this is not found in any copies of the element in the complete *P. lessonae* genome. Perhaps this deletion was present at the time of first insertion into *P. lessonae* genome. Only the right ITR, about 16 bp long, is identified on the basis of reference sequences while the left ITR is not known because of the long deletion in this region. In the transcriptional regulatory region, only the TATA box is found. Both complete consensus nucleotide sequence of the element and its transposase coding ORF and regions show the highest similarity to element in the lesser hedgehog (*Echinops telfairi* - consensus sequence from Repbase; Novick et al., 2010). Similarity between aa sequences of transposases is 93% (556/601). None of copies of PL hAT-2-ET element on *P. lessonae* genome has an intact ORF. Moreover, the truncated 5' UTR region, and several other insertions and deletions in both UTRs, the transcriptional regulatory region, and the ORF indicate very ancient transmission of this element to *P. lessonae* genome. Or the element was present in the very ancient common ancestor of both species.

A

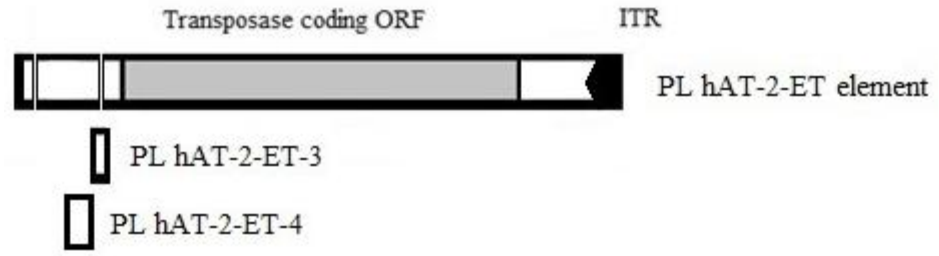


Figure 2.14. Structure of the PL hAT-2-ET element and its consensus sequence. A) Structure of PL hAT-2-ET element and its copies in the serum albumin gene with black coloured triangles indicating inverted terminal repeats and gray coloured rectangles representing transposase encoding region. B) The consensus sequence of the 2914 bp PL hAT-2-ET element and with translations of the nucleotide sequences indicated below. The putative TATA box is underlined and shown by bold letters. Region of the sequence representing ITR is underlined with black.

B

```
TAATGCGAATGGTCAGCGGTCAGTGTTAATGCTAATGGTCAGTGCTCAGTATTAATGCTAATGGTCAGCGGT
CAGTATTAATGCAAATGGTCAGCGCTCAGTGTTAATGCAAATGGTCAGTGCTCAGTATTAATGCAAATGGTC
AGCGCTCAGTATTAATGCAAATGGTCAGTGCTCAGTATTAATGCAAATGGTCAGCGGTCAGTGTTAATGCAA
ATGGTCAGTGCTCAGTGTTATCGCATGGGGGCCCCAAACTGGTAATCTGCCTAGGGCCCCATGGGAACTTA-
----------CAGACAGCCGAGGAGTAGAAAACCCAATTTAATTGACAGTAAGTGCATTTATATTCTGATTG
CTATTCAGTTGTATGATGTTGTATGTTGTGTGCTGTGTAAGCCCCGGTTCACACTGTTGCGATCTCTGAGCA
GTGCGAGTTCAGCCATATGCTTGTATGGCTGAACTTGCATTAGATTCGGAAGAAAAAAGGCACACGTGCCTT
CTTTTTTCCTGCAGTGGAATCGGATCGCATGGGTCTTCTCACCCATGCGATCAGATTCCTGTGCGAGTTCAC
------------------CACAGGGCAGTGTGAACTGGAAATATGGTGCGGGAACCGGCACGATTACAGAGC
CGGTTCCCGCACCGCACCAGTGTGAGCCTGGGGTAAAAGCGGAGTTCCACCAACATGGGCACTGGTGAGGCT
GAAATGATGTGGACTGGTAAGGCTACATTGATGGACACTGATCAGACTGCATTGATGGGCAGTGCAGTCTGT
                                                   TatA Box
ATGTCTCTGTGTGGGCAAAGTTATTGCTGGTATATTGTTTTTGTAGCGCTGTATATATATATTGGTATTTTA
CTAATAGCAATTTGGAATCCCTAGGAAACAatgatatcaaaaaaaagaaaaattgactctgagtgcagggta
                              M  I  S  K  K  R  K  I  D  S  E  C  R  V
ttcaaagaacagtggacttacgattactttttcacgcagtacaaagaaagagctgtttgtctgatatgccag
F  K  E  Q  W  T  Y  D  Y  F  F  T  Q  Y  K  E  R  A  V  C  L  I  C  Q
aatatagtgtctgtgttcaaggaatacaatttgcgtcgacactacgaaactcaacataaagataaatatgat
N  I  V  S  V  F  K  E  Y  N  L  R  R  H  Y  E  T  Q  H  K  D  K  Y  D
tgtttggtcggacaagtgagaaaagataaaatattaaaactgaaaaatggattgacaactcagcaaaatact
C  L  V  G  Q  V  R  K  D  K  I  L  K  L  K  N  G  L  T  T  Q  Q  N  T
tttgtgaagcaaaagcagctaaatatatcatcattgcgagcaagttttcaagttgccaagctcatagcgtgc
F  V  K  Q  K  Q  L  N  I  S  S  L  R  A  S  F  Q  V  A  K  L  I  A  C
actggcagaccattcgtagagggagaatttgttaaagaatgccttctttctgttgccaaagagatgtgtcca
T  G  R  P  F  V  E  G  E  F  V  K  E  C  L  L  S  V  A  K  E  M  C  P
gagaaggctgatttatttagtacagtgagtctttcaggacctacaattacgcgaagaattgaagaaatggga
E  K  A  D  L  F  S  T  V  S  L  S  G  P  T  I  T  R  R  I  E  E  M  G
gaaaatttgcatctgcatttgcaaaactcctcaaaaaaactatgctatttttcattggcactcgacgaaagc
E  N  L  H  L  H  L  Q  N  S  S  K  K  L  C  Y  F  S  L  A  L  D  E  S
aatgatgttcgtgattctgcacaacttctaattttcatttgtgggacaaatgaatatttcgaagtcacagag
N  D  V  R  D  S  A  Q  L  L  I  F  I  C  G  T  N  E  Y  F  E  V  T  E
```

Figure 2.14. (continued).

```
gagcttgctgcactgaaaagcatcaaaggaacaacaacaggagaggatatctatgaaaaagtttgccaaact
E  L  A  A  L  K  S  I  K  G  T  T  T  G  E  D  I  Y  E  K  V  C  Q  T
atgaatgatttggagctggactgggctaaactagccagtgtgacaactgatggtgctcctagcatggtgggg
M  N  D  L  E  L  D  W  A  K  L  A  S  V  T  T  D  G  A  P  S  M  V  G
tctatgaaaggagtggttgcacgcattaaaaaagagatggacaaacacaaccattcacatccaatagccata
S  M  K  G  V  V  A  R  I  K  K  E  M  D  K  H  N  H  S  H  P  I  A  I
cactgcctcatccaccaacaagcactgtgttgtaaatcattgaagttggactctgtcatgaaaattgtggta
H  C  L  I  H  Q  Q  A  L  C  C  K  S  L  K  L  D  S  V  M  K  I  V  V
tcttgtgttaacttcattagagctcatgcactaaaccacagacagtttcaggaatttctgtctgagctaaat
S  C  V  N  F  I  R  A  H  A  L  N  H  R  Q  F  Q  E  F  L  S  E  L  N
gttgcctatgaagatattctgtaccacacagaagtccgttggctgagtcgagggagagttttgaaacgtttt
V  A  Y  E  D  I  L  Y  H  T  E  V  R  W  L  S  R  G  R  V  L  K  R  F
tatgacttacttccacaggtttctgcttttatgctttcgaaaaacaaagaagtaccagagctcaaagatgca
Y  D  L  L  P  Q  V  S  A  F  M  L  S  K  N  K  E  V  P  E  L  K  D  A
gaatggaaatggcaccttgcctttctgacagatgtaacagagctactcaacagtttcaatgttcaacttcaa
E  W  K  W  H  L  A  F  L  T  D  V  T  E  L  L  N  S  F  N  V  Q  L  Q
ggaaaggggaagctcatctgtgatatgcattcacatgtgaaagcatttcaagtaaaattagacctcctcatt
G  K  G  K  L  I  C  D  M  H  S  H  V  K  A  F  Q  V  K  L  D  L  L  I
aaacaagtgaaggaggaaaacttctgccatctccccacgactcaaaaccttttggcggaaaaaccagcagtt
K  Q  V  K  E  E  N  F  C  H  L  P  T  T  Q  N  L  L  A  E  K  P  A  V
gcattcccaaacaaaacatgtgtggatttactagaaattttgcaaaaggagtttcaatttagatttaaagag
A  F  P  N  K  T  C  V  D  L  L  E  I  L  Q  K  E  F  Q  F  R  F  K  E
cttcatctccatgaacaggacatacagcttttccggaacccattttctgttgacattgaaattgttgatccg
L  H  L  H  E  Q  D  I  Q  L  F  R  N  P  F  S  V  D  I  E  I  V  D  P
atttaccaaatggaattggctgaactacagaattgtgactctctgaaagacgcattcaaatcaagcagcctt
I  Y  Q  M  E  L  A  E  L  Q  N  C  D  S  L  K  D  A  F  K  S  S  S  L
actaatttctatgcatctctcccctctgagacatatcctaatctcaggaaccatgcactcaaaattgcaacc
T  N  F  Y  A  S  L  P  S  E  T  Y  P  N  L  R  N  H  A  L  K  I  A  T
atctttggcagcacctatgtctgtgaacagactttttcccgaatgaaacatctgaaatctccaaccagatcc
I  F  G  S  T  Y  V  C  E  Q  T  F  S  R  M  K  H  L  K  S  P  T  R  S
agactaactgatgaacacttgcatcacttgctacgactagcagtgacaaatatggaaccggacattgaccat
R  L  T  D  E  H  L  H  H  L  L  R  L  A  V  T  N  M  E  P  D  I  D  H
```

Figure 2.14. (continued).

ctcattagccaaaagcaggcccatacttcccattgaAATACTGGTAAGTTTCTTTATTTAACTTTACTTGTT

L I S Q K Q A H T S H *

CTTCATTTTAAATATTGTATTTGTTCCCGTTTTGTTTTGTTTTTTTTGCTTCATAATAAGATATGTGCAGTG

TGCATAGGAATTTGTTCATATTTTTTTTTTCAAACTATAGTCCGGCCCTCCAATGGTCTGAGGGACAGTGAA

CTGGCCCCCTGTTTAAAAA**GTTTGAGGACCCCTG** **2914 bp**

Figure 2.14. (continued).

2.3.2.1.2.3. PL hAT-2-OG Element

This element has only one very short truncated copy (75 bp) in intron 10, which overlaps a very short region in the transcriptional regulatory region (Fig 2.15). To obtain a consensus sequence of this element, the reference sequence of the hAT-2-OG from Repbase database (Novick et al., 2010) was blasted against the *P. lessonae* genome; the search returned 514 hits. Because the element is considerably truncated in both the UTRs and ORF parts, all copies of the element from 60 bp to 1797 bp were used to derive a complete consensus sequence (PL hAT-2-OG). Although it contains an intact transposase coding ORF (601 aa), it has a deletion of about 41 bp before the translation initiation and two short deletions in the 5' UTR region. These parts are not found in any copies of the element in the *P. lessonae* genome. Only the right ITR (15 bp) is identified on the basis of the reference sequence. Both the complete consensus nucleotide sequence of the element and its transposase coding ORF and regions show the highest similarity to element in the greater galago (*Otolemur monteiri* - consensus sequence from the Repbase; Novick et al., 2010). Similarity between aa sequences of transposases is 92% (601/553). None of copies of PL hAT-2-OG element in the *P. lessonae* genome has an intact ORF. Additionally, several other insertions and deletions both in UTRs, the transcriptional regulatory region and ORF indicate very ancient transmission of this element to *P. lessonae* genome.

A

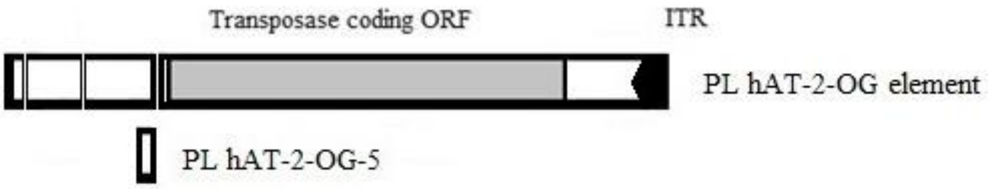


Figure 2.15. Structure of the PL hAT-2-OG element and its consensus sequence. A) Structure of thePL hAT-2-OG element and its copies in the serum albumin gene with Black coloured triangle indicate inverted terminal repeats; and gray coloured rectangles represent transposase encoding region. B) The consensus sequence of the 2790 bp PL hAT-2-OG element and positions where nucleotide sequences are translated indicated below the ORF. Region of the sequence representing ITR is underlined with a black colour.

B

```
CAGTGTTAATGCAAATGGTCAGCGCTCAGTGTTAATGCAAATGGTCAGCGGTCAGTGTTAATGCAAATGGTC

AGCGGTCAGTGTTAATGCAAATGGTCAGTGCTCAGTGTTATTCGCATGGGGGCCCCAAACTGGTAATCTGCC

TAGGGCCCCATGGGAACTTAA---------------------GGAGTAGAAAACCCAATTTAATTGACAGTA

AGTGCATTTATATTCTGATTGCTATTCAGTTGTATGATGTTGTATGTTGTGTGCTGTGTAAGCCCCGGTTCA

CACTGTTGCGATCTCTGAGCAGTGCGAGTTCAGCCATATGCTTGTATGGCTGAACTTGCATTCGATTCGGAA

GAAAAAAGGCACACGTGCCTTCTTTTTTCCTGCAGTGGAATCGGATCGCATGGGTCTTCTCACCCATGCGAT

CAGATTCCTGTGCGAGTTCACA-------------------CAGGGCAGTGTGAACTGGAAATATGGTGCAG

GAACCGGCACGATTACAGAGCCGGTTCCCGCACCGCACCAGTGTGAGCCTGGGGTAAAAGCGGAGTTCCACC

AACATGGGCACTGGTGAGGCTGAAATGATGTGGACTGGTAAGGCTACATTGATGGGCACTGATCAGACTGCA

TTGATGGGCAGTGCAGTCTGTATGTCTCTGTGTGGGCAAAGTTATTGCTGGTATATTGTTTTTGTAGCGCTG

-----------------------------------------CTAGGAAACAatgatatcaaaaaaaagaaaa

                                                   M  I  S  K  K  R  K

attgactctgagtgcagggtattcaaagaacagtggacttacgattactttttcacgcagtacaaagaaaga

I  D  S  E  C  R  V  F  K  E  Q  W  T  Y  D  Y  F  F  T  Q  Y  K  E  R

gctgtttgtctgatatgccagaatatagtgtctgtgttcaaggaatacaatttgcgtcgacactacgaaact

A  V  C  L  I  C  Q  N  I  V  S  V  F  K  E  Y  N  L  R  R  H  Y  E  T

caacataaagataaatatgattgtttggtcggccaagtgagaaaagataaaatattaaaactgaaaaatgga

Q  H  K  D  K  Y  D  C  L  V  G  Q  V  R  K  D  K  I  L  K  L  K  N  G

ttgacaactcagcaaaatacttttgtgaagcaaaagcagctaaatatatcatcattgcgagcaagttttcaa
```

```
L  T  T  Q  Q  N  T  F  V  K  Q  K  Q  L  N  I  S  S  L  R  A  S  F  Q
gttgccaagctcatagcgcgcactggcagaccattcgtagagggagaatttgttaaagaatgccttctttct
V  A  K  L  I  A  R  T  G  R  P  F  V  E  G  E  F  V  K  E  C  L  L  S
gttgccaaagagatgtgtccagagaaggctgatttatttagtacagtgagtctttcaggacctacaattaca
V  A  K  E  M  C  P  E  K  A  D  L  F  S  T  V  S  L  S  G  P  T  I  T
cgaaggattgaagaaatgggagaaaatttgcatctgcatttgcaaaactcctcaaaaaaactatgctatttt
R  R  I  E  E  M  G  E  N  L  H  L  H  L  Q  N  S  S  K  K  L  C  Y  F
tcattggcactcgacgaaagcaatgatgttcgtgattctgcacaacttctaattttcattcgtgggacaaat
S  L  A  L  D  E  S  N  D  V  R  D  S  A  Q  L  L  I  F  I  R  G  T  N
gaatatttcgaagtcacagaggagcttgctgcactgaaaagcatcaaaggaacaacaacaggagaggatatc
E  Y  F  E  V  T  E  E  L  A  A  L  K  S  I  K  G  T  T  T  G  E  D  I
tatgaaaaagtttgccaaactatgaatgatttggagctggactgggctaaactagccagtgtgacaactgat
Y  E  K  V  C  Q  T  M  N  D  L  E  L  D  W  A  K  L  A  S  V  T  T  D
ggtgctcctagcatggtggggtctatgaaaggagtggttgcacgcattaaaaaagagatggacaaacacaac
G  A  P  S  M  V  G  S  M  K  G  V  V  A  R  I  K  K  E  M  D  K  H  N
cattcacatccaatagccatacactgcctcatccaccaacaagcactgtgttgtaaatcattgaagttggac
H  S  H  P  I  A  I  H  C  L  I  H  Q  Q  A  L  C  C  K  S  L  K  L  D
tctgtcatgaaaattgtgatatcttgtgttaacttcattagagctcatgcactaaaccacagacagtttcag
S  V  M  K  I  V  I  S  C  V  N  F  I  R  A  H  A  L  N  H  R  Q  F  Q
gaatttctgtctgagctaaatgttgcctatgaagatattctgtaccacacagaagtccgttggctgagtcga
E  F  L  S  E  L  N  V  A  Y  E  D  I  L  Y  H  T  E  V  R  W  L  S  R
gggagagttttgaaacgtttttatgacttacttccacaggtttctgcttttatgctttcgaaaaacaaagaa
G  R  V  L  K  R  F  Y  D  L  L  P  Q  V  S  A  F  M  L  S  K  N  K  E
gtaccagagctcaaagatgcagaatggaaatggcaccttgcctttctgacagatgtaacagagctactcaac
V  P  E  L  K  D  A  E  W  K  W  H  L  A  F  L  T  D  V  T  E  L  L  N
agtttcaatgttcaacttcaaggaaaggggaagctcatctgtgatatgcattcacatgtgaaagcatttcaa
S  F  N  V  Q  L  Q  G  K  G  K  L  I  C  D  M  H  S  H  V  K  A  F  Q
gtaaaattagacctcctcattaaacaagtgaaggaggaaaacttctgccatctccccacgactcaaaacctt
V  K  L  D  L  L  I  K  Q  V  K  E  E  N  F  C  H  L  P  T  T  Q  N  L
ttggcggaaaaaccagcagttgcattcccaaacaaaacatgtgtggatttactagaaattttgcaaaaggag
L  A  E  K  P  A  V  A  F  P  N  K  T  C  V  D  L  L  E  I  L  Q  K  E
tttcaatttagatttaaagagcttcatctccatgaacaggacatacagcttttccggaacccattttctgtt
F  Q  F  R  F  K  E  L  H  L  H  E  Q  D  I  Q  L  F  R  N  P  F  S  V
```

Figure 2.15. (continued).

gacattgaaattgttgatccgatttaccaaatggaattggctgaactacagaattgtgactctctgaaagac

D I E I V D P I Y Q M E L A E L Q N C D S L K D

gcattcaaatcaagcagccttactaatttctatgcatctctcccctctgagacatatcctaatctcaggaac

A F K S S S L T N F Y A S L P S E T Y P N L R N

catgcactcaaaattgcaaccatctttggcagcacctatgtctgtgaacagactttttcccgaatgaaacat

H A L K I A T I F G S T Y V C E Q T F S R M K H

ctgaaatctccaaccagatccagactaactgatgaacacttgcatcacttgctacgactagcagtgacaaat

L K S P T R S R L T D E H L H H L L R L A V T N

atggaaccggatattgaccatctcattagccaaaagcaggcccatacttcccattgaAATACTGGTAAGTTT

M E P D I D H L I S Q K Q A H T S H *

CTTTATTTAACTTTACTTGTTCTTCATTTTAAATATTGTATTTGTTCCCGTTTTGTTTTTTTTACTTCATAA

TAAGATATGTGCAGTGTGCATAGGAATTTGTTCATAGTTTTTTTTTTTTTTAAACTATAGTCCGGCCCTCCA

ATGGTCTGAGGGACAGTGAACTGGCCCCCTGTTTAAAAA**GTTTGAGGACCCCTG** **2790 bp**

Figure 2.15. (continued).

2.3.3. Sequence Evolution and Phylogenetic Implications

The following calculations are based only on protein coding exon sequences of WPWFs. Nucleotide frequencies of exons 1-14 and the corresponding transition/transversion rate (R) were estimated under the discrete GTR+G model (5 categories, G=0.05) with MEGA6.06 (Tamura et al., 2013). All positions with less than 95 % site coverage were eliminated resulting in a final data set of 1587 positions. The estimated nucleotide frequencies were A=23.7 %, T=25.2 %, C=17.8 %, and G=22.3 %; the R-value amounted to 0.73, which was used as an input parameter in a codon-based z-test to test whether positive selection is operating on the gene. The z-test was performed for all sequences (scope=overall average) on the basis of the modified Nei-Gojobori method (Nei and Kumar, 2000) as implicated in MEGA6.06 under the alternative hypothesis $d_N > d_S$ (positive selection) where d_N is the number of non-synonymous substitutions per non-synonymous site and d_S is the number of synonymous substitutions per synonymous site. As a result, the null hypothesis ($d_N = d_S$) could not be rejected ($p=0.161$), i.e. sequence evolution of protein coding exons is expected to follow a neutral model of sequence evolution.

Based on the full sequence length of 1815 bp (from the start to the first stop codon), 58 variable sites (3.2%) were found; 34 (1.9%) were parsimony informative. The corresponding values for the 605 aa are 43 (7.1%) and 27 (4.5%), respectively. Pairwise sequence comparisons revealed 8 to 39 nucleotide and 7 to 33 aa differences (Appendices 2.3 and 2.4).

ML analysis of albumin exons clearly supports the sister group relationship of *P. lessonae* and *P. bergeri* and indicates a close relationships of *P. ridibundus* and *P.* cf. *bedriagae* from Anatolia as already suggested by previous studies (e.g. Plötner et al., 2010; Akin et al., 2010b; Plötner et al., 2012). Moreover, *P. epeiroticus* is closely related to *P. ridibundus/P.* cf. *bedriagae* which coincides with the results of phylogenetic reconstructions based on the first intron of the SA gene (Plötner et al., 2009; 2012) and our mtDNA phylogenies (e.g. Plötner, 1998, Plötner and Ohst 2001; Plötner et al., 2010; Akın et al., 2010b). In contrast to former hypotheses, however, the SA exon data do not support a sister group relationship between *P. shqipericus* and *P. lessonae+P. bergeri*. Instead, *P. shqipericus* represents a distinct lineage; this corresponds to the results of protein electrophoretic investigations (Beerli et al., 1996).

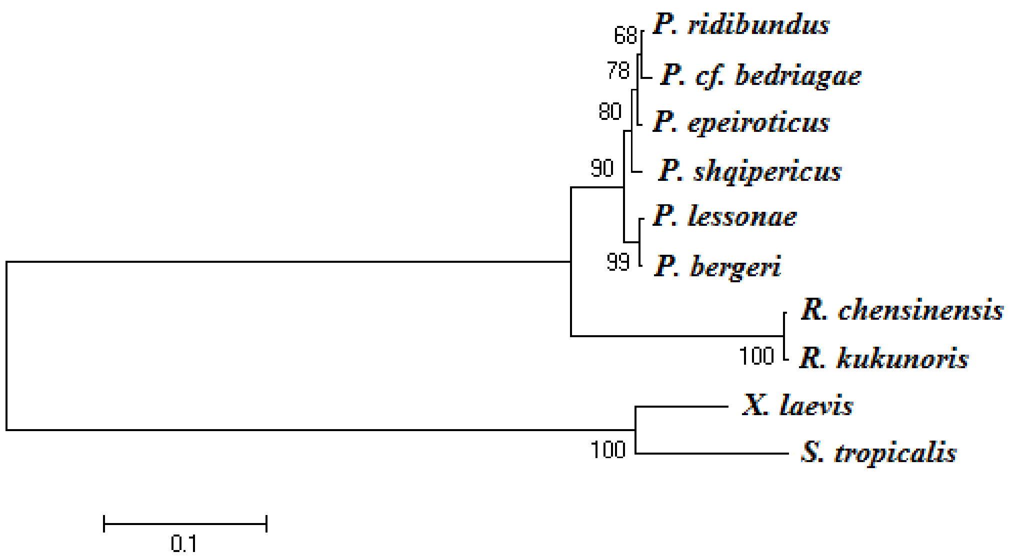


Figure 2.16. Phylogenetic relationships of main western Palearctic water frog species based on nucleotide sequence of protein-coding albumin exons. Numbers on the branches show bootstrap values.

2.4. References

Akın, Ç., Bilgin C.C., Beerli, P., Westaway, R., Ohst, T., Litvinchuk, S.N., Uzzell, T., Bilgin, M., Hotz, H., Guex, G.-D., Plötner, J. (2010b) Phylogeographic patterns of genetic diversity in eastern Mediterranean water frogs were determined by geological processes and climate change in the Late Cenozoic. *J Biogeogr* 37: 211–2124.

Arensburger, P., Hice, R.H., Zhou, L., Smith, R.C., Tom, A.C., Wright, J.A., Knapp, J., O'Brochta, D.A., Craig, N.L., Atkinson, P.W. (2011) Phylogenetic and functional characterization of the hAT transposon superfamily. *Genetics* 188: 45-57.

Beerli, P., Hotz, H. & Uzzell, T. (1996) Geological dated sea barriers calibrate protein clock for Aegean water frogs. *Evolution* 50**:** 1676-1687.

Benjamin, B., Yves, B., Corinne, A.-G. (2007) Assembly of the Tc1 and mariner transposition initiation complexes depends on the origins of their transposase DNA binding domains. *Genetica* 130: 105-120.

Benson, G. (1999) Tandem repeats finder: a program to analyze DNA sequences. *Nucleic Acids Res* 27 (2): 573-580.

Binder, R., Horowitz, J.A., Basilion, J.P., Koeller, D.M., Klausner, R.D., Harford, J.B. (1994) Evidence that the pathway of transferrin receptor mRNA degradation involves an endonucleolytic cleavage within the 3'UTR and does not involve poly(A) shortening. *EMBO J* 13: 1969-1980.

Bowes, J.B., Snyder, K.A., Segerdell, E., Gibb, R., Jarabek, C., Noumen, E., Pollet, N., Vize, P.D. (2008) Xenbase: a Xenopus biology and genomic resource. *Nucleic Acids Res* 36(Database issue): D761-767.

Brezinsky, L., Wang, G.V., Humphreys, T., Hunt, J., (1990) The transposable element Uhu from Hawaiian Drosophila-member of the widely dispersed class of Tc1-like transposons. *Nucleic Acids Res* 18: 2053– 2059.

Bucher, P. (1990) Weight matrix descriptions of four eukaryotic RNA polymerase II promoter elements derived from 502 unrelated promoter sequences. *J Mol Biol* 212: 563–578.

Calvi, B.R., Hong, T.J., Findley, S.D., Gelbart, W.M (1991) Evidence for a common evoloutionary origin of inverted repeat transposons in Drosophila and plants: hobo, Activator and Tam3. *Cell* 66: 465-471.

Cereghini, S., Raymondjean, M., Carranca, A.G., Herbomel, P., Yaniv, M. (1987) Factors involved in control of tissue-specific expression of albumin gene. *Cell* 50: 627-638.

Cereghini, S., Blumenfeld, M., Yaniv, M. (1988) A liver-specific factor essential for albumin transcription differs between differentiated and dedifferentiated rat hepatoma cells. *Gene Dev* 2: 957-974.

Church, D.M., Goodstadt, L., Hillier, L.W., Zody, M.C., Goldstein, S. et al. (2009) Lineage-specific biology revealed by a finished genome assembly of the mouse. *PLoS Biol* 7(5): 1-16.

Chénais, B., Caruso, A., Hiard, S., Casse, N. (2012) The impact of transposable elements on eukaryotic genomes: from genome size increase to genetic adaptation to stressful environments. *Gene* 509: 7-15.

Clark, K.J., Carlson, D.F., Leaver, M.J., Foster, L.K., Fahrenkrug, S.C. (2009) Passport, a native Tc1 transposon from flatfish, is functionally active in vertebrate cells. *Nucleic Acids Res* 37(4): 1239-1247.

Conway, L., Wickens, M. (1985) A sequence downstream of AAUAAA is required for formation of simian virus 40 late mRNA 3' termini in frog oocytes. *Proc Natl Acad Sci* 82: 3949-3953.

Danckwardt, S., Kaufmann, I., Gentzel, M., Foerstner, K.U., Ganzert, A.S., Gehring, N.H., Neu-Yilik, G., Bork, P., Keller, W., Wilm, M., Hentze, M.W., Kulozik, A.E. (2007) Splicing factors stimulate polyadenylation via USEs at non-canonical 3'end formation signals. *EMBO* 26: 2658-2669.

Edgar, R.C. (2004) MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res* 32(5): 1792-1797.

Fanali, G., Masi, A., Trezza, V., Marino, M., Fasano, M., Ascenzi, P. (2012) Human serum albumin: from bench to bedside. *Mol Aspects Med* 33: 209-290.

Felsenstein, J. (1985) Confidence limits on phylogenies: An approach using the bootstrap. *Evolution* 39:783-791.

Gibbs, R.A., Weinstock, G.M., Metzker, M.L., Muzny, D.M. et al., (2004) Genome sequence of the brown norway rat yields insights into mammalian evolution. *Nature* 428 (6982): 493-521.

Graber, J.H., Cantor, C.R., Mohr, S.C., Smith, T.F. (1999) In silico detection of control signals: mRNA 3'end-processing sequences in diverse species. *Proc Natl Acad Sci* 96: 14055-14060.

Goldberg, M.L. (1979) Sequence analysis of *Drosophila* histone genes. Ph.D. dissertation, Stanford University, California.

Gu, H., Gupta, J.D., Schoenberg, D.R. (1999) The poly(A)-limiting element is a conserved cis-acting sequence that regulates poly(A) tail length on nuclear pre-mRNAs. *Pro Natl Acad Sci* 96: 8943-8948.

Gupta, J.D., Gu, H., Chernokalskaya, E., Gao, X., Schoenberg, D.R. (1998) Identification of two cis-acting elements that independently regulate the length of poly(A) on Xenopus albumin pre-mRNA. *RNA* 4: 766-776.

Hickman, A.B., Perez, Z.N., Zhou, L., Musingarimi, P., Ghirlando et al., (2005) Molecular architecture of a eukaryotic transposase. *Nat Struct Mol Biol* 12: 715-721.

Hillier, L.W., Miller, W., Birney, E., Warren, W. et al. (2004) Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. *Nature* 432 (7018): 695-716.

Hillier, L.W., Graves, T.A., Fulton, R.S., Fulton, L.A., Pepin, K.H. et al. (2005) Generation and annotation of the DNA sequences of human chromosomes 2 and 4. *Nature* 434 (7034): 724-731.

Hu, J., Lutz, C.S., Wilusz, J., Tian, B. (2005) Bioinformatic identification of candidate cis-regulatory elements involved in human mRNA polyadenylation. *RNA* 11: 1485–1493.

Izsvak, Z., Ivics, Z. & Hackett, P. B. (1995) Characterization of a Tc1-like transposable element in zebrafish (Danio rerio). *Mol Gen Genet* 247: 312–322.

Jurka, J., Kapitonov, V.V., Pavlicek, A., Klonowski, P., Kohany, O., Walichiewicz, J. (2005) Repbase Update, a database of eukaryotic repetitive elements. *Cytogenet Genome Res* 110:462-467.

Katoh, K., Kuma, K.-I., Toh, H., Miyata, T. (2005) MAFFT version 5: improvement in accuracy of multiple sequence alignment. *Nucleic Acids Res* 33(2): 511-518.

Kazazian, H.H. (2004) Mobile elements: drivers of genome evolution. *Science* 303: 1626-1632.

Kempken, F., Windhofer, F. (2001) The hAT family: a versatile transposon group to plants, fungi, animals, and man. *Chromosoma* 110: 1-9.

Kugler, W., Wagner, U., Ryffel, G.U. (1988) Tissue specifity of liver gene expression: a common liver-specific promoter element. *Nucleic Acids Res* 16 (8): 3165-3174.

Leaver, M. (2001) A family of Tc1-like transposons from the genomes of fishes and frogs: evidence for horizontal transmission. *Gene* 271: 203-214.

Lukacs, M.F., Harstad,H., Bakke,H.G., Beetz-Sargent,M., McKinnel, L., Lubieniecki, K.P., Koop, B.F., Grimholt, U. (2010) Comprehensive analysis of MHC class I genes from the U-, S-, and Z- linaeges in Atlantic salmon. *BMC Genomics* 11: 154.

MacDonald, C.C., Wilusz, J. Shenk, T. (1994) The 64-kilodalton subunit of the CstF polyadenylation factor binds to pre-mRNAs downstream of the cleavage site and influences cleavage site location. *Mol Cell Biol* 14: 6647-6654.

Mantovani, R. (1998) A survey of 178 NF-Y binding CCAAT boxes. *Nucleic Acids Res* 26 (5): 1135-1143.

Miller, L.L., Bly, C.G., Watson, M.L., Bale, W.F. (1951) *J Exp Med* 95: 531.

Miller, L.L., Bale, W.F. (1954) *J Exp Med* 99: 125.

Miskey, C., Izsvak, Z., Plasterk, R.H.A., Ivics, Z., (2003) The Frog Prince: a reconstructed transposon from Rana pipiens with high transpositional activity in vertebrate cells. *Nucleic Acids Res* 31: 6873-6881.

Minghetti, P.P., Ruffner, D.E., Kuang, W.-J., Dennison, O.E., Hawkins, J.W., Beattie, W.-G., Dugaiczyk, A. (1986) Molecular structure of the human albumin gene is revealed by sequence within q11-22 of chromosome 4. *J Biol Chem* 261: 6747-6757.

Mount, S.M. (1982) A catalogue of splice junction sequences. *Nucleic Acids Res* 10(2): 459-472.

Munoz-Lopez, M. Garcia-Perez, J.L. (2010) DNA transposons: nature and applications in genomics. *Curr Genomics* 11: 115-128.

Murthy, K.G. Manley, J.L. (1995) The 160-kD subunit of human cleavage-polyadenylation specifity factor coordinates pre-mRNA 3'end formation. *Gene Dev* 9: 2672-2683.

Nei, M. & Kumar, S. (2000) *Molecular Evolution and Phylogenetics*. Oxford University Press, New York.

Novick, P., Smith, J., Ray, D., Boissinot, S. (2010) Independent and parallel lateral transfer of DNA transposons in tetrapod genomes. *Gene* 449: 85-94.

Pace, J.K., 2nd, Gilbert, C., Clark, M.S., Feschotte, C. (2008) Repeated horizontal transfer of a DNA transposon in mammals and other tetrapods. *Proc Natl Acad Sci USA* 105: 17023-17028.

Peters, T.Jr., Anfinsen, C.B. (1950) Production of radioactive serum albumin by liver slices. *J Biol Chem* 182: 171-179.

Plasterk, R., Izsvak, Z., Ivics, Z. (1999) Resident aliens: the Tc1/mariner superfamily of transposable elements. *Trends Genet* 15(8): 326-332.

Plötner, J. (1998) Genetic diversity in mitochondrial 12S rDNA of western Palearctic water frogs *(Anura, Ranidae)* and implications for their systematics. *J Zool Syst Evol Research* 36: 191-201.

Plötner, J. (2005) Die westpaläarktischen Wasserfrösche. Von Märtyrern der Wissenschaft zur biologischen Sensation. Laurenti Verlag, Bielefeld.

Plötner, J., Ohst, T. (2001) New hypotheses on the systemtics of the western Palearctic water frog complex (Anura, Ranidea). *Mitt Mus Natkd Berl Zool Reihe* 77 (1): 5-21.

Plötner, J., Köhler, F., Uzzell, T., Beerli, P. (2007) Molecular systematics of amphibians. In: Heatwole, H., Tyler, M. (Eds.), Amphibian Biology, vol. 7. Phylogeny and Systematics. Surrey Beatty & Sons, Chipping Norton, pp. 2672–2756.

Plötner, J., Köhler, F., Uzzell, T., Beerli, P., Schreiber, R., Guex, G.-D. & Hotz, H. (2009) Evolution of serum albumin intron-1 is shaped by a 5' truncated non-long terminal repeat retrotransposon in western Palearctic water frogs (Neobatrachia). *Mol Phylogenet Evol* 53: 784–791.

Plötner, J., Uzzell, T., Beerli, P., Akın, Ç., Bilgin, C.C., Haefeli, C., Ohst, T., Köhler, F., Schreiber, R., Guex, G.-D., Litvinchuk, A. N., Westaway, R., Reyer, H.-U. & Hotz, H. (2010) Genetic divergence and evolution of reproductive isolation in eastern Mediterranean water frogs. Evolution in action. Case studies in adaptive radiation and the origin of biodiversity. Special volume from the SPP 1127 ‘Radiations – Genesis of Biological diversity’ of the DFG (ed. by M. Glaubrecht), pp. 373–403. Springer, Heidelberg, Berlin.

Plötner, J., Baier, F., Akın, Ç., Mazepa, G., Schreiber, R., Beerli, P., Litvinchuk, S.N., Bilgin, C.C., Borkin, L., Uzzell, T. (2012) Genetic data reveal that water frogs of Cyprus (genus Pelophylax) are an endemic species of Messinian origin. *Zoosyst Evol* 88: 261-283.

Pocwierz-Kotus, A., Burzynski, A., Wenne, R. (2007) Family of Tc1-like elements from fish genomes and horizontal transfer. *Gene* 390: 243-251.

Proudfoot, N.J. (2011) Ending the message: poly(A) signals then and now. *Gene Dev* 25: 1770-1782.

Rebollo, R., Romanish, M.T., Mager, D.L. (2012) Transposable elements: an abundant and natural source of regulatory sequences for host genes. *Annu Rev Genet* 46: 21-42.

Reed, R. and Maniatis, T. (1985) Intron sequences involved in lariat formation during pre-mRNA splicing. *Cell* 41: 95-105.

Rothschild, M.A., Oratz, M., Schreiber, S.S. (1988) Serum albumin. *Hepatology* 8: 385–401.

Rubin, E., Lithwick, G., Levy, A.A. (2001) Structure and evolution of the hAT transposon superfamily. *Genetics* 158: 949-957.

Ruskin, B., A. Krainer, T. Maniatis, Green, M.R. (1984) Ex- cision of an intact intron as a novel lariat structure during pre-mRNA splicing in vitro. *Cell* 38: 317-331.

Ryffel, G.U., Kugler, W., Wagner, U., Kaling, M. (1989) Liver specific gene transcription in vitro: the promoter elements HP1 and TATA box are necessary and sufficient to generate a liver-specific promoter. *Nucleic Acids Res* 17(3): 939-953.

Sargent, T.D., Jagodzinski, L.L., Yang, M., Bonner, J. (1981a) Fine structure and evolution of the rat serum albumin gene. *Mol Cell Biol* 1: 871-883.

Sargent, T.D., Yang, M., Bonner, J. (1981b) Nucleotide sequence of cloned rat serum albumin messenger RNA. *Proc Natl Acad Sci USA* 78: 243-246.

Schorpp, M., Döbbeling, U., Wagner, U., Ryffel, G.U. (1988a) 5'-Flanking and 5'-Proximal Exon Regions of the Two Xenopus Albumin Genes: Deletion Analysis of Constitutive Promoter Function. *J Mol Biol* 199: 83-93.

Schorpp, M., Kugler, W., Wagner, U., Ryffel, U. (1988b). Hepatocyte-specific promoter element HP1 of the Xenopus albumin gene interacts with transcriptional factors of mammalian hepatocytes. *J Mol Biol* 202: 307-320.

Schwarz, G.E. (1978) Estimating the dimension of a model. *Annals of Statistics* 6(2): 461–464

Solovyev, V.V., Shahmuradov, I.A., Salamov, A.A. (2010) Identification of promoter regions and regulatory sites. *Methods Mol Biol.* 674: 57-83.

Tamura, K., Stecher, G., Peterson, D., Filipski, A., and Kumar, S. (2013) MEGA6: Molecular Evolutionary Genetics Analysis Version 6.0. *Mol Biol Evol* 30: 2725-2729.

Tang, H. (2007) Genome assembly, rearrangement, and repeats. *Chem Rev* 107: 3391-3406.

Tavaré, S. (1986) "Some Probabilistic and Statistical Problems in the Analysis of DNA Sequences". *Lectures on Mathematics in the Life Sciences (American Mathematical Society)* 17: 57–86.

Thompson, J.D., Higgins, D.G., Gibson, T.J. (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res* 22 (22): 4673-4680.

Tunner, H.G. (1979) The inheritance of morphology and electrophoretic markers from homotypic crosses of the hybridogenetic *Rana esculenta*. *Mitteilungen aus dem zoologischen Museum in Berlin,* 55 (1): 89-109.

UTRdb and UTRsite (RELEASE 2010) a collection of sequences and regulatory motifs of the untranslated regions of eukaryotic mRNAs. *Nucleic Acids Res* 38 (Database Issue): D75-D80.

Uzzell, T. (1979b) Immunological distances between the serum albumins of Rana ridibunda and Rana lessonae. *Proceedings of the Academy of Natural Sciences of Philadelphia,* 130: 1-10.

Uzzell, T. (1982) Immunological relationship of western Palearctic water frogs (Salientia: Ranidae). *Amphibia-Reptilia* 3: 135-143.

Uzzell, T., Hotz, H. (1979) Electrophoretic and morphological evidence for two forms of green frogs (Rana esculenta complex) in peninsular Italy (Amphibia, Salientia). *Mitteilungen aus dem zoologischen Museum in Berlin,* 55 (1): 13-27.

Westley, B., Wyler, T., Ryffel, G., Weber, R. (1981) *Xenopus laevis* serum albumins are encodedin two closely related genes. *Nucleic Acids Res* 9(15):3557-3574.

Yazawa, R., Cooper, G.A., Hunt, P., Beetz-Sargent, M., Robb, A.,Conrad, M., McKinnel, L., So, S., Jantzen, S., Phillips, R.B., Davidson, W.S., Koop,B.F. (2008) Striking antigen recognition diversity in the Atlantic salmon T-cell receptor alpha/delta locus. *Dev Comp Immunol* 32 (3): 204-212.

Zhang, Y.-X., Lai, R., Lee, W.-H., Zhang, Y. (2005) Frog albumin is expressed in skin and characterized as a novel potent trypsin inhibitor. *Protein Sci Sep* 14(9): 2469-2477.

2.5. Appendices

Table 2.3. Comparison of SA exon and intron lengths among distinct vertebrate species. Start and stop site positions of individual exon and intron within the serum albumin gene of *P. lessonae*, the lengths of each exon and intron of the serum albumin gene for *P. lessonae*, *S. tropicalis, X. leavis, G. gallus, R. norvegicus, M. musculus* and *H. sapiens*, and the average lengths of exons and introns of the albumin gene for each species are given in this table.

P.lessonae			**LENGTH (bp)**						
E/ INT	**START**	**STOP**	***P. lessonae***	***S. tropicalis***	***X. laevis***	***G. gallus***	***R. norvegicus***	***M. musculus***	***H. sapiens***
E1	1	116	116	117	117	93	94	125	118
Int1	117	634	518	494	487	1487	704	707	709
E2	635	698	64	67	67	61	58	58	58
Int2	699	1802	1104	636	866	754	912	921	1454
E3	1803	1935	133	133	133	133	133	133	133
Int3	1936	4450	2515	585	717	919	1616	1151	1832
E4	4451	4656	206	206	203	215	212	212	212
Int4	4657	7004	2348	541	604	705	952	657	549
E5	7005	7137	133	133	133	133	133	133	133
Int5	7138	10080	2943	1112	878	1066	903	888	824
E6	10081	10178	98	98	98	98	98	98	98
Int6	10179	12023	1845	561	385	1277	1519	1372	1587
E7	12024	12153	130	130	130	130	130	130	130
Int7	12154	12730	577	618	620	879	986	1007	1293
E8	12731	12939	209	215	215	215	214	215	215
Int8	12940	17408	4469	660	718	549	747	806	1399
E9	17409	17541	133	133	133	133	133	133	133
Int9	17542	17636	95	211	624	828	1070	1106	1088
E10	17637	17734	98	98	98	98	98	98	98
Int10	17735	20907	3173	1767	792	137	1145	1166	1177
E11	20908	21046	139	139	139	139	139	139	139
Int11	21047	25794	4748	946	1310	518	327	317	418
E12	25795	26018	224	224	224	224	224	224	224
Int12	26019	27796	1778	1090	766	530	1000	1882	1192
E13	27797	27929	133	133	133	133	133	133	133
Int13	27930	30742	2813	141	142	1019	574	569	614
E14	30743	30788	46	55	65	57	62	68	68
Int14	30789	32317	1529	921	935	276	1062	1123	770
E15	32318	32460	143	134	135	30	139	144	163
Mean ±SD	Exons		133,67 ±49,71	134,33 ±48,92	134,87 ±47,50	126,13 ±57,75	133,33 ±50,57	136,2 ±49,01	137,00 ±49,62
	Introns		2175,36 ±1399,94	734,5 ±412,99	703,14 ±274,17	781,71 ±369,56	901,21 ±407,40	976,57 ±382,06	1064,71 ±426,52

Table 2.4. Alignment of *P. lessonae* scaffold 10.7 with the serum albumin cDNA of *P. shqipericus*. Yellow coloured regions indicate exonic positions, grey coloured regions show intronic sequences, green coloured areas represent DNA transposons belonging distinct families; pink coloured regions indicate distinct types of LTR and non-LTR retroelements; blue coloured regions show simple repeats and low comlexity elements; and conserved regulatory motifs in both 5' and 3' regions of the albumin genes are also shown.

```
U40452_P._shqipericus         ---------------------------------------------------------------------------------------------------- [  100]
scaffold39565_10.7_P._lessonae AACACTTGGTTCTAAACTGTATACACATGCAATAAACATAATGCATACAGGAAGGACAATATACAGTGGCTGTGTTTGCCACACTGCTCCCCCAGAAGCA [  100]
U40452_P._shqipericus         ---------------------------------------------------------------------------------------------------- [  200]
scaffold39565_10.7_P._lessonae AGCCGGCATACACAGTCTGATCCTAATGGATCGTCTTGGGGATGTCCGGGGAGTACTCACGGATCATTTGTCAATGTCTGTTTGCCTGGATAATTCGTTG [  200]
U40452_P._shqipericus         ---------------------------------------------------------------------------------------------------- [  300]
scaffold39565_10.7_P._lessonae GCGTTGCCGTTTTGCTTCCCAGGGCAGTAGTGGATGATAAAGTCAAAAGGCTGCAGCGCCAAACTCCAGTATCTTCTGGCCCATAGTCTGTCGGTAGGAG [  300]
U40452_P._shqipericus         ---------------------------------------------------------------------------------------------------- [  400]
scaffold39565_10.7_P._lessonae GCTTGCGCACAGTCCCCTCCAAAACGCACAGTGACAGTGGGTTCTGTCACACTGTTCTGTCACACAGGGCAATCTTAGAAGAAAACCTGTTAGAGTCTGC [  400]
U40452_P._shqipericus         -------------------------------------------Tc1-10_XT------------------------------------------------ [  500]
scaffold39565_10.7_P._lessonae AAAAGACTTGAGACTGGGGCGGAGGTTCACCTTCCAGCAGGGGAACGACCCTAAACATACAGCCAGAGCTACAATGAAATGGTTTAAATCAAAGCATATT [  500]
U40452_P._shqipericus         ---------------------------------------------------------------------------------------------------- [  600]
scaffold39565_10.7_P._lessonae CATGTGTTAGAATGGCCCAGTCAAAGTCCAGACCTAGATCCAATTGAGAATCGGTGGCAAGACTTGAAAATTGGAGTAAACTGGAGTGGACTGGAGTAAA [  600]
U40452_P._shqipericus         ---------------------------------------------------------------------------------------------------- [  700]
scaffold39565_10.7_P._lessonae TGCGAGGAATGTTTGAGAGTTTAGGAGCCCAAAGGAATTGGTTTTTATACAACTGCTCCTCCTTCCTCTTTGATCTTCCTACATGCTAATGATGAAGGTC [  700]
U40452_P._shqipericus         ---------------------------------------------------------------------------------------------------- [  800]
scaffold39565_10.7_P._lessonae TGGTAAGCAGCCTCTTTAGAGCACTTTGTTTGGTGTTGTGTGCTATCACTTGACACAATCATCGGTGATGGGATCTTCAGTGTATGGACTCTTAAATATC [  800]
U40452_P._shqipericus         ---------------------------------------------------------------------------------------------------- [  900]
scaffold39565_10.7_P._lessonae ATCAGAATATAATTTACTCAGCACTGCTTGTTTGGATTTTTACTATTAATCTTTCTGCTATCAACAGATTACTGCTAGCTGCTTTAGAGTGACATTTTAT [  900]
U40452_P._shqipericus         ---------------------------------------------------------------------------------------------------- [ 1000]
scaffold39565_10.7_P._lessonae GGTTCTTTCAGATGGAGCGCAGATGTTATTTGTGTTAAGACTTGAAAATTGCTGTTCGTAGACACTCTCCATCCAATCTGACAGAGCTTGAGCTATTTTG [ 1000]
U40452_P._shqipericus         ---------------------------------------------------------------------------------------------------- [ 1100]
scaffold39565_10.7_P._lessonae CAAAGAAGAATGGGCAAAAATGTCCCTCTCTAGATGTGCAAAGCTGGTAGAGACATCCCCAAAAAGACTTGCATCTGTAATTACAGCCAAATTCTAGAAA [ 1100]
```

Table 2.4. (continued).

```
                                                                       Tc1-10_XT
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 1200]
scaffold39565_10.7_P._lessonae GTATTGACTCAGGGGGCTGAATATAAATGCACGCCACACTTAGACGCCAAAAGATATTTATTTGTAAAATATGTTAAAAACCATTTATCATTTTCCTTCC [ 1200]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 1300]
scaffold39565_10.7_P._lessonae ACTTCACTATTATGTGCCACTTTGTGTCGGTCTATCACATAAAATCCCAATAAAATACATTTACGTTTTTGGTTGTAACATAACAAAATGTGGAAGATTT [ 1300]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 1400]
scaffold39565_10.7_P._lessonae CAAGGGGTGTGAATACTTTCAAGGCATTGTATACGGAAATGAGGTGGCTCTACTGCATCAGATCATGTACTAGATACATGATCTGGCACTTCCAGGAAGG [ 1400]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 1500]
scaffold39565_10.7_P._lessonae GGGTGTGTGCGCGCACTGCTGGGGACCCAGCCCTTTTTGTGATTAAACACAGCAGATGTCGATCAGCAGGTGCCAATGGATTACCGCCGGCATCTGCCAA [ 1500]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 1600]
scaffold39565_10.7_P._lessonae TCACCGGGGAATTCACACAGGACAGAGCCATGCCTATGTAAACAAGGCAGAGCTCTGTCATGTCAGTTAAGGAAGTAATGGATTTTCTTTCCCCGCTAAG [ 1600]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 1700]
scaffold39565_10.7_P._lessonae CAGGGAATAAAATCCATTACCTAATAGAATAAATATCTTAATCACCGCAACTAAATATACAAAAAAATATATATAAAAAATTGTAATTTTAAAGTTGTGA [ 1700]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 1800]
scaffold39565_10.7_P._lessonae ATTGATTGCTGCCAATACTCCACACGTATATTCACCTCACTTTCAATAATATCAGTGTCAAATTAGTACAGTGCAATCATCTATCTCAATATTGCGATAT [ 1800]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 1900]
scaffold39565_10.7_P._lessonae ATAAAAAATCACTAAATATGTGTACACATATAACCTCCATATATTTCACAATCTGTGACAAAATATAACTTGCTCAAGTGAAAATTCCAAATTCATATGC [ 1900]
                                                                  (AATA)n
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 2000]
scaffold39565_10.7_P._lessonae ATTCATATGCACAAGATATATACCAGTGAATAAATAATATATATATAAAAAAAAAAAAGAGAGTCCAAAACGATGAAACCATCCAGTGAAAATAAATGAG [ 2000]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 2100]
scaffold39565_10.7_P._lessonae TCCCAAAAGCGAGTGTTCTTGCCACCTCTGTGTATAACAATCAACTAAAAAGCAGGTGCTCATGTAATCCACCTCCAGTATTCACTAGCAGCTCACCTCC [ 2100]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 2200]
scaffold39565_10.7_P._lessonae GGCTTTGACTCCTATTTCAGCAGAGAGTCAAAGTATAAAAAAGTATAAAATAGGCTCACTCACATTCTGCAGGAGCTGACAGGCAGCTGATTTTACCCTA [ 2200]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 2300]
scaffold39565_10.7_P._lessonae TGACCATTACTATTAGATGGTGGTAAGTCGGTGAATATTGCTTTATGCTGTATATAGCTGGCACGACTTGCAGTGCTGTTCGAAGTGAGTGAGCCTATTT [ 2300]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 2400]
scaffold39565_10.7_P._lessonae TATACTTTTTTTATAATAAATCTGCCTTTACGGAGAGCACTAGATGGTATGTCTTTTGTTTTATATGGCCGAGTAATATACAAGCACCGCATTAAGGAGA [ 2400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 2500]
                                                                                              (TATTT)n
scaffold39565_10.7_P._lessonae GAGTGGGTTTCTGAAATACCCAGGAACATCCATTCATTCACATACGTTTTAGACTATATATTTTATTTTTTTTACATTATTTATTCACTGGTATATATCT [ 2500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 2600]
scaffold39565_10.7_P._lessonae TGTGCATATGAATGCATGTGAATTTGAAGTTTTAACTTGAGCAAGTATTGCTCAAGTCATTTTGTCACAGATTGTGAAATGTATGGAGGTTATATGTGTA [ 2600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 2700]
scaffold39565_10.7_P._lessonae CACATATTTAGTGATTTTTTTTATATATATGACACAATATTGAGATAGTTGATTGCGCTGTAGTAATTTGACACTGATAAAATCCATTACTTGCCTTAGT [ 2700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 2800]
scaffold39565_10.7_P._lessonae AAAAGCACCTCACACAGTACACCACAACACTGTTAACTATATTAAATGTATTAGTGTCACTGGTTCTCAAAAAATGTCAAAAGTGTCAGTTAGTGTTTGA [ 2800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 2900]
scaffold39565_10.7_P._lessonae ATGTCCACTGCAATATCACAGTCCTGCTATAAGTCACTGATCACCGCCATTACTAGTAAAAAAAAATTTAAAAAAATAATGATACCAGTATACTGTATAT [ 2900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 3000]
scaffold39565_10.7_P._lessonae ACCATAGTTTGCAGGTGCTTTAACTTTTGCGCAAACCAATCATTATATGCTAAATGGTATTTTTTTTTACCCAAAACATGTTACAGAATACATATTGGCC [ 3000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 3100]
scaffold39565_10.7_P._lessonae TAATTTTGTCAAGAAATTAGATTTTTTACATTTTTTTTATTGGATATGTTTTATTTTTTTTTCAAAATTGTCGGTTTTTTGTTTCTAGCGCAAAAAATAA [ 3100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 3200]
scaffold39565_10.7_P._lessonae AAAATGCAGTGGTAATCAATTGTAGCAATATTTCCAGGCATTGGGCCTGATGTGGGTCTGCCATGGTTACCGTTACCACCAACAGCACATTTAAGCTTGT [ 3200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 3300]
scaffold39565_10.7_P._lessonae TTCCCAAGTGTGAGATCTGAGACAATGAACAGTCCGGCATCTTTGGTTTTTAGTTTTATTGTAGGAACTTGGATGGGAGAAGGGAATGAGTGGGATACTC [ 3300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 3400]
scaffold39565_10.7_P._lessonae CTCTGGCTCAACTAGGTACAAATCTGGGACACTTGAGGAAAATGCCGCCTAGCGCTGTCTTGGCACTGGCTGAATGCCGACCAACGCTTACTGGCGCTTG [ 3400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 3500]
scaffold39565_10.7_P._lessonae TAAACCTGATTTGCGGTCTGTGAACTGAAACTTGACTTCTATTGCTTCCTCACAGCTCAAAAGTCCTGTTCACTGCTCCCTGTAGTCCTCTGCAACACTT [ 3500]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 3600]
scaffold39565_10.7_P._lessonae AACACTTTACACTTCAGGGCCCAACCACTGGCACCCCTTTTACTCTTCAGGGTAATCTCTGGCACCCCCTTTCTATATTCCTGTACCGGCTAGCTAGCTC [ 3600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 3700]
scaffold39565_10.7_P._lessonae CTGGATCCCTCTGACCTTCTCCAGAGTGGTCCCCTCTCCTAGGCAGACCCCAGGGGCAGTTTGCAGTACTCATGACTCAGAATACTTTCCTGAAACTCGA [ 3700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 3800]
scaffold39565_10.7_P._lessonae CCCCAACGCTCCACTGGTCCTCCGCACACCTGGATCCTTCTCTGCAGCTCAGCTCAGCCCTGTGTCCACTCAGGCCAGCCGCCTGGGACACCCGATACTT [ 3800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 3900]
scaffold39565_10.7_P._lessonae CCTGACAGGATAGACAGCCATCATCTCCCTCCTGGGACTCTGCTTCCCACCAAAGACAATCTGTCATGTGCTCCCCACAGACTTATATCCCCTCCCAGAG [ 3900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 4000]
scaffold39565_10.7_P._lessonae TGCTGTGCAGCAGAATCTGCCCTTCCAGGATGGATATAAGCCCTGGTGTGCTATTGGTCAGGTTTCCTCCACTGCCCAATGACAGCCCTCATTGGGATAC [ 4000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 4100]
scaffold39565_10.7_P._lessonae AGTGGGGAGACTCCCCAACACAACAGGCACACCTGGGAACACATGCCAGCCTAGCTGAAAACATGGCCCTGCTGATAAGCAGACAAGGCCCACTATACTT [ 4100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 4200]
scaffold39565_10.7_P._lessonae TACCTAGCACCTACATTGGAGGGTGCTACACAATTATCACCAAAATAAATCTCTATTTGTGGAACAAAAAAGGACATAAATGTTGTTTGGGTGAAGTGTG [ 4200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 4300]
scaffold39565_10.7_P._lessonae ACATAACTGCACAATTGTATAGTTGGCTATACTTATTCTATGGATCACAGGAGTGCAGTTCATTTTGCACTCCTGTGACCCATTTTGGCTACTTAGCTGG [ 4300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 4400]
scaffold39565_10.7_P._lessonae TCCAGGTTCAGGAAAGAACGGCAGCTAGCTAGGCCTTTTAGAATGCCACTGAGAGCCTGAGCTAGCCACTCCTGCCCTCTCCCTCCACAGCCCAGCACTC [ 4400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 4500]
scaffold39565_10.7_P._lessonae CAGTGGGTGCTGGAGGAGCAGAGCAGAGAGCCAGTGAGTGGCAGTCACCGCTCTCTGCTTGGAACCAAAGGGGAGAACTGAGCAATCATCAGTGTTTAAT [ 4500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 4600]
scaffold39565_10.7_P._lessonae CGCTTTGTTCTCGGGGTAGAGCCAGCGGTGGACAGTTGCAGCTGGGATCGGTGCTGCAGCCATCTAGGGGAGTATGATTTTTTTTTGCTATTTCCATAAT [ 4600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 4700]
scaffold39565_10.7_P._lessonae TCTCTTTTAAGAAACCTGAGATTGGGCAAAAGTACACTTTCACCATCAGGGAAGCAACCTTACATCATACATCTCAACTGTCCCTCATTTGAATGAACTG [ 4700]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 4800]
scaffold39565_10.7_P._lessonae TCCAATTTTTGAAGCCAGATCCCCCTGTCCCTCTTTCCTTCTCAGTTGTCCCTCTCTTTTGGAAAGATGTATAGGCCTATCTAAGAAGTTAAATTACTTA [ 4800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 4900]
scaffold39565_10.7_P._lessonae ATGGTTTAGCCAATTATTTTTTATTTTTGTTTATTAACTCTTTATGTGCCATGTAAGGGGGGGCATGGCAGGGAGTGTGTCCATTTCCTATGCACCGTGG [ 4900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 5000]
scaffold39565_10.7_P._lessonae GCTATAAGGTGTTCCTTTTTTCATCTCAGTTGAGAGGTATGCTTAAATGCGAATCTAAAACCAAACTGTTGTGGTTTAAAAACAAAATCCTAAAGGGCTT [ 5000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 5100]
                                                                                 TC1-RT
scaffold39565_10.7_P._lessonae GGAATGACCCATTCAACACCCACATATCAATTAAACTGAGATTCTGTGGCAAGACTTTAAAATTCCTGCTCATATATGGTCCCTTTTCAACCTAACAGAG [ 5100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 5200]
scaffold39565_10.7_P._lessonae CGATTTTGTCAAGAATAATTGGAAAAAACTGCAGTAATTGCAGCCAAAGGTGATTCTAGGTTTTGATTCAGGGGGATAAATCATGATGGGAACATAAAAT [ 5200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 5300]
                                                   TC1-PP
scaffold39565_10.7_P._lessonae TACTGTTTTACTTTTTTTTCCTATTACCTTTTATGTTACAATAAAATATATGCATCTATAACAGTCTGAGAGCGGTTACGTAGCACCCTGGGTTCTCATC [ 5300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 5400]
scaffold39565_10.7_P._lessonae CATACAGGTTGAGGGTTTCCAGGTTGTGGGTTTGGTACAGAGAAAACTGGTTGTTCAGTGTTCCCTGGAATTAGTCATGATATACAGTGCCTTGCGAAAA [ 5400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 5500]
scaffold39565_10.7_P._lessonae GTATTCGGCCCCCTTGAACTTTGCGACCCTTTGCCACATTTCAGGCTTCAAACATAAAGATATAAAACTGTAATTTTTTATGAAGAATCAACAACAAGTG [ 5500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 5600]
scaffold39565_10.7_P._lessonae GGACACAATCATGAAGTGGAACGAAATTTATTGGATATTTCAAACTTTAACAAATAAAAAACTGAAAAATTGGGCGTGCAAAATTATTCAGCCCCTTTAC [ 5600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 5700]
scaffold39565_10.7_P._lessonae TTTCAGTGCAGCAAACTCTCTCCAGAAGTTCAGTGAGGATCTCTGAATGATCCAATGTTGACCTAAATGACTAATGATGATAAATAGAATCCACCTGTGT [ 5700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 5800]
scaffold39565_10.7_P._lessonae GTAATCAAGTCTCCGTATAAATGCACCTGCACTGTGATAGTCTCAGAGGTCCGTTTAAAGCGCAGAGAGCATCATGAAGAACAAGGAACACACCAGGCAG [ 5800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 5900]
scaffold39565_10.7_P._lessonae GTCCGAGATACTGTTGTGGAGAAGTTTAAAGCCGGATTTGGATACAAAAAGATTTCCCAAGCTTTAAACATCCCAAGGAGCACTGTGCAAGCGATAATAT [ 5900]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 6000]
scaffold39565_10.7_P._lessonae TGAAATGGAAGGAGTATCAGACCACTGCAAATCTACGAAGACCTGGCCGTCCCTCTAAACTTTCAGCTCATACAAGGAGAAGACTGATCAGAGATGCAGC [ 6000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 6100]
scaffold39565_10.7_P._lessonae CAAGAGGCCCATGATCACTCTGGATGAACTGCAGAGATCTACAGCTGAGGTGGGAGACTCTGTCCATAGGACAACAATCAGTCGTATACTGCACAAATCT [ 6100]
                                                                              Tc1-1Ory
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 6200]
scaffold39565_10.7_P._lessonae GGCCTTTATGGAAGAGTGGCAAGAAGAAAGCCATTTCTTAAAGATATCCATAAAAAGTGTCGTTTAAAGTTTGCCACAAGCCACCTGGGAGACACACCAA [ 6200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 6300]
scaffold39565_10.7_P._lessonae ACATGTGGAAGAAGGTGCTCTGGTCAGATGAAACCAAAATCAAACTTTTTGGCAACAATGCAAAACGTTATGTTTGGCGTAAAAGCAACACAGCTCATCA [ 6300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 6400]
scaffold39565_10.7_P._lessonae CCCTGAACACACCATCCCCACTGTCAAACATGGTGGTGGCAGCATCATGGTTTGGGCCTGCTTTTCTTCAGCAGGGACAGGGAAGATGGTTAAAATTGAT [ 6400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 6500]
scaffold39565_10.7_P._lessonae GGGAAGATGGATGGAGCCAAATACAGGACCATTCTGGAAGAAAACCTGATGGAGTCTGCAAAAGACCTGAGACTGGGACGGAGATTTGTCTTCCAACAAG [ 6500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 6600]
scaffold39565_10.7_P._lessonae ACAATGATCCAAAACATAAAGCAAAATCTACAATGGAATGGTTCACAAATAAACATATCCAGGTGTTAGAATGGCCAAGTCAAAGTCCAGACCTAAATCC [ 6600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 6700]
scaffold39565_10.7_P._lessonae AATCGAGAATCTGTGGAAAGAACTGAAAACTGCTGTTCAAAAACGCTCTCCATCCAACCTCACTGAGCTCGAGCTGTTTTGCAAGGAGGAATGGGCAAAA [ 6700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 6800]
scaffold39565_10.7_P._lessonae ATGTCAGTCTCTCGATGTGCAAAACTGATAGAGACATACCCCAAGCGACTTACAGCTGTAATTACAGCAAAAGGTGGCGCTACAAAGTATTAACTTAAGG [ 6800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 6900]
scaffold39565_10.7_P._lessonae GGGCTGAATAATATTGCACGCTCAATTTTTCAGGTTTTTATTTGTTAAAAAAGTTTGAAATATCCAATAAATTGCGCTCCACTTCATGATTGTGTCCCAC [ 6900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 7000]
scaffold39565_10.7_P._lessonae TTGTTGTTGATTCTTCACAAAAAAATTACAGTTTTATATCTTTATGTTTGAAGCCTGAAATGTGGAAAAAGGTCGAAAAGTTCAAGGGGTCAAGGGGGAG [ 7000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 7100]
scaffold39565_10.7_P._lessonae ACTCCAATTTTGGGTCGGGTTTTGCCAGTTACCAGCACACTGACTGTGCAGGTGTGCACAAGATCAGTGTAAGGAAGATGACTAGAGTTCAGGGCTCAAG [ 7100]
```

Table 2.4. (continued).

```
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 7200]
scaffold39565_10.7_P._lessonae    CCAGGACAGAGGGGGATCAGAGCCCAGAGGTCAAAGTGGGAGCCAATGCAGCAGTAAACTCTGAGGTATACAGAACATTTTGAGTTCTGTCTGGAGGACA [ 7200]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 7300]
scaffold39565_10.7_P._lessonae    GAGACAAGGTCTAAGCCTGAGGGCCAAAGCAGCATGGCTACAACATGAAAGCCAGGGGTCTGAAGTATTTGCTTATGGCAGAGAGATGCTAAACAACCTC [ 7300]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 7400]
scaffold39565_10.7_P._lessonae    TGCATTGGTAACCCTTTTGTGTTTTTGTGAGCTTTCTTTTAAATAAAAATGTCCAAAAATGTAACACCAGAATATGAGGAAAGGTCTAATGCGGGTGAAA [ 7400]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 7500]
scaffold39565_10.7_P._lessonae    ATAATGTAAAGCACTGTATGTGGGTTTCTCTTCTGTGAAAAGACGAACTATATTTTAATGTCTCAATACCTGACCTTTACAAGCATTTGGAAACCATGCA [ 7500]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 7600]
scaffold39565_10.7_P._lessonae    GGTTTCAGACGCAGACTGGGATACTGTCATAATCAAGGATCACTTTGCTTAACCTTTTGTTCGTAGTTTCACAGCCTAATCACCAAACGCTTACATTAGT [ 7600]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 7700]
                                                                          CAAT Box
scaffold39565_10.7_P._lessonae    AAAATTATAACTGATCTACAAGGTCTTTCAAAAAATGTGTTGCCAATCCAAGCCCACTTTACAACTGATTCAGTATTGTGTTTTGTCATTCTTTGTGTTT [ 7700]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 7800]
                                                                                                    TATA box:TATA(A/T)AA(G/A)
scaffold39565_10.7_P._lessonae    CTAGAAACGAGCCAAATTGTAATTAATTATAAAGCCAGTCTGGTTAATCATTTCCAAATAGGATGCAAAAATGGTATAAATGTCTGCCTTTCCCTTAGCT [ 7800]
                               Initition site(+1:PyPyAN(T/A)PyPy
U40452_P._shqipericus             ------------------------------------------ATGAAGTGGGCCACTCTGATTTGTCTGTTTATTCTCTCCATAACAACGGAGTCCAGAC [ 7900]
                                                                                                      EXON-1
scaffold39565_10.7_P._lessonae    GATTTAGGCTTCTAAGAGAACCTCCAAAAAACATTTGCCACCATGAAGTGGGCCACTCTGATTTGTCTGTTTATTCTCTCCATAACAACGGAGTCAAGAC [ 7900]
U40452_P._shqipericus             ACTTACAAAAGCGACATCATg------------------------------------------------------------------------------- [ 8000]
scaffold39565_10.7_P._lessonae    ACTTACAAAAGCGACATCATGGTAAGCAAGAATTTTTAGAACAGCAATCTTTATGTCCATACAAATGTGCTAAGTAGGTTTGAGTGTTTTTCTGTCTGTT [ 8000]
                                                                              INTRON-1
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 8100]
scaffold39565_10.7_P._lessonae    TCTTCTCTTTTAATAACTGAGGAAGATGAGGTCTGTTGGGCATACAAATATCGGTACGGTACGGTTAACAGCAAACACGCACATCATAGGTTGAACTGGA [ 8100]
                                                  RanaCR1
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 8200]
scaffold39565_10.7_P._lessonae    TGGACTGATGTCTTTTTTCAACCTCACTAACTATGTAACTATGTAATATATTTATCTGTCCTTTGTATTTTTCTTGCTGTCAAGATGGCCCATCCCTCAT [ 8200]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [ 8300]
scaffold39565_10.7_P._lessonae    TTTACAAAGACCAATAATTGTTTATAAGTTCCCCTAAATGAATTATGTCCCCTTACCGTCTGGTCTAGTGACAGCTTTAATCTAAACAGGAAGTGAGGGT [ 8300]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 8400]
scaffold39565_10.7_P._lessonae GAATATCCCCAACAAGGACACAACAACAGCAATAAAAATCACTACTTTATTGAAAATAAACATGCTCTGAAGTTACATTTTTTGTGACTGCTATGCTTAT [ 8400]
U40452_P._shqipericus          ---------------------------------------AAGAACATCCACGGATAATAAACGATATTGTAAAGGCAGTGGGAAAACCAGCTGTTGAAAA [ 8500]
                                                                                                          EXON-2
scaffold39565_10.7_P._lessonae GTGTTTCCTATGCATTACATTTTTTATCTGTTTTTTTAGAAGAACATCCACGGATAATAAACGATATTGTAAAGACAGTGGGAAAACCAGCTGTTGAAAA [ 8500]
U40452_P._shqipericus          ATT------------------------------------------------------------------------------------------------- [ 8600]
scaffold39565_10.7_P._lessonae ATTGTAAGTATTCAATTTATATAATGTGTTTTATTGTTCTGTAAACACTTTGAAAATTGCATAAAATGCAAACTTCTAGATAAAACTGTTTTCAAAATTT [ 8600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 8700]
scaffold39565_10.7_P._lessonae TATAGTAGAACTATAGGCATTTTTTTTTTATTTTGGATAGAGGGAGGGAGGAATAAAACTCCTTTTGGCCATCTATGTGCCATTGAGGAGATTTACCTTC [ 8700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 8800]
scaffold39565_10.7_P._lessonae ACTTCCTGTTTTATAACCAAAACAAGAAGTGAGAAGAAATCCCTCCAAAATAAGGTAATCCTTTGAGGACCCCCAGGCCATCAGAACTAGTGTCCCCATC [ 8800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 8900]
scaffold39565_10.7_P._lessonae GAAAGATTTCCCTTCTATTGCTATTACAAAATTTGGGATTTCCTTTCACTTTTACTAACGGTAAACATGACAAATAGAGGGTGAATCTCGCTAATGGGGG [ 8900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 9000]
scaffold39565_10.7_P._lessonae CACAGACAGCAATAAAAACTCCCAGGTGTTCTACTGCCTCTCCATTCTGTTCAAAACTAAAGTAAAAGTTTTACCTTTAGTTATACTTTAAGGCTTGGTT [ 9000]
                                                                            INTRON-2
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 9100]
scaffold39565_10.7_P._lessonae ATTATTAAAGTGATGATTTCTAATAGATTTCTTTTTTTTCCACTTCCTCATTATTCTTTTGTTGCCTGGCTTGGTATGTCTAAATAAGGTTGAGCTATAA [ 9100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 9200]
scaffold39565_10.7_P._lessonae AAATTGTAGGCAAGGAAGAAGTTGGTGTTCTAGTAGAAACAAATAGATATTGGATTATTATTTTTTTCAAATAGATATCGGATTATTATTATTTACCATT [ 9200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 9300]
scaffold39565_10.7_P._lessonae TCTATAGTTTAATCATCTCCCATAAACCTACAAAATGTAACAGTTAATACACATGCATAACACGTTTCCATTATTAGTATGTAAATCTGTACGTGAAAAC [ 9300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 9400]
scaffold39565_10.7_P._lessonae ATACATAATTAAGCTATAGCAGGATACAGTATTCAGAACAAACAAAGATAAACTGGAATATTTCCTAAATACTTAGAATTAATTGGATGCAGCCATTTTC [ 9400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 9500]
scaffold39565_10.7_P._lessonae AGGCATTAGTGGTTTTCATTATCCTTCTGATACAGTGAGGGTAACTGGTGTCTGGATGATGGTGGATATGGCAGGGCTTTGTGTACAAGGCCTCTTCATT [ 9500]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 9600]
scaffold39565_10.7_P._lessonae TTAGTGGCTCCATAACATATTCCTGTTTACAGCTACATTTTAAAGACAGATGTTGACACACAATGATTAGAATGAATATGTATTTACTATGCTGCTATGT [ 9600]
U40452_P._shqipericus          -------AGTGTTGGTGATGGTGGCACAGGATTTTGAAAAATGCTCACTGGATGAACATCTGAAAGTCCAGGCAAAAATTATAGAGGCTGTTGATAACTG [ 9700]
                                                                                          EXON-3
scaffold39565_10.7_P._lessonae CTTACAGAGTGTTGGTGATGGTGGCACAGGATTTTGAAAAATGCTCACTGGATGAACATCTGAAAGTCCAGGCAAAAATTATGGAGGCTGTTGATAACTG [ 9700]
U40452_P._shqipericus          CGAAAAACATCCAGAGGAAGCTGAGTGTAAAAAACCAGCG------------------------------------------------------------ [ 9800]
scaffold39565_10.7_P._lessonae CGAAAAACATCCAGAGGAAGCTGAGTGTAAAAAACCAGCGGTAAGCTCTCCTTGGCTCCTTCCCCGCAAGCTTTACATAATAATATAACAGACATTTTTA [ 9800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [ 9900]
scaffold39565_10.7_P._lessonae AGTTGCAGTGGTGCAGAATACAGGGATCAAGAGTATGTAACACACATTGTGCAGGGTTTAACAGTATGTAACACACGGAGTCCAGGGTCAAGAGTTTGTA [ 9900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [10000]
scaffold39565_10.7_P._lessonae AAGCACAAAGTGCAGGGGGTCAAGGGATCATAATGACAAATTGCAGGGGTTAAAAGTGCATAGCACAGTATTTAGGGGTCAGGAATACATAGCGTACAGG [10000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [10100]
scaffold39565_10.7_P._lessonae CCAGTATACACAGTAGGACCAAAAACAACCCTCTTCTCTCAGTACAAATGTCCCCCCTCAGTACAAATTCTCCCCTAAATGCCCCCAGCAGTGGTGTATT [10100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [10200]
scaffold39565_10.7_P._lessonae TAGGTTTTGTGCTGCCCTAGGCCTGACTAAACTTGTGATCCCCCTAATTTAAATATGACGCACCCCTTCCTGTAAAGGCCACACCTCTTCCTGTTTATGA [10200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [10300]
                                                                                       hAT-2_TS
scaffold39565_10.7_P._lessonae CCCGCCCTGTCATCTGTAAACCACAGACCACAACCACAGTCTATCAGTGCCCATCAGTGTAGCCTCATCAGTTCCCAGAAGGTCAGCCTCAGCAGTGCCC [10300]
                                          (ATCAT)n
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [10400]
scaffold39565_10.7_P._lessonae ATCATCATACCATCATATCATACCATATCAAACCAGGACGTAGCAGTGTGACTGCTTTATGGGGGTGCCAGACTGATTTGCCTCCTGGACCCTGCCCTCC [10400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [10500]
scaffold39565_10.7_P._lessonae AGCCCAATTTGCCCTATAAGACTGGCACTATACTAAAAGTGTGTAGCGCAAGCCGTCAGGGACTCTTTTTAGTGGGGGAGGAGGCTGTTTTTTTCTCATG [10500]
                                                                          hAT-32_TS_CPB
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [10600]
scaffold39565_10.7_P._lessonae CGTGGTGCAGCTTTTTTGCTGCCCCCCTGCAAAGTGCTGCCCTAGGCCTGGGCCTTGTTGGCCTAGGCCACGATAAAGCACTGGCCCCCAGTACAGATCT [10600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [10700]
scaffold39565_10.7_P._lessonae TTCCCCAAAAATCCCTCCCAGTAGAGAGCTCTTTTTGCGCAAATCATCCTCAGCAAAGGATCCCCTTCCCCCCAAGTTTCTTTTATTACAGACCTCCCCA [10700]
```

Table 2.4. (continued).

```
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [10800]
scaffold39565_10.7_P._lessonae     CCAATACAGACCTCTCTCCCCCCCAGTACAGACCTTTTTCTCCCCAGTACAGACCTCTCCTCCCCCAGTACAGACCACAAGAGACCCCTCCCCCAAATTT [10800]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [10900]
scaffold39565_10.7_P._lessonae     CACTTACCAGACCTCAGATACAATGGAAGGGCACAGTGAAGGGGTAGTCCTTGGCAGTGTCACTTGACACTGTGCATCAAAGCTAAGGAGGAGCTTACAG [10900]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [11000]
scaffold39565_10.7_P._lessonae     GGCCCTCAGCTCTGTACATTCACTGTGTCTGAGGTTTCGATTAAGCCAATGTCTGCAGTGCAAATGGCGGAACATAAAATAAAAAAGTCAGGTGGTCACA [11000]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [11100]
scaffold39565_10.7_P._lessonae     GAACCAGAGCCCTGAGCTAGTGACATCTCTGCACTTCACCACTGGGCAGCTGAAGACAACTTTGGGGATGTTTGTTTTACCAGGGACAGACCCCTCAAAA [11100]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [11200]
scaffold39565_10.7_P._lessonae     TAGGGACTATCTCCTAAAAATTGGGGACAAATAGCAACTTTAACTTAAAGTGTATTTAAAGTCCAAACTTTGGAAGAGCCTTCTCTGAGTTTGAAGGCTG [11200]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [11300]
scaffold39565_10.7_P._lessonae     AGAGAGATCTGTCTCATCCTTACTGCATCTCCCTGCAGCAACCTACCACATCCTACCATGTCATTACTGCTCTCCCTGCAGCAACAAATCATTGGTATAT [11300]
                                                                                     INTRON-3
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [11400]
scaffold39565_10.7_P._lessonae     TCAATTTCTTTTTAATTAAATAGTTTCTTACTGTGTTTTTTTGCTTTCTTGTAATGTTCTCCATGAGTTCCCAAACTTCTTTATTTTCCCTGCCAGCTTC [11400]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [11500]
scaffold39565_10.7_P._lessonae     TACCAGTTTTCTAGAATAGACTGTGCATACCTACCCATGCGTGAGATTTCACAAAATCCTCCTGTAATTTCTATGTAACACATCCCAGGAGGCACTTCAC [11500]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [11600]
scaffold39565_10.7_P._lessonae     GCAATCTTGCCTGTGCATCAGGCCTCGCTAAGTCCTCCTGGCCCAGGCCAGGATTTAAGAAAAAAAAATGTAAAAAAAAAATAAACTTTTTAAATACATTT [11600]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [11700]
scaffold39565_10.7_P._lessonae     TTTTTGGGCAAATGTGTAAGAAAGAGGGGAAAAGAGGCACTAGAGGGGACCTTCCTGAAATGAGTAAAATTTTGCTTTAAGAAAACATATTTGAACATAA [11700]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [11800]
scaffold39565_10.7_P._lessonae     TTTATAAACCAGAGCTTAGTGTCCCTTTTAGTGTGATGCTAAATTGGGTTCCTTATATAAAAGCACTGACCCACTAATACTGACATCATACCCTTTAATG [11800]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [11900]
scaffold39565_10.7_P._lessonae     ATCCTAGACCTTTCTACTATATTTTAGAGGCTTATTCTACTCATACCTAATGCACAAGTGGTGGAAATCACTAATTAAACAACAGTCTTCACTGTTTTAT [11900]
```

Table 2.4. (continued).

```
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [12000]
scaffold39565_10.7_P._lessonae AAATAGATTGCGACATGTGCTTTCATATAGTCATTGCAGGGTTAAATTACAATTGCCCCCCTTCCCCACCTAACATTAGCCCTTAACCATGGGCCACATT [12000]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [12100]
scaffold39565_10.7_P._lessonae TCCTTAAAAATCCCCAACTGCATGTGTGTGTTAGACCCCTTTCACATGGTAAGGACTCCTTTGAGAGCAGCAGGGGATCAGTCTGCTGATCAGAGCCATG [12100]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [12200]
scaffold39565_10.7_P._lessonae ATCTGCTCTATGGGAGTAAATGGACTCCGCTGTCTGTTTACACCAGCCGGTCCATGGAGGTGAATAGACCATCAGGGGAACATGATCGTACCCTTCATGT [12200]
U40452_P._shqipericus             -------------------------------------------------------ATTGAACTGTATCATGACATAGTTTGCAAAGAAGAAGACATAGAC [12300]
scaffold39565_10.7_P._lessonae GAAAGGGGCCTAAAACTGCCTTCTTTAATTGTGTGTGTGTCTCTTGTGTCTGCAGATTGAACTGTATCATGACATAGTTTGCAAAGAAGAAGACATAGAC [12300]
U40452_P._shqipericus             CAGCTCTACCCCTGGACTACAGAGTGTTGTGGCAAAGCGGAGGCAGAGAGGACCAAGTGCTTTTATGAGCATAGAGAAGTTCGAGTTGAGGAATATAAGA [12400]
                                                                                 EXON-4
scaffold39565_10.7_P._lessonae CAGCTCTACCCCTGGACTACAGAGTGTTGTGGCAAAGCGGAGGAAGAGAGGACCAAGTGCTTTTATGAGCATAGAGAAGTTAAAGTTGAGGAATATAAGA [12400]
U40452_P._shqipericus             TACCAAATATTGAAGAATCCTGCAAAGAACACAAAGAGCACCCACAACGTGCCTTCTCTTA--------------------------------------- [12500]
scaffold39565_10.7_P._lessonae TACCAAATATTGAAGAATCCTGCAAAGAACACCAAGAGCACCCACAACGTGCCTTCTCTTAGTGAGTTTATTTTAGTATTTTATATATACCATTGTACTT [12500]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [12600]
scaffold39565_10.7_P._lessonae GTAAAGCCCAATTGCCCACCACGTGTTATGATTTGTCATGATTTGACTTTTTTTTTGGAAATGCCTAGAAATAACTTTGTCCTATCATGGAAGCCTAATA [12600]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [12700]
scaffold39565_10.7_P._lessonae AATATGTATGGTGCCATGATTTGCCACTAGAAAAGGAAATTTATGGTGTGTATTGATACAATTTTCCTAAATGTCCAATTTAATTTTCACCTTCCTCTGG [12700]
                                                                               CR1-2_XT
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [12800]
scaffold39565_10.7_P._lessonae ATCAACTGTGGGTATAGGATTGTGTATATGGGATTGTATGATTGTTTTTTTTATTGGTTGAACTAGATGGACTTGTGTCTTTTTTCAACCTGACTAACTA [12800]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [12900]
scaffold39565_10.7_P._lessonae TGTAACTATGTAAGTCTCATACTTTTTTAACCTCTTTACAGCCCATTCAGACTGGCGCGACACGACTTTGTGGGGCAACCTGTGAAGTCGCGGTGCATAG [12900]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [13000]
scaffold39565_10.7_P._lessonae CTTGCACTGCGACTTCGGCGCGACTTGCACGGACTTCATATAATTGAAGTCAATGCAAGTCGCCTCCAGGTCGCCTCAAAGTAATACAGGAGCCTTTTTC [13000]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [13100]
scaffold39565_10.7_P._lessonae TAAGTCGGAGCGACTTGTGTCGCTCCTATTAGAATGGGTCCTGTACTACTCAATGGCGAGCGACCGACCGCGACTTGTCAGGCTAGTCTGAATGGACTCT [13100]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [13200]
scaffold39565_10.7_P._lessonae TAGAGTTATGTATCCCTTCATGTTATGATTTGGGGCTGTTTTTTGTTTTATTTCTAAAAAAATAATCTTTTCTCATAGTGATGTCTGCCTTTATATTACA [13200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [13300]
scaffold39565_10.7_P._lessonae GTGGTCTTTGCTGGCAGAATTGAGTAACAGCCACACCTGTCATCACAAATGTCCTTACACAGACCTCTATTATAGAGAAGGTTAGGAGGTGTGTCTGACC [13300]
                                                                                  INTRON-4
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [13400]
scaffold39565_10.7_P._lessonae ATATCTGTGTGAATTACTGTGAGCACTGGGTCATTTCTAGTGCCTATTGGACAACACAGTTCTTCTTAAACTGGGCATGGATGGTTAGGCACTGATGTTG [13400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [13500]
scaffold39565_10.7_P._lessonae GGAGAGAAGGCCTGGCTTGCAGTCTGTACTCTAATTTATCCCAAAGGTGTTCTATCGGGTTGAGGTCAGGACTGTGCATGGCAGTCAAGTTCCTCCACCC [13500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [13600]
                                                                                   TS1_FR3
scaffold39565_10.7_P._lessonae CAAACACATTAATCCATGTCTTTATGAACCTTGCTTTGTGCAATGGTGCACAGTCATGTTGGAACAGAAAGGAGCCAACCTCAAACTGTTCCCACAAAGT [13600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [13700]
scaffold39565_10.7_P._lessonae TGAAAACATGAAACTGTCCAAAATTTCTTGGTATGCTGATGCCTTAAGAGTTCCCTTCACTGGAACTAAGGAGCCAAGCCCAACCCCTGAAAAACAACCC [13700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [13800]
scaffold39565_10.7_P._lessonae CACACCATAATCCCCCCTCCACCAAATGATTTGGACCAGTGCCCAAAGCAAGGTCCATAAAGACATGGATGAGTGAGTTTGGGGTGAAGGAATTTGACTG [13800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [13900]
scaffold39565_10.7_P._lessonae TCCTGCACAGAGCCCTGACCTCAACCCGATAGAACACCTTTGGGATGAAATAGAGCGGAGACTGCAAGCTAGGCCTCTCCAAAATCAGTGTCTGACCTCA [13900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [14000]
                                                                                 TS1 FR3
scaffold39565_10.7_P._lessonae GAAATCCGCTTCTGGAAGAATGGTCAAACATTCCCATAGACACTCCTAAACCTTGTGGACAGCCTTCCCAGAAAAGTTGAAGCTGTTATAGCTGCAAAGG [14000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [14100]
scaffold39565_10.7_P._lessonae GCCAACTCAATATTGAACCCTACGCTCTAAGACTGGGATGCCATTAAAATTAATTTGCGTGTAAAGGCAGGTGCCCCAATACTTTTGACAATAAAGTGTA [14100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [14200]
scaffold39565_10.7_P._lessonae TGTGAACCTGACCTAAGACAGGAAGTGTGTTACTGGTTGGATCACCGGGTGAAAGTAAGGGAAAAAAAACCTAATACAAGAAAACAAATGCAGCCATCAC [14200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [14300]
scaffold39565_10.7_P._lessonae ATCTAAGGATCGCTAAGCTACAATATATTATATATATTTTTTTGGGTTCAATACTGCTTTAAAGTAAAGTTGCTTTTAAATCTGCTCACTGTTTTGCCCT [14300]
```

Table 2.4. (continued).

```
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [14400]
scaffold39565_10.7_P._lessonae CTTTTACACTAAATGGTGGAAGTATACCTGTGATCATGTCAAACATACAATACCTGCGCAGGAAAATTTGAAAAAAAAAAAAAAAAATAGAGCTTCTTCTG [14400]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [14500]
scaffold39565_10.7_P._lessonae ACATGTTCAGCTCACTTTGCTTTTCTTCATACTTTAGTATATCAGGCTGGCAGGATTTACACTTGCATTTATTTTTTTTTTTCAAATACATTTTATTAAA [14500]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [14600]
scaffold39565_10.7_P._lessonae AGAATTCACCATTACAATGTATAGAACTTTGACAAAAGTCAGGATTTGCGTTTTTTATAATTCGCAAGGAACATGTTAATAGGCTAAAATGAGAGAGACA [14600]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [14700]
scaffold39565_10.7_P._lessonae ATATAACAAACATGTTGCACACTTGCATTTTTATATGTGACTTTAGAATTCATCTATCACCGACTTGATCACAATAAAGTCTTACTTGACTGCTTTTGGC [14700]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [14800]
scaffold39565_10.7_P._lessonae ACTGCTGTACTAACCAGTAACAAAGTCCCTATACAGCATGTTTGTGTGGCATTATGCTCAGTACATTCATTCAGGATTTGTAATGATTCTATTTTTTTTT [14800]
U40452_P._shqipericus              ---------CTACCTCTCCAATATTGCTAAAAGACATTCAAAACTCTATCCACCAGCTGTTCTGGGTTTTGCTATACAATACAATGAAATCACTACTGAA [14900]
                                                                                                   EXON-5
scaffold39565_10.7_P._lessonae ACATTTCAGCTACCTCTCCAATATTGCTAAAAGACATTCAAAACTCTATCCACCAGCTGTTCTGGGTTTTGCTTTCCAATACAATGAAATCACTACTGAA [14900]
U40452_P._shqipericus              TGTTGTGCTGCAGAAGACAAAGCCAAGTGCTTTGGTGAACGG---------------------------------------------------------- [15000]
scaffold39565_10.7_P._lessonae TGTTGTGCTGCAGAAGACAAAGCCAAGTGCTTTGGTGAACGGGTATGCCATTAAACTTCTTGAAATTAAACAATGTTATTGCACATGTAGGCTTCCTTCG [15000]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [15100]
scaffold39565_10.7_P._lessonae TACGGGGCGATTACATTTGTGTCCCATGTGTGTTTACCTGCATGGGGATACACAGATGTTTCTGCACCCTGTGCCGAGTAATCCCATTCTTGTCTATTGG [15100]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [15200]
scaffold39565_10.7_P._lessonae ACACAGCGGCTGCATGGACACAGCTGCCATATGACACCAGTGGGTGCGGGTCCCCAAATGCACGTGCACGGTTATCACATAGGGAGCAGCGCTGTGTCCG [15200]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [15300]
scaffold39565_10.7_P._lessonae TGCAGTTGCTGCGCCCCAAGACAGCTATGGGTCTGCTGGCACGGGGGTTTGCATGCAACACCTGCGCATCCCCATGCTGGTAAAACAGAGCCTCGCCCCG [15300]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [15400]
scaffold39565_10.7_P._lessonae GGACGTGGATGTTATGGCCTGGTGTGAACTAAGCCTTAAAGTGTATGTCTGAGAAAAATAATTAAAAAAAACATATGTAGTACAGATCTGCAATATATAC [15400]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [15500]
scaffold39565_10.7_P._lessonae ACAATTGCACATGTTTTATTATTTTAAAAAAAATGCATCAAGTACAGAAAATGGCTTGTGGATTGCCAGAAACCCAGTGATTTCCTAATATCCTGTTGTT [15500]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [15600]
scaffold39565_10.7_P._lessonae GGCTGACAGCACAATGCTTCTGCTGCATTGAATTCAGTGGCAGTGTTGTCAGTCCTGCCCAATTCTCTTCTGCTGGATTACTAAACTCCAGTAGTCCGCA [15600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [15700]
scaffold39565_10.7_P._lessonae GGCAGAACAAATAGTACTGTTTTGGATTTCAGCATAACAAAGGCCTTGGGCTGTCATCTGCAACAGTAAGTTGACACTTTGGTGAACGGGTATGCCATGA [15700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [15800]
scaffold39565_10.7_P._lessonae AACTTCTTGAAATTAAACAATGTTATTGCACATGTAGGCTTCCTTCATACGGGGCGATTACATTTGTGTCCCATGCGTATGCACCAAGTGTCCCATTCAT [15800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [15900]
scaffold39565_10.7_P._lessonae CCATAGGTGCATACTGCTCTAAATCTTAGTATTGATCGGTGCCTCCTATGCCTCCCAGATTGCTTTTGCCTGCGTTTAGATGTTCCTACTTTATTGTAGT [15900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [16000]
scaffold39565_10.7_P._lessonae TGTAAACGCTTACATATACCTAGTGAAGTGAACAGGCTGATACACAGCGATGAAACACATCCTCCTACATAAGTTGTACCTGTTATCTGCCACCCTCTCT [16000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [16100]
scaffold39565_10.7_P._lessonae TTCTACAGCCATTTAAAGTCAGAGCTTTAGGAGACAGGGTGGGGAACTGACATCACACACACTGCACAGCACAGAGAGGAGAGCTGAGTGTACCCTGAGA [16100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [16200]
scaffold39565_10.7_P._lessonae CCTGAGTGGAGGGAATGGACACACCTCAGGGAAACATGCACAGCTGAGGCTGTCAATCACCCGCTGTGTGCTGGAGGGAAGGAGGGGGGGGGCAGGGCC [16200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [16300]
scaffold39565_10.7_P._lessonae TTGGCATCACATACCTCCTAACCTTTTGAGATAGAAGCGAGGGACACCTATTAGCAAAAGTGTGTAGTCATAGGACACACCCCCTGCCACACCCAATTAA [16300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [16400]
scaffold39565_10.7_P._lessonae AGGAGAATTATACAAAAAAATGATTAGTTAAACCCACAAGCGGTTTTTTTTTTATACCACTATTATTCCTTTTTATTGGCTTTTGACATTTACAAATGTA [16400]
U40452_P._shqipericus          ----------------------------------------------INTRON-5---------------------------------------------- [16500]
scaffold39565_10.7_P._lessonae GCAATTTAGAAATTGGATAAAGGTTTAGCACTGGGAAACCCTTTTTGATAGATAAGCAATGTGTTTTATATACAACTATATAGATCAGACCAAAATAAAG [16500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [16600]
scaffold39565_10.7_P._lessonae GACAAAGGAGGAGGAAAAAGGGACATAGGGACTTTGTTCCAAATCAGGGAGAGTCCCTCAAATTAGGGACAATTGGGAGCTATGGCATTAGCATAAACTG [16600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [16700]
scaffold39565_10.7_P._lessonae TGAAATGTAACTCATGCAGATAGCAGAAAAAGGAGAGAGCAGACAGGAAGACATGCTATAGATTGAGGCAAGTATACACGATAGAATGATATACTTTGTT [16700]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [16800]
scaffold39565_10.7_P._lessonae CATTTTTTATTTCAGAGGTTTAAATCCACTTTGCATTTGCGTGCGATTAGCCACATTTGGAGTGCCTAATCAGATCAGACATACAGAATTCTGTTTTCTG [16800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [16900]
scaffold39565_10.7_P._lessonae TAAACACAGCTAATCTGACTTCACCTAAATGCACGTAAAAGCACAGTTTGAATGGCCAATTAAAAACTCATTACATGCATTTACTGTTTATGCATTTAGA [16900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [17000]
scaffold39565_10.7_P._lessonae AAAGTCCTCTGAATTATATAAATGCAGGTTTGACACTGAATGAGAACAAAATGCATAATAAGTTTTATTACCTCAAAAGAAAAACTATTACAGGGAATCT [17000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [17100]
                                                           (T)n
scaffold39565_10.7_P._lessonae ACAAAGGTTTGGGGACAATTTCTTTTTTTTTTTTTTTTTTAACATTTATTCTTTAAAATTGATGTTTTAAATGTTTTATTTTTCTATATGTGTGAATAAT [17100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [17200]
scaffold39565_10.7_P._lessonae CAGTGAAACCTCCACTTCCTTTGAATGTGATACAAAATAATATATATGTAAATACTCTAAATTCAACACAAAATCAATATAAATTTTCAGTTGCAGCTGT [17200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [17300]
scaffold39565_10.7_P._lessonae GCGCTCCTTATTGATTTCAGCACACTAAAAACAAAAATCAATTGTATCCTGTATAGTGCAGTGCAACAGAACAATTATGTGATAAATTCCTGGAAATCAA [17300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [17400]
scaffold39565_10.7_P._lessonae ATATAACTCAATATTAATTTGTGAAAAATAGAACCAGTCCTTTCAGAACACCATTATATAAATAAGAGTCCATAAACAGACGTGTTCCTCCACCAACAGT [17400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [17500]
scaffold39565_10.7_P._lessonae GCTCTTCAATCGATGGTATTGTGAAAGGACTAGTTCTATTTTTCACAAATAAATATTGAGTTATATTTGATTTGGAGGAATTCTTTACAAAATTGTTCTT [17500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [17600]
scaffold39565_10.7_P._lessonae TTGCGCTGCACTATACAGGTTCCAATTATTTTTCTATATGTATACAATCGTTTTACATATAAATATTTAATACGTGGCAAGCGACTCCCAGAATCCAATG [17600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [17700]
scaffold39565_10.7_P._lessonae AGTTAGCTGTAGATAGTCTGGCAGTAGCTTATGTTTTCTCACGCTTTGTTTAAAACCTTGGGCAAAGACATCTGATAAGGGATGAGTCACTGCAAAGGCT [17700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [17800]
scaffold39565_10.7_P._lessonae CGTTTGTCTTTCAGCTTGAGCTAGGCAGCACTGTAAACAACAGATAAATACAAGCAGTGGATATAGTATATAATATGCAAAAATATACCTTCTGCTATTT [17800]
U40452_P._shqipericus          -------------------------------------------------------------------------------------ATGCCCCAGGTAAAA [17900]
scaffold39565_10.7_P._lessonae CTTTATGTGTCTGCTTTGTGCTTGTATATGTGTATATATATATATTTTTTTTTTTTTATGTTTGAAACAATACTTTCTTTTGCAGATGCCCCAGGTAAAA [17900]
```

Table 2.4. (continued).

```
                                                   EXON-6
U40452_P._shqipericus              AAACTAACAAACTATCTTGAGGATAAACATAAACAGAAATGCCGTGTTCTTAAAGAATTTCCAGAAAGAGTTTCTCAAGCACT----------------- [18000]
scaffold39565_10.7_P._lessonae     AAACTAACAAACTATGTTGAGGATAAACAGAAACAGAAATGCCGTGTTATTAAAGAATTTCCAGAAAGAGTTTCTCAAGCACTGTAAGTATCTATTCCCA [18000]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [18100]
scaffold39565_10.7_P._lessonae     ATCCAGGAAATATATGTAGGGGAAATGTGGAGAGCTTTATTTTTATCTTTAGCGCCTTACCGCTCGCCCATTTCCATCTTTGACAGCTCAATCTCTGTGC [18100]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [18200]
scaffold39565_10.7_P._lessonae     TGGGAGCATGCAGTGAGCGCGCTCTCAGCACAGAAACCTATGCTGTCCATAGAGGGATATGTGGGCCATGTGGGTGTTAATACCCATCTTTGGGCCACTG [18200]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [18300]
scaffold39565_10.7_P._lessonae     CTCATATAACTATATACATGCCAGAGTACCTTCATCACTATGTTGCTATAAATTTACCCTGACCTCTATTCTTTTGGTTGGGGAGGGGGGAACAAGCAGC [18300]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [18400]
scaffold39565_10.7_P._lessonae     TGACCTTGCTAGCTCAGCAAGAACAGCACAGATCGGAATGGGACCGAGTGTTACCTGCACTTTGTCCCCTGTGGGATTCACGAATGATTTTTAAGGTGGG [18400]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [18500]
scaffold39565_10.7_P._lessonae     TGTGATACTTCTTCCTTAAAATCCCTGTCAGGTTATTTCTTATGTCTGTGTCCAATCGGAAAGAATTACCTTTAGTTTCTGCTCTGAAGACGCAACAGGA [18500]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [18600]
scaffold39565_10.7_P._lessonae     AGTAAGAGGAAATTTCTCCAAAGTGAAGGGAATTGCCCCTGAGACAGTTTTCACAGAAACATTTGTTCAGTGGCATCTTAAGAGCATTATAGGCCCCCGG [18600]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [18700]
scaffold39565_10.7_P._lessonae     GCAATGCAGTACACTGGGGCCCCGCCTGCAAAATCACCCACAAGAATAAACATGCTAATTATCATTAAGGCTATATTTATTGGTACAGCAGTGCCATGCT [18700]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [18800]
scaffold39565_10.7_P._lessonae     AATGACAGCTTCCAAGTTCCGCGGCTGAGTTCGGTTAACACACACACACAGACGGGAGTCAGACTCGACTGTCCTGTGTGTGCCTGTTCCTGTGGGGGCG [18800]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [18900]
scaffold39565_10.7_P._lessonae     GACAGGCATTCTGCAGTTGTGGGCTCCCCCTCCACGGCATATGTGGCCTGACAGCAACGCAGGGCCGACAGGCACTTGCCACCTGCTAAGTTCGGTGGCG [18900]
                                                                                INTRON-6
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [19000]
scaffold39565_10.7_P._lessonae     GCATGCACATGGGAATCAGGACTAATGCTTGGCTGGGGCTGAGCCGCTGGGCAGGTGGGTCCCCCCGGGCAAGTGGGGCCCCCGGGCAACTGCCCAGCAT [19000]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [19100]
scaffold39565_10.7_P._lessonae     GCCCATTCTGTAAGATGGCCCTGCATTTGTTCCCATTTAAAAATTTACCTTTGACTCTTGTTTTGGTGACAGCTGTAGAATTTTGGATTTTCTATCACTT [19100]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [19200]
scaffold39565_10.7_P._lessonae TCATGCATGACAAATAGAGACAATGATGCTGATTTACTAAAGGAGCTGATCATTTTTCCACATTTCTTTTATGTGAATATTATCTCAGCTATCCAATCAC [19200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [19300]
scaffold39565_10.7_P._lessonae ATATAAAGCAAATTCCTATTTATCATGATTGGATAAATGAAGTGAGTAATTACATTTTATTGTGACAAATCTCAACTTCTTAAGGGACCATTCACACACC [19300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [19400]
scaffold39565_10.7_P._lessonae TTTTCAGTGCAGTGCATTGCGCTAACACGCATGTTACTGCAACACACGTTAACACACCTTACTTGCATTGCAGTGCAATTCATTTTTAATGGCAGCCCAA [19400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [19500]
scaffold39565_10.7_P._lessonae CACATCAAGGCAACACAGTGTTGCAGAGATCCACCATGTTTTGTTATGTGCGACCGTTCATTGTGGGGCTCTGAGTTGCCAATATTGGTGAATGTCCGAA [19500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [19600]
scaffold39565_10.7_P._lessonae TTTTGTGGATGTGTCCGTATGTTGGCAGCCCATATATGGGTGAAAAAAAGTGCTTTAACACAACGCACTAGGGCACCAAGGTCTAAATGGGGAGACAAAC [19600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [19700]
scaffold39565_10.7_P._lessonae GACAATAAAAGCTTAACAGGGGTTTCTGACTGCATCAAAAGCAAACAAAAAAAGTTTTGGCTTTATATATACTTTAAGATTATTGTACAATATAAACAAT [19700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [19800]
scaffold39565_10.7_P._lessonae ATAATAACACAGTAATAAAAATGTTCTTTTATCAACTATTTCAACATTGATATTATTATAATGTTATTTCTGCTTACGAGTACAAGCCTTTTTTTCGATG [19800]
U40452_P._shqipericus          ----------------------------AACACTAGTTCAAGTATCCCAAAGGTTTGGTAATGCAAAATATGACGATGTGGAAAAAGTCACCATTGAAAT [19900]
                                                                                               EXON-7
scaffold39565_10.7_P._lessonae CGGTAACTGCTTCTTTCTCATTTATCAGAACACTAGTTCAAGTCTCCCAAAGGTTTGGTAAGGCAAAATTTGAAGATGTGGAAAAAGTCACCATTGAAAT [19900]
U40452_P._shqipericus          TGCACATTTGAATGAAGATTGTTGCAAAGGTGATGCCGTGGAATGTATGATTGAAAGG------------------------------------------ [20000]
scaffold39565_10.7_P._lessonae TGCACATTTGAATGAAGATTGTTGCAAAGGAGATGCCGTGGAATGTATGATTGAAAGGGTAAGCCTGTGCACCAAACATTTTAATATCTCCTTCATCACA [20000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [20100]
scaffold39565_10.7_P._lessonae TTTGGGCCTTCTTTACACTTGTGGTTAAGTGGTGGTAAAAATAGGTGGTTGACCTGTGTTACTATCACCCAAAGGCAGCTGTGGGGGTGAAGCAGGGGGG [20100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [20200]
scaffold39565_10.7_P._lessonae TGGGGTTAATACATATGCTTCGGCAAAAATGATTTCCCCTGTTGTGTTGGGCTGTATGGCAAACTAATGCAAAATATTCAAGTGGATGGGGCTGCGCCAC [20200]
                                                                         INTRON-7
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [20300]
                                                                                   (A)n
scaffold39565_10.7_P._lessonae AACCATTAGGCTTACAGTTGTGGCACAGTATGTCCATTGAAAAAAGTCCATTCAACTGTAAAAAAAAAAAAAAGAAAAAACAGGCATTCAGGAGGCTCTA [20300]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [20400]
scaffold39565_10.7_P._lessonae CTGCCACCCCCTTGCCACTCTGTAAAAAGCGACCCTCCTCAAAATGCTTTTCACAAATAGCCACAAGTGTACATGAGTCCTAAAACTTTTACCTAATACA [20400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [20500]
scaffold39565_10.7_P._lessonae GTAAGTAATTTGACATCTGATAAGGATACATGCCTATATCTCTCAAGCCTGTTTTTTTTTTTTCAATTCATTGGGGACAAGGTGTAATCAATAAATACGA [20500]
U40452_P._shqipericus          -----------------------------------ATGGAAGCAACGGAACATATTTGTTTAGCTAAGGAGAAATTATCAAGCAAACTAAGTGACTGTTG [20600]
scaffold39565_10.7_P._lessonae TGTTATCATGCATATGTATTTTATATCTTTGACAGATGGAAGCAACGGAACATATTTGTTTAGCTAAGGACAAATTATCAAGCACACTAAATGACTGTTG [20600]
                                                                                                        EXON-8
U40452_P._shqipericus          TGCTAAAGGTGTTTTAGAACGAACACCCTGTATTCTTGCCCTACCAAACGAGGAACCTGACTTGCCCATAGAACTGAAAGAATATTATGAAGATGAACAT [20700]
scaffold39565_10.7_P._lessonae TGCTAAAGGTGTTTTAGAACGAACACCCTGTATTCTTGCCCTACCAAACGAGGAACCTGACTTGCCCCTGGAACTGAAAGAATATTATGAAGATGAACAT [20700]
U40452_P._shqipericus          GTTTGTGAGAACTATCAAAAAGACAAGAGAAAATACCTTGCCCA-------------------------------------------------------- [20800]
scaffold39565_10.7_P._lessonae GTGTGTGAGAAATATCAAAAAGAAAAGAGAAAATACCTTGCCCAGTAAGTATACCTTTTAATGTTTATACAATTGCCATCAAGTTGGGTGTCCTCCGAAC [20800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [20900]
scaffold39565_10.7_P._lessonae TCTACCATAACCCAAACTCTGAACTTTTGCCTTTTTGTACTCCAATGAGCTTCGGGCTGGAAACTAACCTTACATCGTTTCAGATCTGTCAGTGACTACT [20900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [21000]
scaffold39565_10.7_P._lessonae TTAATATTACTTATATTATTCTCACAGTATTGCAAATGTGTGCTATATCAATCTTTTCATTTATTTGTTTTTGGACCACTTAATTCTGACAGGTTAAAGA [21000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [21100]
scaffold39565_10.7_P._lessonae AGAAAAATGATTGATTTTTTTTTTCTGAAGTTAAAAAGTCTTAATACTGTTTATATACTATAGCTATATTTATTTATTTATTTATTTATTTATTCGAAAA [21100]
                                                                                                           (TATT)n
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [21200]
scaffold39565_10.7_P._lessonae GAAATGAAAAGAAAAAGAGCAAACAGAACAAACAATGCAGGCTCCAGATAAAAAATTGCCATAGTCATATTATAGTGTGAATACGTATGCGCTGCTATTT [21200]
                                                                                                  (AGATAA)n
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [21300]
scaffold39565_10.7_P._lessonae GCAGAACGTGATACAAACAATCTTAGTATCTATACTAATAATCAAGGGACAGAAAAAAGAAAGAAAAAGAAGAAAAATAAAGGATAAAGATAGAACAGCA [21300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [21400]
scaffold39565_10.7_P._lessonae GCAACTGTTATAATAGTGACCTCTAACACTAAGATACAACACTAATAGACAAAAAAAACTGTGCGCTTGTTCATAAACAATCCCTATATATGCTTAAAAC [21400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [21500]
scaffold39565_10.7_P._lessonae AATTCATCTAATAAAATATTCAATTGTGCAATACACCATTCATGTGATGAAACATTCAGTAAGGATGGTGGAACCATACAAATTAAAAAGGGAAAAAAAA [21500]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [21600]
scaffold39565_10.7_P._lessonae ACAAAGTCCAAAAAATGTGCTCGTAAGTTCAATATCAACGTGTATGTGGTCAATCCACAAAAAGATTGTAATCATTCATCCAGCAATGTGTAACAATCCT [21600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [21700]
scaffold39565_10.7_P._lessonae TTAAAAATTGTGATGATAGGACAGAACCACCACCAGCAGGTGAAATCACTGCTCACCTTACAGAAAGACCAATTGGTCAAAACACGCTTAATCACCAGAT [21700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [21800]
scaffold39565_10.7_P._lessonae AGCTCAAGGGAACTGATCTCTTCCACTGCAATGGTCTCCCTCCCTGGATCACCAGATAAATCCACCGATCAATCTCTGTGGGTTTTCACTTCCAATTTTT [21800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [21900]
scaffold39565_10.7_P._lessonae GTAAATCAAGTTTCCAGAAGGTTCTGCAGAAGGAAGAAGTGACGCAGCAGAGATAAGGAATCACACATGGCTCCCGCCGGGTTTCAAACTTTGGGGCTGC [21900]
                                                                                             KibiDr1
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [22000]
scaffold39565_10.7_P._lessonae ATTTCAAGAGAGGTTTCTTGGGTCCATCCTGAAGCGTTTCCTTTTTTTTCCATTTTTAATTTGTATGGTTCCACCATACTTTCTGAATGTTTCATCACAT [22000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [22100]
scaffold39565_10.7_P._lessonae GAATGGTGTATTGCACAACTGATTATTTTATTGGATTAATTGTTTTAAGCATATATAGGGATTGTTTATGAACAAGAGCACTGATTTTTTGTCTATTATT [22100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [22200]
scaffold39565_10.7_P._lessonae GCCATAGTTATATTGACAAACAATCACAGTCCACCACTGAAAATTAACATAGTTTACCCTCATAGCATGCCCACTGTACTACAGAATAGGGCCAACATAT [22200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [22300]
scaffold39565_10.7_P._lessonae CAGTATATAAACAAGAAGTTATTCATTACTGACCATATTGACAACAATATTAAATAAGTAGTCTGTCCACATCCATTGGGGAAAGCCCAGAGGTATCTAA [22300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [22400]
scaffold39565_10.7_P._lessonae CCACAGGGGCCATAATTTCTTAAACTTGCCAGGGTGTCCTCTGTGTTGAAAAATATACTTTTCCAACCGTAGGGTATCCCCCATTTGGGTAGTCCATTCC [22400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [22500]
scaffold39565_10.7_P._lessonae AGGCCATAGGAGGGTCAGCCGCCTTTCAATGCCTGAATATAAGCTTATGGGCCTGGAAGAGACAATTGCCTGTTTAGGATTATCCTCAATTGGGAGGTCA [22500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [22600]
scaffold39565_10.7_P._lessonae TTCAGAATATCTAATAAACATGGTTTATTGTCTGCCTGGATGTTGACCTGGAATACCCTATTAATGGTATTAAGGATACCTGTCCAGTAGAGATGTAACT [22600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [22700]
scaffold39565_10.7_P._lessonae TAGCACAGTGTCACTGTCTATATTTTTAATATATACTTATACACCATTTTTGTTTTCCCATGGACACCTTTAACAAAGGATACCCAGAGCATTATGAGTT [22700]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [22800]
scaffold39565_10.7_P._lessonae CAGTAAAGGGGGACACGGCAGAATTTGTTTACTTATGAATACTTGTTGAGAGATGAGCACTATGTAATGATTTGGCGTCTCTCTCTCTCTGCAGTTGGGC [22800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [22900]
scaffold39565_10.7_P._lessonae AGGGAGGCAGAACCTTGATGCCCTGGGCTCACAGTAAGTGGGATGAATGATGATAGGTGTCATTCAGCCTGGAAAAGGAGTGGCATCAGGGAGTCTGCTG [22900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [23000]
                                                                                         Helitron-1_DR
scaffold39565_10.7_P._lessonae AAGACAACACTAGAGATCGGGTGGATATACAGTATCTCACAAAAGTGAGTACACCCCTCACATTTTTGTAAATATTTTATTATATCTTTTCATGTGACAG [23000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [23100]
scaffold39565_10.7_P._lessonae CACTGAAGAAATTACAATTTGCTACAATGTAAAGTAGTGAGTGTACAGCTTGTATAACAGTGTAAATTTGCTGTCCCCTAAAAATAACTCAACACACAGC [23100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [23200]
scaffold39565_10.7_P._lessonae CATTAATGTCTAAACCGCTGGCAACAAAAGTGAGTGTACCCCTAAGGTAAAATTGGGCCCAAAGTGTAAAAATTTTGTGTGGCCACCATTATTTTCCAGC [23200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [23300]
scaffold39565_10.7_P._lessonae ACTGCCTTAACCTTCTTGGGCATAGAGTTCACCAGAGCTTCTCAGGTTGCCACTGGAGTCCTCTTCCACTCCTCCATGACGACATCACGGAGCTGGTGGA [23300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [23400]
scaffold39565_10.7_P._lessonae TGTTAGAGACCTTGCGCTCCTTCAACTTCCGTTTGAGGATGCCCTACAGATGCTCAATAGGGTTTAGGTCTGGAGACATACTTGGCCAATCCATCACCTT [23400]
                                                                       INTRON-8
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [23500]
scaffold39565_10.7_P._lessonae TATCCTCAGCTTCTTTAGCAAAGCAGTGGTCATCTTGGAGGTGTGTTTGGGGTCGTTATCATATTGGAATACTGCCCTGAAGCCAGAGTCCCTGAAGGGA [23500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [23600]
scaffold39565_10.7_P._lessonae GGGAATCATGCTCTGCTTCAGTATGTCACAGTACTTGTTGGCATTCATGGTTCCCTCAAGGAACTGTAGCTCCCCAGTGACGGCAGCACTCATGCAGCCC [23600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [23700]
                                                                      TC1DR1
scaffold39565_10.7_P._lessonae CAGACCATGACACTACCATCACCATGCTTGACTGTAGGCAAGACAAATTTGTCTTTGTACTCCACACCTGGTTGCCGCCACACACGCTTGACACCATCTG [23700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [23800]
scaffold39565_10.7_P._lessonae AACCAAATAAGTTTATGTTGGTCTCATCAGACTACAGTACATGGTTCCAGTAATCCATGTCCTTAGTCTGCCTATCTTCAGCAAAACTTTTGCGGGCTTT [23800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [23900]
scaffold39565_10.7_P._lessonae CTTATGCATCATCTTAAGAAGAGGTTTCCTCTTGGGACGACAGCCATGCAGACCAATTTGATGCAGTGTGCGGGGTATGGTCTGAGCACTGACAGGCTGA [23900]
```

Table 2.4. (continued).

```
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [24000]
scaffold39565_10.7_P._lessonae   C?CAGCAATGCTGGCAGCACTCATACGTCTATTTCCCAAAGACAAACTCTGGATATGATGCTGAGCACGTGCACTTGAATTCTTTGGTCGACCATGGCGA [24000]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [24100]
scaffold39565_10.7_P._lessonae   AGCCTGTTCTGAGTGGAAACTGTCCTGTTAAACCACTGTATGGCTTTGGCCACCTCGCTGCAACTCTGTTTTAGGGTCTTGGCAATCTTCTTATTGCCTA [24100]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [24200]
scaffold39565_10.7_P._lessonae   GGCCATCTTTATGTAAAGCAACAATTCTTTTTTTCAGATTCTCAGAGAGTTTATTGCCATGAGGTGCCATGTTGAACTTCCAGTGACCAGTATGAGCAAA [24200]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [24300]
scaffold39565_10.7_P._lessonae   TGAGAGCGATAACACCAAATTTTACACATCTGCTCCCCATGCACGCCACTAACGGGTCAAATGATACCAGGGAGGGAAAATGGCTAATTGGGCCCAGTTA [24300]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [24400]
scaffold39565_10.7_P._lessonae   TTTTGAGGAGTTATTTTGAGGAGACAGCAAATATACACTGTTAAACAAGCTGTACACTCACTACTTTACATTGTAGTAAAGTGTAATTTCTTCAGTGTTG [24400]
                                                                          Helitron-1_DR
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [24500]
scaffold39565_10.7_P._lessonae   TCACATGAAAAGATATAATAAAATATTTTCAAAAATGTGAGGGGTGTACACACTTTTGTGAGATACTGTATATTCAGTGCAACATTCCACAGCTTTGGAA [24500]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [24600]
scaffold39565_10.7_P._lessonae   TAAAAAACACACAGTTCAGAACTGGTCCCATCCAAGAATAGCGAGATGCAGTGGCGGCTGGTGCATTGGAGGCGCCGGACACATAGAGTTCAATGGGGTT [24600]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [24700]
scaffold39565_10.7_P._lessonae   TTTTTTTCTGAAGCACCTGATTAGAGCCAGAGGCTCTAATAGGCTTCAGAAAAGGGTGGGTCTGGGGCGCAGAGCACTGCGCCCTAGCCCACCCATTTGT [24700]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [24800]
scaffold39565_10.7_P._lessonae   GTGACAATAGCGAATGAAAATTCGCTATTGTTACACGGATCCTCCTCTTGGCAGATCAGGAAGCGGGTCCGAGACCCGTTTTCTGATTGTCCGAAAGGCG [24800]
                                                                                 GA-rich
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [24900]
scaffold39565_10.7_P._lessonae   AACCCATGCCATTGGCCAAGGAGGAGGAGGAGGCAGGAGGACTTGAGGAGACGCAGGGAGACGCGGGGGACTGAGGAGAAGCCATCACTGCAAATCAGGT [24900]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [25000]
scaffold39565_10.7_P._lessonae   AAGTGCACTGGTCACTCTGCAGTGAAGGGGGCACAATGGTGATTCCTGATGACTCTTGGGATGTATGACATCATTTTGGCCTATGCCAGAAACTAGAAAA [25000]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [25100]
scaffold39565_10.7_P._lessonae   CAGCTAAGTTTGAAAGAAGTAAATATAATCTACTTTCCTGTCTATCTACTAATGCTAGCAGCGTAAGGACTAAAATAGTTAATGTCGATTGAGCGTGTTT [25100]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [25200]
scaffold39565_10.7_P._lessonae AGTTCCACTTTAAGTGACTGCATGTTTTTTTTTAAATGATCAAAGTGTTAAAAGTGCATATTTAACGTTCTGGTTATGTCACTTTAAACAGTCATTTGCA [25200]
U40452_P._shqipericus          -------------CTTTACGCATGATTATTCCAGAAGTCACCAGGAATCATCTCCTCAATCGTGTTTACGAGTTTCTAGAGGATTTGAAATGCTGCTGGA [25300]
                                                                                       EXON-9
scaffold39565_10.7_P._lessonae TTTGTTTCTCCAGCTTTACGCATGATTATTCCAGAAGTCACCAGGAATCATCTCCTCAATCTTGTTTACGAGTTTCTAGAGGATTTGAAATGCTGCTGGA [25300]
U40452_P._shqipericus          AAAGTGCTGTGCTAGTGCAAACTCTGCTGAGTGTCTCAAGGATGCC------------------------------------------------------ [25400]
                                                                                                 INTRON-9
scaffold39565_10.7_P._lessonae AAAGTGCTGTGCTAGTGCAAACTCTGCTGAGTGTCTCAAGGATGCCGTATGTATATGAATGTTACTGTTACAGTCCAAATAGTAAATGTGTGTGTGTGGT [25400]
U40452_P._shqipericus          -----------------------------------------CCTAAATTGTTAGAAGCTGCACTAAAAGAAAATGAAGAGATATCTAAACAGAACTGTGG [25500]
                                                                                                     EXON-10
scaffold39565_10.7_P._lessonae TTTTTTTTTCATTTAAAGTATTTATTTTATTTTCATTTCAGCCTAAATTGTTAGAAGCTGCACTAAAAGAAAATGAAGAGATATCTAAACAGAACTGTGG [25500]
U40452_P._shqipericus          TGCCTTGGAGAAGCTTGGGTTTAATGATTTTTATATTCA------------------------------------------------------------- [25600]
scaffold39565_10.7_P._lessonae TGCCTTGGAGAAGCTTGGGTTTATTGATTTTTATGTTCAGTAAGTTAAGCGTGTAGCATTTACAATTTTGAACATTTTATCAAAAGTCATATAACATAAG [25600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [25700]
scaffold39565_10.7_P._lessonae CAAGGTTTCTCTGAAGGAATTACTAAATTTGGTAGAAAACCAAACTAAGGATTGTATAGTGTAATGTAATTGTTTAGTGCTTTTTCACACTAGCATGATG [25700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [25800]
                                                         hAT-2_ET
scaffold39565_10.7_P._lessonae CGGGAACCAGAGCCGGTTTCCACATCACACAGGACTCGCAGCCAGTTCACACTGCCCTATGCAAACCGCAACGGGTGTCAATAGAAAGTTAATGACACCC [25800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [25900]
scaffold39565_10.7_P._lessonae CCAGATCAGTTTGCATATTGCAGTGCAAACTGTCAAATGGTGCAGGAATCGGGTCGCATTAGGTGCAATCTGATTCCAGTGCAGACCAAAATAAGGGTCC [25900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [26000]
                                                           hAT-2_ET
scaffold39565_10.7_P._lessonae TGCACCGTTTTGGTCCAGACGTGATGCAAATTCAGCCATATAACCTGTATGGCTGAATTTGCATTGCACAGACGTCGCATGTGATCTGCACAGCAATGCG [26000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [26100]
scaffold39565_10.7_P._lessonae GTGCGAATCACATACGACGTCTGGCATCGCGCTTGTGCCAACTAGCACTTAAAGCTGAACTTTGGGAAAACAGCACAATTACTTGTGTTTAGATATATTT [26100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [26200]
scaffold39565_10.7_P._lessonae CCATGCATTTAAAGCACTCAGAGTTTCTATTCTGCCACTGGACCCACAGATTTTCATATTTTTTTAACAAGCTAAACTGAATACAATCAAAAGCAAGTAA [26200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [26300]
scaffold39565_10.7_P._lessonae ATGCTTAGTGTGCATTATCCTATTTACTGTAAAATCATTACATGAATTTACAAACTTTTAGAAATGTTCTTTAACCACTTGCTTACTAGACACATATACC [26300]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [26400]
scaffold39565_10.7_P._lessonae CCCTTCCTGCCCAGGCCAATTTTCAATTGACAATTCCGCGGTCATGCTACACGACACCTATATGAAATTTTTATCATTTTTATTTTCACACAAATAGAGC [26400]
                                                                                          A-rich
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [26500]
scaffold39565_10.7_P._lessonae TTTCTTTTGGTGGTATTTAATCACCGCTGGGTTTTTTATTTTTATGATAAACAAACAAACAAAACATAAAAATTTAGAAAAAACAAACCAAAACAGTTTT [26500]
                                                                                            hAT-2_TS
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [26600]
scaffold39565_10.7_P._lessonae CCAAATAGGTAATTTTTCTCCTTCATTGATGTGCGCTGATAAGGCTGCACTGATGGGCACTGATAGGCTGCACTGATGGATACTGATAAGGCGGCACTGA [26600]
                                                                                         hAT-2_OG
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [26700]
scaffold39565_10.7_P._lessonae TAGGTACTGATAGGTGGCACTGATGGGCACTGATGAGGCATGACTGGTGGGCACTGATTAGGCTGCACTGATAGGCACAAGTAGATGGCACTGATAGGTG [26700]
                                                         hAT-2_TS
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [26800]
scaffold39565_10.7_P._lessonae ACACTTAAAGGCACTGATAGGTGGCACTGATAGGCGGGACTGATGGGCACTGATAGGTTGCACTGATGGGCACTGATTGGCAGCACTGATAGGTGGCACT [26800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [26900]
scaffold39565_10.7_P._lessonae GGTGGGCACTCATTAGCAGCACTGGTGGCCACTGTGTGGGACTGATTTCCCTCTTACATAAGCCGGTAAGCGGCTTTATTCTTTTCTCTTCATGCTGTCA [26900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [27000]
scaffold39565_10.7_P._lessonae GCGTGAGGGGAAAAAGAAGCAGATGCCTGGCTTCTGTTTACATCATGTGATCAGCTGTCATTGGCTGACAGCTGATCAGGTAGTAAAGCGCCCGCAGCAT [27000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [27100]
scaffold39565_10.7_P._lessonae GGGAGGACATCCATGTACACCCTTTCTGCATTTTATGCCATCTTTCGGCTATAGTGCGGGCACCAAGTGGTTAAAGGCATACATTTATATAATTCCGTGC [27100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [27200]
scaffold39565_10.7_P._lessonae CCCTGTGAAAGAGGCCTTACATTTTCAATGTGTGGCTTTCCAGTAGCCATTTGGGTTCCTGCCATGGCACAAAAACATAGTGGTAGGGTTCTAGATTGTT [27200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [27300]
scaffold39565_10.7_P._lessonae TGGTGATTTGTATGTAATAGTATATAAATGTAATTAGCAATTTTTGTTTTCTATGTGAATGAATAATTTCATAGCTACCTAATATGCAAGGGTTCTTCAA [27300]
                                                                INTRON-10
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [27400]
scaffold39565_10.7_P._lessonae AATGCACTTTTCTAAAACTCCAATTAATATAAAAAAGTGCGTAAACTTTTTAACCCTCCTCTTATGTTAGAATTCTGTTACTATCCATGATGTTAGGGTC [27400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [27500]
scaffold39565_10.7_P._lessonae GGTTTTGACCCGTGTTTTAAATCAGCCATAAAATACCCTCTGAATAATTATTTATCATAAAATTTGTTTCTTACCTCTTGGTTACCTTGTTAGGCTTCTT [27500]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [27600]
scaffold39565_10.7_P._lessonae TATCCTTGAAAAGATTGGTTTTAATATTTTTGGTGTGACCCCTTAGACCTTTCTTTTGATAGCATACCTCTCATTTTCAAATTTAAAAAATGGTAAAATA [27600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [27700]
scaffold39565_10.7_P._lessonae AACCAGCAACTCTGAAATGTATTGGTCCTATGTTTCTTTACTTTATTTAGAGAAGCAGACAAGCAGGCAAAGAGATATGCCCCTCCCTAACTACAGCTCA [27700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [27800]
scaffold39565_10.7_P._lessonae CAGGGTTGAGAGGTGATTGGCTGTCAGTGTTACTAAGCAGAGAGAGTGTTTATGATTTCAGTTTTGGAACTTATTAGTGTCCTAAAATCCTATATTATAA [27800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [27900]
scaffold39565_10.7_P._lessonae CTGGGTCAAAATTGACCCTAACACCATGAACGTCTTAATTTTCACCACAGTATTTTATAATTTAGTGAAAAGGATTATTTTTCTATTACATTGTTTAAAT [27900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [28000]
scaffold39565_10.7_P._lessonae AGAGGTTCCTGACAAAGTAAAACAATCTTGATGCAATAAACAAATTTATGTGATACTTATAGACATTCAAAACCTGAAAACGGGTCGGTTCTGACCCTAA [28000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [28100]
scaffold39565_10.7_P._lessonae CACAAGAGGAGGGTTAAAGACCCCTCATATAATACAGGCAGGACTGGGTACAGACTGGAACAATTCATTTTTGCAATATTAACCATGTTATTACACTTTT [28100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [28200]
scaffold39565_10.7_P._lessonae CTTACATGAGTATTTTTCTTTAATTTCCCCTCACTGGGCCACCACTTCCACTATTTTAGTACATATTAGCAGCTATTAGTTTGTTTACCCAAAGGAAGAA [28200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [28300]
scaffold39565_10.7_P._lessonae AGAATGCCTTAAATAAATAATTACAAGAGAGGTGATAGGGCTCAAACCCTCATTTTGGTTCAAGGGCTGTGTGAATTGTGAGGGTAGGCTGAGACTGGTT [28300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [28400]
scaffold39565_10.7_P._lessonae CATTGTTAGCAAAGAATCTGCTAGAATCTGTGAGTGATCCTCACCAACAAATCCAGAAAGAGTTTTTAAACCCTTCCAGAAATAATTTCCAAACCCTTCT [28400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [28500]
scaffold39565_10.7_P._lessonae CCCTCCCTTTACTTGCTGTCCTGTGTGATGCCAGTCAAATAAACAGAAAGGGAGAAATATGAAACAGATTGAAAGTTGGGAGAAATCTCATGGCAAGAAA [28500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [28600]
scaffold39565_10.7_P._lessonae AATTTGACAGATGTTCTAACCCACCCATCTTCCCGATATCCATAACTGAAGGTTCTAACCCTTCTATCCTCTAGTCAAAGCTAGGGGGAGAAAAAAAGTT [28600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [28700]
scaffold39565_10.7_P._lessonae TTAGCAGGAGTTGGCATTTTAAGTTGGTTGAAAATATACAACACTTAAATAATGATCTTTGGTCCAGTTGGCCATTAACACTTTGCTAAGAACCGGTTTT [28700]
```

Table 2.4. (continued).

```
U40452_P._shqipericus              ------------GCTGCTTGTTAGATACTTTGGAAAGATGCCTCAGGTAACAGCCCAAACACTTGTTGAATTAACTGGTAGAATGGCCAAAATTGGAGTC [28800]
                                                                                        EXON-11
scaffold39565_10.7_P._lessonae     CCTTTTTTCCAGGCTGCTTGTTAGATACTTTGGAAAGATGCCTCAGGTACCAGCCCAAACGCTTGTTGAATTAACTGGTAGAATGGCCAAAATTGGAGTC [28800]
U40452_P._shqipericus              TACTGCTGTGGCTTGCCTGACAACAAGAAGCAACCCTGTGCTGAAGAAAAG------------------------------------------------- [28900]
scaffold39565_10.7_P._lessonae     TACTGCTGTGGCTTGCCTGACAACAAGAAGCAAACCTGTGCTGAAGAAAAGGTAAGCTCTTCTTGTTTTCTATCCTTTCAATAGATTTTTATTGATTTTC [28900]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [29000]
scaffold39565_10.7_P._lessonae     AAAATAACAAAGGGATAACAACACTCCAACATGGAGGATAACATAGGGATTGGTACAGTAATAACAAAAGGGAGAAAGAAAGAAAAACAGCTCTTCTTGC [29000]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [29100]
scaffold39565_10.7_P._lessonae     TTTCTGTATAATATCTAGTATTGGGCAGATTTATTTCCTAAACTTGAAACACAATGAAATATTCTGGGTAGGATATATTGGATATAGGACATATATTGAA [29100]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [29200]
scaffold39565_10.7_P._lessonae     AGTGATGGTTCTAAAGTCTAAATGTTTTTTTACTGTAATGCATTCCCTGCATTAAGGTAAAAAATGTCCCACTACTTTTTGTGCCCCCACCCAAACACCT [29200]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [29300]
scaffold39565_10.7_P._lessonae     GACTCCTCCACCGGTCCAGCACTGTCCTATCTGCTCCTTCTTCCTGGTCTCACAGGAGACTCTGAGAGCTGCGGCAGCCATATGCCGCTGTCAGTCAAAT [29300]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [29400]
scaffold39565_10.7_P._lessonae     CCTGTAAGGGGGTAACAAGGGTGTGACTAAGCTGCGCTGTGTGTTATATAAACAGCTTGCTGAGGGGGCACCTGTCGGAAGAAAGAGCGCAAAGCACTGG [29400]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [29500]
scaffold39565_10.7_P._lessonae     TGGGGGACCGCCAATGAAAAGGTTAGCCACTGCTTTATGCACTGTTGTTGCACAGAGAAGGCAAGTATAACCCCAAGTATAACCCCTTTCTTTATTTTAA [29500]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [29600]
scaffold39565_10.7_P._lessonae     TAAAAAGAAAAAACCTTTAATATTACTTTAAATTAACATGGCAGCTAATATACAGCATCTGTCTTTTTGGCTACAGCTCTATGCAAAAATCCTTTCATTG [29600]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [29700]
                                                                                Tc1-13_Xt
scaffold39565_10.7_P._lessonae     CAATTTTTTTCTTGGTTTCCTTGCATAAACTGCAAGTTTCATATCCCCCCAACCCCCCCACAAAATTTTAATGAGATTTAGGGCTTTGACTTTGCCAATC [29700]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [29800]
scaffold39565_10.7_P._lessonae     TATAACCTTTTATTTATTTTTTGAGCCATTCCTTGATGAACTTGCTAGTGATCTGAATCATTGAAGGATTGTTGTGTTTAAACATCTGTTTCCAATGTAA [29800]
U40452_P._shqipericus              ---------------------------------------------------------------------------------------------------- [29900]
scaffold39565_10.7_P._lessonae     CCTAAAGTGGTTCTAAAGGCAGAATTTTTTTTTTCTTTTTACCTTAATGCATTTCATGCATTAAGGTAAACCCCTTAGCACCCCTTTATACTTACTCACG [29900]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [30000]
scaffold39565_10.7_P._lessonae AGTCACGGCCAAACAACCCTATTTTTGATTTGTCAGTGCACCACACATTAGGGTAATTTACTAAAACTAGAGAGTGCAAAATCTGATGCAGCGGTGCATG [30000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [30100]
scaffold39565_10.7_P._lessonae GTGGTCAATCAGCTTCTAACTTCAGCTTCTTCAATTAAGCGTTGATAAAAAAAACTAGAAGCTGATTGGCTACAATGCACAGCTGCACTCTCCAGTTTTA [30100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [30200]
scaffold39565_10.7_P._lessonae ATCAATCAACCCCATTATATAATATGACAGCTTAAATGCCCACCGAAGACCAAATAAAATAAAAGGTATAAGCTATCCCAAGCGCTTAAAATGAGGACCA [30200]
                                                                                                            (AT)n
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [30300]
scaffold39565_10.7_P._lessonae CTCACCAATAATTATATTGGCTATGCAGCTACTTAGCTTAAAAATATGGAAAAAAAATATATATAATAGATAGATACTCAACAATATCTCTATGTATATA [30300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [30400]
scaffold39565_10.7_P._lessonae TAGTAGCGCAAACTTGTCACAAAGCAAGTGCCAAAAGTACTGTGCCAAACTGCACAAAGTCCAAAATGCAATAAATGTCACATAGGCAGCAGGAAAAGCT [30400]
                                                                          INTRON-11
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [30500]
scaffold39565_10.7_P._lessonae CAGAAATGACACAAACAGTCCATATTCCTTCACTCTATCTCCTGGGATGACAATATACAGAGACGTGTTTCTCAAAAGGATCACCACCGCCACCGTGCTC [30500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [30600]
scaffold39565_10.7_P._lessonae CAAGGGGGGAGGAGAATTACCCACTCACCAGATGCTGTGGCCCAACCCACTTTCGTGTTTGAGCATTCAGGCTTATAATGATGGTCACTGGTCCAGAATA [30600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [30700]
scaffold39565_10.7_P._lessonae TCCACAATGGGAATCACACCAGCACAGTCAAAAGAAGCTCAGCAGCATATGGAGAGGAGAGAACATAATCCCAATAGCGTGATACCGTTTAAAAAGGTTT [30700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [30800]
scaffold39565_10.7_P._lessonae TATTAAATAAAACATAAGGTAGTACACTCACATTTCTTGTATGTCATCAAACACAAATAACAGTCACAAATAGGAGAGGAATGCCCTTCGGGAGATGATG [30800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [30900]
scaffold39565_10.7_P._lessonae TCCAGGCTCCACGCCGTGGACGCCGCGCCTTCCGGGTGGTCCAAACTCCTCTTACAAAACCTGGTTACACCGCCTGGTCACGCCCCGACACGTTTCGTGA [30900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [31000]
scaffold39565_10.7_P._lessonae TTTCCACTTCTTCCCCGGGAGCGTGACCACGGCGGCTTGGCGGTAACCTTAAATACCCATGCCCAACACCCCACAGGGCGGGGCCTGGATTGACAACATC [31000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [31100]
scaffold39565_10.7_P._lessonae GGCCATTGGTGTTTACTCCGGTGTATTGACCAATAACAGACTAGATTTACAGGATCACTTCCTCTCAATCTACTAATCTCCATGGTAAAACACCCTATGA [31100]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [31200]
scaffold39565_10.7_P._lessonae CCCGGAAATAGGGTGGAGTCGAGGTGGATACCTGTAGAATACTGGCCAATAGCGGGCTGAGACAACACAATGACCCTCTATCTCGCCGCTATTCACTGTA [31200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [31300]
scaffold39565_10.7_P._lessonae ATAGGCCGTCCTACAACCCGGAAGTATAACACATTGGAAGTTAATTACACCCTATGCCAAAGGCAAAATAACACCAAACCCTCAACGACCAATGGACCGA [31300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [31400]
scaffold39565_10.7_P._lessonae TGATGCACATACAAAACACAAAGTGTATGTACATAATTAAAACGATATGAATCCTATCACTTTCCATTGGTAGTAACTATCGTGCTCTGGCCAATCACAG [31400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [31500]
scaffold39565_10.7_P._lessonae TGATTTAGCTGTACGCCCAATCAGCTAAACATCCTCCTTAGTTGACCTATGGCCCGGAACAATAATACAGAGTCCCGCCCGGATGTATGGACTCCACCCA [31500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [31600]
scaffold39565_10.7_P._lessonae CCAGAAAGATCAAGGAGTTTTCATGTGTACATAGTACACTAAGCACAGCAGCGCCATCTACCAATGGACTAGTGGTACAATGTAAGGAAAAATTTGGTAA [31600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [31700]
scaffold39565_10.7_P._lessonae TCTGTATGGAAATTGGTTTAATCCATGTACCAGAAAATATTAATAATAATAAACAAAATCATGTCTCACCAGAAAAAAGAACACGAATCTACTGGAAACT [31700]
                                                   (AAATAT)n
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [31800]
scaffold39565_10.7_P._lessonae AATAAGCAAAATTAAAATATAATATAAATATAAATATAAATAAGGTAAAATCATTAAAATGACACTAAACCCATGACCAATGTTAAAGCAACATAAGTCA [31800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [31900]
scaffold39565_10.7_P._lessonae CAAGTTTAGGGACATAATTGTGTGCGCGGACACTTTGGAGGATCATGGTCCTCCCAACGCACATCATCAGAAAATTAAAAAATGTAGATATAGAATTGGA [31900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [32000]
scaffold39565_10.7_P._lessonae AACTAAAATCAATAATCACTAATAAAACAATTTAAATCCAACTCTATATTTAATCCAACAGGGCTCAAAGATTGGGTCTGGAATATCCATTTCGTTTCGC [32000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [32100]
scaffold39565_10.7_P._lessonae ACTTTGACAATTCCCTGACCCAATTCGCACCCCTCCACGGGGGTGTCACCCGCTCAACACCCCAGAACTGTAGACAACTGGGGTCCCGTTGGTGGTGTGA [32100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [32200]
scaffold39565_10.7_P._lessonae GCGGAAATGGGCTGGGACACTGTGCTCTTTTTTACCCTTGATAATATTGCTGATGTGCTCCCCAACTCTAATTGTCAAAGTACGTTTAGTTCGTCCTATA [32200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [32300]
scaffold39565_10.7_P._lessonae TAAATGATTTTGCAGGGACACATTAAAGCATACACCACATGTGTGGTGTCACATGTGATGAAATGCTTAATGTCAAAGTCCTTGTCAATTGCTGCAACAT [32300]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [32400]
scaffold39565_10.7_P._lessonae GAAAGGACTCATGTCTCCTCAGATTTTGGGGGGTGTAAGAACATGACTTACATCTTCCACATTTGTGAAACCCTCGTCTGCCCGGAAAGAAAGAAGTGTC [32400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [32500]
scaffold39565_10.7_P._lessonae CGGGGGGTTAAGGATCTTCTTCACCACTCTGTCCCCAAAACTCGGGGCCCTACGATAAATGAAGGATGGGACATCAGGCAACACAGGCCCCAATACGGCG [32500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [32600]
scaffold39565_10.7_P._lessonae TCCATCTGCAAGATGTTCCAATGGGTTTTGAAGATGGCTTCTACTTTTTTGTGGTCCTCACAATAGTCAGACAAGAAGCTCCATTGTTTATCGTCAGATC [32600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [32700]
scaffold39565_10.7_P._lessonae CATTTGTGGGTCTCGTCACATTCTGCAAGCATGCAGCTCGAGGGATATCCAAAATATTTTCAATCTCTTTCTCAAGAGATTGTTCGTCATATCCCTTTTG [32700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [32800]
scaffold39565_10.7_P._lessonae GATAAACCTCTCCTTAAGAACATTAGTTTGGGCAATATAGTCTTCTTCAAATGTACAGTTCCGTCATACTCGCATGAACTGGCCACGCCATTGTTACAGA [32800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [32900]
scaffold39565_10.7_P._lessonae AGACCTGGTCTTTTCCAATCTGTTTAATGACAAACTGTAGGCTTGCTTTAATATTCTTTTTAGACAGCAACGGCTTTCCGTTCATGCAGGTTAAATTGGT [32900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [33000]
scaffold39565_10.7_P._lessonae GCAATCTCTTTTTCCAAATTGTAGATGTTTGCAGTTTGCCACCAACTGTTACAAGAGTTACCTGCAGATCCTGCAGTTAAATGGGTTCTTGGAGACTTAT [33000]
                                                                                        Tc1-13_Xt
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [33100]
scaffold39565_10.7_P._lessonae AGCATCAAACAGTAGACTCTTGGGCTAACTTTGTCATCCCTGACCAAGCAGTTGTTCGAAATCTACGCCACTCATAGATTTTTTTTTCCTTACAATGGAA [33100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [33200]
scaffold39565_10.7_P._lessonae TGACTAATTCACACAATTTGACCATTTTTTTTACATTTTTTTGTCACGCTCATAGGCATCAACAGCCTTCTTTTTAAAGGCCTTAGAGAGCTCTAGTGAT [33200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [33300]
scaffold39565_10.7_P._lessonae GTTGGCATAATAGCACCATACGTCAGTAGCAAAGTAAACACCAGACCCTAGATTCCTGAATTTCATCTAACAGTTTCCACCCACATACTTCCCTAAAGAG [33300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [33400]
scaffold39565_10.7_P._lessonae ATTCTAATCATTGACACCTAATCTGGATCACTCAGTTCTAATGTTATGGATTTGAAGTAGTGCAAAACGTAAAGATGTACTTGAGACAAATTTTCGTTCA [33400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [33500]
scaffold39565_10.7_P._lessonae TTTAGTTTATGACAATGAATGAATTTAAATTTTAGATATCATTTATCCAAGTAATCTTTATATGTAGATTGAAAAGTAAATTCTATTTTTTTTATTATAA [33500]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------C [33600]
scaffold39565_10.7_P._lessonae CCATATGCTTGCTTTGAACACACCATTTTTTCATTTAGAAATCCTGTTTAAAATATCCTCACTAAACCTCTCAATGTTTTCTAATATTTTACATCACAGC [33600]
U40452_P._shqipericus          TGGATATTCTTTTGGGAGAGATGTGTGAAAGGGAAAAGAAAACATTCATAAATGACAATGTTCACCATTGTTGCGTCGACTCATATGCTAATAGAAGACC [33700]
scaffold39565_10.7_P._lessonae TGGATATTCTTTTGGGAGAGATGTGTGAAAGGGAAAAGAAAACATTCATAAATGACAATGTTCACCATTGTTGCGTCGACTCATATTCTAATAGAAGACC [33700]
                                                                      EXON-12
U40452_P._shqipericus          ATGCTTCACTAAACTTGGACCTTATGCTAATTATGAAGCACCAGTATGGGATGAAAGTAAGCTCCACTTTACTGCCGACATGTGTAAAGGTTCAGCAGAT [33800]
scaffold39565_10.7_P._lessonae ATGCTTCACTAAACTTGAACCTTATGCTAAATATGAAGCACCAGTATGGGATGAAAGTAAGCTCCACTTTACTGCCGACATGTGTAAAGGTTCAGCAGAT [33800]
U40452_P._shqipericus          GACCAGCTAAAGACGAAACTGGT----------------------------------------------------------------------------- [33900]
scaffold39565_10.7_P._lessonae GACCAGCTAAAGACGAAACTGGTGTAAGTTTTGGAAAAACAGCCATGAGAGGCTTTAAAGATTGTCACATAACACAATGCATGCAATAGCATACATGCTA [33900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [34000]
scaffold39565_10.7_P._lessonae ATATGGGTTAACTTGCAATTTTATGGTGTGTATTTTACATGTCTTGTTTTTCTTTGTTTCCTGTTTAAACTGTTGTCCTTCCTTGCTGCATTGCTCTAAA [34000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [34100]
scaffold39565_10.7_P._lessonae ATGCACCCTGCCTATTTTTTTTTTTTTTAATTGCGCGATGCAGGTTATTGGTTTGAACTACCACTGAAAACAATAGTATTTTACATGTCCTGTTCTATGTT [34100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [34200]
scaffold39565_10.7_P._lessonae CAGATATGAGAAATGTATTCGATTTATCAGGGTTTATTATTTATTAATGAAAGTGCTGCCTAAAAATGTCACCAGGTCCAATTTTTACTGCGTTAAACTC [34200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [34300]
scaffold39565_10.7_P._lessonae ATTCAAAAAGCAGCATGGGTATTAATGCAACACATAGTGTAAATGGGGCCTTCAGAAGTGTTGTATAAGATTTAAACCCCTGTTAGGTTTGCTGTATCTC [34300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [34400]
scaffold39565_10.7_P._lessonae TTTTTAAGAGATTCAACCTCTGTTAGGAATTCATCTGTGGCTTCCTATGGTGGCACATGGAGAAGAGGAGAAACCCAGAGTGCCAGAGGGGGACCGGAGC [34400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [34500]
                                                                                                               (T)n
scaffold39565_10.7_P._lessonae AGAGGAGGATTGGGGCTGCTCTGTGCAAAACCATTGCACAGAGCAGGTACGTATGATGTGTTTTATTTTTTTTTATTTTTTTATTTAACATTACACTCTC [34500]
                                                                      INTRON-12
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [34600]
scaffold39565_10.7_P._lessonae TTTAAAGCAAAGCCTGCAGTGGCAGACCAGGTAAGTCAAGCTTCCAATGCAAATCTGGAGTAAGACTGAAGAGAGAAAATATATGATTGGAGCACCACGT [34600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [34700]
scaffold39565_10.7_P._lessonae GGATGTATCAAAGTCCACAGATAACAAATTTATTTCCTTAAAAGGTTAGACAAAAAGTATGTAAACAATGGATGCATTTTAGGGGCTAAGCCCTACCCTC [34700]
```

Table 2.4. (continued).

```
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [34800]
scaffold39565_10.7_P._lessonae  TTCATCAAGTGTTATGGTTGTACATGGACCAAAAAAAATGAATTCTTTGTCCTTTAAGTAGACAGAGGATCTGGGTGATACCTAAGACTGGGTTCATATA [34800]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [34900]
scaffold39565_10.7_P._lessonae  TATGCAAATTTCCCCGCATCCAATTCGCATAACAGGAGAGTGTGACCTGCTCTCAATGGAGCAGGTACACACAGCTCCAAGGTGGCCACGGTCCACATTG [34900]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [35000]
scaffold39565_10.7_P._lessonae  GAAAGGGCCTGTGCATCTTTGGTTCCGATTCAAGTGCAAATTCAGGCCAGAATACAGACCTGATTTGCACCTGAATCGGCGAACAGGGATACACCGGACC [35000]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [35100]
scaffold39565_10.7_P._lessonae  CCATGCTGTGAACAGCATATATAAACCCAGCCTCAAGGTTGCATTGTGTTCTGTGTTGGCTTTGCTGGCAGCTAGATTTTGCAGTGACCGTGGGAGAAGC [35100]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [35200]
scaffold39565_10.7_P._lessonae  TCTAACCCTCCTCTGCCCTGAGGGCTGGTTCACACCAGATGCAGTCCAGTGAATTTTTATTCTGCCTCAAAAACACAAGCACAGTGTTTAACATGGATTA [35200]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [35300]
                                                                 (CAGTG)n
scaffold39565_10.7_P._lessonae  CAATAGCCCTACTTTACACCAGTGCAGTGCGGTCCAGTGCAGGCAAGAAAAGTAGAACATGTTAAATTTTTTCTGTACAGAATGCCTCTGGAACACAGCA [35300]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [35400]
scaffold39565_10.7_P._lessonae  AACACATCACAAATGCCCTGGAATGCATGAAAAAACTTGCATGCAGAAATGCATAGGGACACAGAAATTGTGGTGTGAACCAGCCCTCAAACAAAAATGG [35400]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [35500]
scaffold39565_10.7_P._lessonae  AGTTTGGATTTAGGAGATGCTCATTGATCCCATAAAACCACACTCTACATCATACCTTTCAACTAGAAGTATTTATTAAGTACCTAACAAGAACCCTAAC [35500]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [35600]
scaffold39565_10.7_P._lessonae  TGGTAACCTTGCAACCTTAAATTGAAACATACATTATGGGTGCATGAAGTCATAAATTTAATTTCTTAACATTGTTTAAAATTATATAATTTTCTTTACA [35600]
U40452_P._shqipericus           -ATTGTTGGTTGAATTTTTGAAAATGAAGCCTACCTGTGGGAAAGAAAAACTTACGGAGGTTATCGAATCCTTTAGAAAAACAGTTGTAGAGTGTTGCGC [35700]
                                                                                          EXON-13
scaffold39565_10.7_P._lessonae  GGTTGTTGGTTGAATTTTTGAAAATGAAGCCTACCTGTGGGAAAGAAAAACTTACGGAGGTTATCGAATCCTTTAGAAAAACAGTTGTAGAGTGTTGCGC [35700]
U40452_P._shqipericus           AGCAGAGAACCAGCAGGCATGCTTTGATGAGAAG------------------------------------------------------------------ [35800]
scaffold39565_10.7_P._lessonae  AGCAGAGGACCACCAGGCATGCTTTGATGAGAAGGTATGTAATGTGACTGCTGTGCAATGTGTATAATGCCAACTACAATGGAACACGTGCTTCAGTGAA [35800]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [35900]
scaffold39565_10.7_P._lessonae  GGTGTATATTTGCGTTTTGTCTATATCTGTTGTTCATGCAAAAAAGGTTCTGTTTTGCAAAGGAAGAACTGTTAGCTAAATATAAATTGTGGATGTTCTG [35900]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [36000]
scaffold39565_10.7_P._lessonae ATTCCCATATCTACAGTGTTGTCACGAGCAGCTAATCATTTTAAGTGTTATTCAATCAGCATTATCACTCTTACAGTAGATAGTGCTTACAATAATTGGT [36000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [36100]
scaffold39565_10.7_P._lessonae ATAAATCCAATGTTATTAGCGATCCGAAGTAAAAGTTAGGGTTTCTTAATGTATAACTAGGGACAAAACTTTTTTTTTGTTTTGGATAGAGGGGAGAGGG [36100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [36200]
scaffold39565_10.7_P._lessonae ATTAGAACACCTGTCAGTTTTTATTGCTTTATCATTGAAAGTGAAAGTAATATAAAATCCCAAATTTTGGGTTGTCCCCAGAAAAGTAATTGAGGGGAAA [36200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [36300]
scaffold39565_10.7_P._lessonae ACTTCCAATGGGGACACTAGTTCTGGTGACCTGGGGGTCCCCAAGGAATTCCCTTAATTTGCAGGGATTTGCTCCCACTTCCTGTTTTGGCTATGGGACA [36300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [36400]
scaffold39565_10.7_P._lessonae GGAAGTGAAATCTCCCCAATGGGACACAGATGGCGAAAAAAAAAATCTGATAGGGGTTATAACCCTCCCTTACCAACCCGCCCTATCCAAACTGAAAAAA [36400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [36500]
scaffold39565_10.7_P._lessonae AATGTTTTGCCTATAGTTCTACTTTAAGTCATGGGAGAGCTGCTTACCATGCATGCACAATGACCACCTTTTAGCAGCTGGGTCTGCTATTGCTACAAAA [36500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [36600]
scaffold39565_10.7_P._lessonae TTCAGCTTGGGGAACAATTGAGGTATTGGTGCAGGTGGATGCTTCTTATCTAGGAGGGTTCATTAGTGGGGCAATGAGAGGGGCCAAGAAAGGGGCTGTA [36600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [36700]
scaffold39565_10.7_P._lessonae ATGGTGTCATAAAAATGGTTAGATTAATAGAGGTATAGACACATGTAATATATTAAAACCAAAGTTTATTACACAAAAACTTATTCTTATAAAAACAGAA [36700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [36800]
scaffold39565_10.7_P._lessonae TACCCATACAATAGAATGAAGCTTCACTCTGAGGTCAACTTCTGCTCCAGCTAAACAGGTTAGGTTGTCCAGTGTTACCTTGAGCTATATGTTGCTGTCT [36800]
U40452_P._shqipericus          -----------------------------------------INTRON-13-------------------------------------------------- [36900]
scaffold39565_10.7_P._lessonae CACTATGAACACTTTCCTTTTTCATTTTTGCACACCTGTTTATTGTTGGCTGGGCATCTGGCCACTGATGCACCTGTTTGAGTCCACCTTGACCTGGATC [36900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [37000]
scaffold39565_10.7_P._lessonae TTTGGTCCAATGGGTCTATAAGAGTGGCATATCCCCCATGGTTGCAGTGTGAGGTTGTTTTTTTTCTTCATGCATGTTAACAGACGTAGGTGCCTGGATT [37000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [37100]
scaffold39565_10.7_P._lessonae AATATTGCTAAATACAGCCTTCTATAATAGGAGGGTTCATTATCATTTGGGACAAGCTTTCTAATGCATCTATTTGATGCTCCTGCCTTCTCTTAGAGAC [37100]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [37200]
scaffold39565_10.7_P._lessonae AGGGGATTATTGGCCAACTAGGTACAAAATGGCAAGATATGTCTGCTAGATCTTCGTGACTATTTGTTTCCTAAATGTCAACTATACTCAGATTAAAGTC [37200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [37300]
scaffold39565_10.7_P._lessonae TAAGGTCACCATTTAAAAAAACATATTAATGTACATCTTTTTTTTAGGAACAAAATGTACAAATACAGTATTTTCTTCGACAGGAGCCTGTAGAGCATTG [37300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [37400]
scaffold39565_10.7_P._lessonae CACCCGAGAACAATGGGTGCAATGTCCAGCTTCAGCAGACACTGCCTAAAGCTCTCTGCCATACCACTACATGGGCAGACAGTTTCTTAGCTGTAGGCAG [37400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [37500]
scaffold39565_10.7_P._lessonae TGTGAATGAACTATGAGCACGTTCATCAGCATGCTCAGAGTTTCCTGATACTACAAGTCCGTTTGTTGTAGTGGAATATGGGACATGTATTTTGTTCATA [37500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [37600]
scaffold39565_10.7_P._lessonae TATTCCTGCTATTTTCAAAATATGACAGTGGGTGCAGGGAGAAGAACCCCCTCCTACTGTCACTGGGTGGTGAAGTGGGTAAGGGGAGAATGCGTAATAG [37600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [37700]
scaffold39565_10.7_P._lessonae TAACATGTTACACCCTAATAACGGGTGTAATATGTTACTAATGGTGAACTTATCCATTAACCCACACTAATTAAAATGCTACACAAACGGTATAGTGAAC [37700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [37800]
scaffold39565_10.7_P._lessonae TGTTTTCTTGATGGCCTATCTAATAAAAATGTACTATATAACAATAAATAGAATACATATTCACTGTGTGATAGTGAATTTAGCAAATACTCACTTTGTA [37800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [37900]
scaffold39565_10.7_P._lessonae ATTCTAGCTGCTTGATAATGCATTTGATGAATGCACACTGGGCCTAATTTACTAAAGATGTGAAATGAAGTTAAGTAATCTTGGTTACCTTTTTAAGGAG [37900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [38000]
scaffold39565_10.7_P._lessonae CAGTCCACCCAAAACTAATCTCCAGTTTTTAGTAAATGCTAAAAAGGTACGCCAACTATCCTTTTCTTGGGAACACTGTTGGTGAGCTATATGCACTGGA [38000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [38100]
scaffold39565_10.7_P._lessonae GTTCCTGGATCTGCACACCTCTTAAATATGAGGAGGTCTTGCTTTGCTTGTTGGGTTTTTAATGTACTTTATACTGTGTGATGGAGCATGAAGAGGAAAG [38100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [38200]
scaffold39565_10.7_P._lessonae GAGTTAACATTTTTGGCAGGCAAATCTTACTGCCAAGGTATGTAAGATATGCAATAAACCAGGGGGTTCACATACCCAAACTTTATTTTAATAAATATTA [38200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [38300]
scaffold39565_10.7_P._lessonae TGCATTTTATTGAATGTTTGACATGAACACAGGAATATCCCATCATACTTTAGTAAATCACAGTTGTCTGTGCATCTTTCAAATACTTGATGCTAAATAG [38300]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [38400]
scaffold39565_10.7_P._lessonae TGTATCTAACGAATATTGGGTTATATGCACAAAAAGAGTGCTTATTAGTTAGTAGAAACCTATAGAAACCTATCCTTGTGCACAATGTACATTATTCACA [38400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [38500]
scaffold39565_10.7_P._lessonae AATACCCACTGCTTGGTAGTGCAACTAGCAAGTTATGTTAGATGCCTTATAGGCTGTTGGGTGAAGATGACTTTTTATTAAAAGTGACTGAAATGTTTTG [38500]
                                                                                                                 3'UTR region
U40452_P._shqipericus          -----------------------------------------------AAAGGAGGCCTTCATGAAATAATTAAGGACCATTGACATGGAACAG------- [38600]
                                                                                          EXON-14
scaffold39565_10.7_P._lessonae TATCTTCTTTAATAATAAATGAATTCTGTTATTTGTGTATATTTTAGAAAGGAGGCCTTCATGAAATAATTAAGGACCATTGACATGGAACAGGTAAGTC [38600]
                                                                                                         STOP CODON
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [38700]
scaffold39565_10.7_P._lessonae TTGCAGTGTGCATGAATGGTATATGTATTTGTATTTCTACCTTGTAGACATAAATAAGTGGTCTTCTAGGTTGGATATTTTTACATCTTAGACCAATATA [38700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [38800]
scaffold39565_10.7_P._lessonae ACTTTACATATACCATACCTGTGAAAGCTGAAAATCATTGAAGTAGACACCGCGATTATAGTGATTTCTGCTAGTTTTGGGGTCCTGTGCTGAATGGCTG [38800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [38900]
scaffold39565_10.7_P._lessonae CCCTGCTGCATTGTGAACGCAGGATGTCGCCCTCTCAGCACAAGCACATTTTAGAGACCACTTTGCATTCTCCCAGTGCATGCAAAGCATTCTCTGATTA [38900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [39000]
scaffold39565_10.7_P._lessonae GATGAGCTAGGTAGGAGGGTCAGGGACGTCACAATTTCCACCTGCTTCATGCTTTGCATTCACTGAGAAAATGTAAAGCATTCTCTGAATGGCGCCCATG [39000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [39100]
scaffold39565_10.7_P._lessonae CCAAACGGGCAACCTTATGTGTTCAGAAAGCTGCAGGGCAGCTGCTCAGCATGGAGCCCAGAAGCTACAGTGTCTTGGTCCATCTGCAGTGCCCCTCTGT [39100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [39200]
scaffold39565_10.7_P._lessonae ACCCCATCTAATTCTGGCTGCTTACTGCAGAGTGCTGAGTTCCACTTCAATCGAATACCTTTTTTAAACTTGGTCTGTTTATAATGTACATGTTAAAGCA [39200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [39300]
scaffold39565_10.7_P._lessonae GAACTTAACTCACTAAAACAAGATTTTCCTATTTTGTCCCTCTTCCCTTCTTCTTACAAGGATGCTAAAAAATGTATTATAATTTTTTTACCTTTGTGTT [39300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [39400]
scaffold39565_10.7_P._lessonae ACTTTTTGTGCTTGTCTGTACTTTCTGGTTTCCAGCCTAGGCCTGGCACAGCTGTCTACTGGAATCACTGTATCACAGTTATCCCAGGAGGCAGTGTGTT [39400]
                                                                       INTRON-14
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [39500]
scaffold39565_10.7_P._lessonae ACCAAGCTGCAACTTTGCTGTGCATGTGCGCACATGCGGTGAATTTCCGCGCATGTGCACAAATGCTAGAGGGTGCTAAAGCGCCCATCTCCCAGTAGTT [39500]
```

Table 2.4. (continued).

```
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [39600]
scaffold39565_10.7_P._lessonae    GGCGGCATTTGTGCACATGTGAGGAACTCCGCTGCATGTGCACAGATGGACTGCCAGTCTTTGCCAGCTCTCAAATACCTGGAAGAGAAAAGTTTAGATG [39600]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [39700]
scaffold39565_10.7_P._lessonae    TGCGCAGTATGTAAGAGCAACCTAGGAAAAACAGCACAAAACGAATTAATAATGATACATTTTATTCAGTGCACTCTTTTAGGAAGGGTGTTTAAGGGGA [39700]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [39800]
scaffold39565_10.7_P._lessonae    TATTTTAGCTGGCATTATAAGTACACATTACTCATCTTCTTTTACCTTTCATATGTACATAATTTTTTTTTTTTTTCGTGGGCAGTTTGGATTTATTTTT [39800]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [39900]
scaffold39565_10.7_P._lessonae    ATTCTTTCAGCTGTGTTATGATTGGCATGCTAATCGCAAAGCATGTGTTCTCCTGTTCCTGACACAGGAGGGGAGACAAACCAAACAAATAAAAAAGCAT [39900]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [40000]
scaffold39565_10.7_P._lessonae    TGGGGTTTCTCAATTTGTTGCATTCCAGCAACTAATCAGATTCAAACTGCACTTGAAAATTACTGTTGAACCTCCTCTACCACATATCATATATGTAGGG [40000]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [40100]
scaffold39565_10.7_P._lessonae    ACCAAAGTTCCTCAAACAATGTCAAGCTTCCTTGACCTTGGTACTTTAAGTCTAATGGACCTGACTTATTTATGTTGGTTTCTTTGCAGTGTATAAACCA [40100]
                                                                                                                 (3'UTR region continued)
U40452_P._shqipericus             ----------------------GCCAAAAGCTGATAGAACAAGACTGTGTTGAGCCACAGGGTTAAACCATCATCAACTGGTCACTGATACATGTCTCTG [40200]
                                                                                                                       EXON-15
scaffold39565_10.7_P._lessonae    GAACTTTCCTTTCTTCAAACAGGCCAAAAGCTGATAGAACAAGACTGTGTTGAGCCACTAGGTTAAACCATCATCAACTGGTCACTGATACATGTCTCTG [40200]
U40452_P._shqipericus             AAGACTCAAGTAGAAAAAAACAATCATTTTACTGCAAAAATAAAAAATAAATTCTTTATGACTGG----------------------------------- [40300]
scaffold39565_10.7_P._lessonae    AAGACTCAAGTAGAAAAAAACAATCATTTTACTGCAAAAATAAAAAATAAATTCTTTATGACTGGATGTTCTTGGTGTCTGTTTTTATGAAAAGCAGTGT [40300]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [40400]
scaffold39565_10.7_P._lessonae    TATAACTGATACTATACAACATAACATAACATAATGAAGAAGTTAAAGCCTCATTTAAAGTTAAAGACTCCGTTTTATAGTCAAATATATGTTTATTCAA [40400]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [40500]
scaffold39565_10.7_P._lessonae    GCTTCACCATATCAAAATGATATAAGAGCCAGTAGTTTGTCAAATGTGAAGGAGTAAATATGGGATCCAACAAGGACAGGGTACCCAACCATATACAAAA [40500]
                                                                                       A rich
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [40600]
scaffold39565_10.7_P._lessonae    AATCCCCCAATAAACCGGCATATATTAAACTGGAAATGATAACAGACAAGAAAACAAAAAGAAAGAAAAAGAAAATAAGCTAAACAACATAAGTCCATCC [40600]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [40700]
scaffold39565_10.7_P._lessonae    TTCTCTGCCCTATGGAAGCAAAAAAGGGAGGATTGACATCCAAGGGCCAGGCCTCAAAGCAATTATAACAATTGTAGAGTAGGTGTATCCCAAGAGATAG [40700]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [40800]
scaffold39565_10.7_P._lessonae ACAGGGGAGAAGAGGAGAAAGAGTAGACAAAGTACGAGAAGCAAAGAAAGAGAGAAAAGATGGTGTGGGTCCCGAGGGAATCTCGAGGCCAGGAATGAGG [40800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [40900]
scaffold39565_10.7_P._lessonae GGGGAATAAAAGGAGTAGAATCCTCTTGGATAAGGGGAAGCCCAACACATGATAACTAGAGGGGGCCCAAGGAGTATCCTGGAGCTCCATCTCAATAAAC [40900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [41000]
scaffold39565_10.7_P._lessonae TGCCGAGGAAGAGGAGATAAGATTATCCTATCCTGTAAGATACAAGCTGCTTAAAAGAATCTGATGATGAAAAATGTATCCAGACATACCAGAGTGGGGT [41000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [41100]
scaffold39565_10.7_P._lessonae GAATTTAAAGACTCAGTTTTAAACTTTTTGATGTTCTCCTAGCAAATCATAACATATGCACACATGTTAAAAAATAATTCCAGGTATATTTGTTTACATA [41100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [41200]
scaffold39565_10.7_P._lessonae GTTACATAGGTTCATCTTGTAGCACTGTAACTATCCATATACTATACCTTTGGGATCCCTCTAGAAAATCATCTGGAAATCAATGCAGTGGGCATCACTA [41200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [41300]
scaffold39565_10.7_P._lessonae CTCCACCACTACTCCATTGATCTCTGTTAGCTCATTCCACGTTAGCTCAGTTTCGTACAAAGCAGGTAGTCTGTGAACAAATTACTTTAAGCTGTCAGGT [41300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [41400]
scaffold39565_10.7_P._lessonae GTTAAAATATGTATATTTAGCCCCTACACTGCACCTAGTGAATAAACAGCATGGAAACTTAGCTTTGAACTAATATTGAAATGGCCAAAATAATACAATG [41400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [41500]
scaffold39565_10.7_P._lessonae TATAGGATATTTAAATACCCCTATTAGAGGTGCCTTTGTCTTGCGATGTTGACATCTTAAAACAAAATGGGCCTAATGAATGAAAAGTCTTCTAGTCCAA [41500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [41600]
scaffold39565_10.7_P._lessonae AAATGTTCTTGTTGTCCAAAGTAATCAACTAGCTCTAATGCTTGGGCTATAAACATGACAGTTGTTAACTGATTGCAATTGCTAACTAGAACACTTTTTT [41600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [41700]
scaffold39565_10.7_P._lessonae TATATAAGAAACCAAATATAAAGTGTCAATCTATACTGAAATATGGAACCTATAAAATTTTGAAGGCCAGGCAATATTTATGAAAGGCATAATCTTAACC [41700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [41800]
scaffold39565_10.7_P._lessonae AATTGGACATGCACTTCAAGCTACACCTGAAATTTTCAAGGGTACTTCCAGTTGGTAAAGTAAATTCACTATATCAAATTAAAAAAGCAAACAGATATTT [41800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [41900]
scaffold39565_10.7_P._lessonae GTCATGAATTTGCTAGTTCTTTCCCAGGTACAGAGGCGGTCAGGCACACAGCAACACTTCACTCATTCTGGCTCAATATTCAGTCTAGATTCTAGAAGAA [41900]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [42000]
scaffold39565_10.7_P._lessonae TGCCTTTTTGTAATTTAATACTGTAGAATAACAGGGGAGGTTGAAGGGGTGTGAGATACTCCAAAGCGCTTAACACAGCTTGAAGAGGACACTCCTCTGT [42000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [42100]
scaffold39565_10.7_P._lessonae CAGCAGTAGCAGTTACAAGGACATATTGACTAGTACAATCTGAGGATGCACAGCTGAAGACTATATAGTAGTAAGTAGAAAATTTGCTATAGGCTTGGAC [42100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [42200]
scaffold39565_10.7_P._lessonae AATCAACGGATGTACAGCTGGAGACCAGGCAGGAGTATATAGCCTACAGATAGTCATAGACTTGGACAGTCTATGGGTGCACAGCTGAAGACCATGCTGG [42200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [42300]
scaffold39565_10.7_P._lessonae TGTATGAAGCATACAGACGCTACTCACCAGGCATGCCTCATAGTCAGTCCATAGGTAAAGTCCCAACATAAAGCCAGCATCCAGTCCAGAAGTGCCTCAG [42300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [42400]
scaffold39565_10.7_P._lessonae GGGGATCAGCCTCCTGGAGCTCACTGATCAATTCCCCACTGGGAAAGAGATGATCTACCCTGAACTCCAGCCTATTTAACAGGAACCCATCCACACAGGG [42400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [42500]
scaffold39565_10.7_P._lessonae GCATATCTACCACGAGGCAAACAACTAGGCAGAAGGAACACTATAAACATGCCCAGACTGGCAGTAGGGTACACTGACCATTTACTAGGTGGGCCGGGCT [42500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [42600]
scaffold39565_10.7_P._lessonae GCAAGGCCACATGTCCTACCAAGAACTTTCTTCCCCCAGCTCCCCTTTCACTCACTGTTTATGGCTGCTTATACACTATGCCCCACCCATCACACACTCT [42600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [42700]
scaffold39565_10.7_P._lessonae ACCAGTCAGAGGTTACAGCACTCTGCAGAGCCCTGTTCACTGTATCCAATGAGGACGCTGCTGACATCTCCATCCTCACCTACCAGGTGTGCCTGGCTCT [42700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [42800]
scaffold39565_10.7_P._lessonae CTGTACTGTGTGTGTTCAGCGAGTGCTCAAAGGAGCATGAAGATGCTGGGAGAAAGGGGGAGACCGGAGATGACAGGGTGCCCAGGACTACTGCTACTCT [42800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [42900]
scaffold39565_10.7_P._lessonae GCACTACTCTGGTTCACTTCCCCTCCCTCCTGGCAGCAGACTTGAGACAATCAGGGAACAGGAGTGCTTGAACCAATCTGTGGCGGGGAGAGGACTTGCT [42900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [43000]
scaffold39565_10.7_P._lessonae ATGCAGGTGCCATGATTCATGGGAACTGCATTTCTTGAAGGGGCGTTGCACCATACATAGAGGAGGCTATTGGCTGTGGAATTTAATACCCTGGATTCCC [43000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [43100]
scaffold39565_10.7_P._lessonae TGCAACTAGTAGTAGGAGAAGAGCAGCACTTTCCTGGGCAAGTTACCAGAGATCGGGGTTGTGCCACATGGGAAGAGAAGGAATGCAGACCTTTGCTGTC [43100]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [43200]
scaffold39565_10.7_P._lessonae TGGGTCTGGGGCCCCACTACAAGGGAGAGCGAGAGAACTGATGAGAGCTGAGCCAGAGCCATGGAGGACCATATGACATGTCTACATCAGGGCTACATCA [43200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [43300]
scaffold39565_10.7_P._lessonae CAGTGTTCTGGCACTGAAGCTGGGAGGTCTGTTGCCCTGTCTGTCTACAGCCAGTGAGGATTGAGACTTTGGGACAACTGATCAAGCATGCTGGACCTGA [43300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [43400]
scaffold39565_10.7_P._lessonae TACCCTGCATACCAGGAATGGTGAGGGGAACTACTGAGCTTAACCCCTTGCTGCCCGCATTTAAGTTAATGCTAACAAAGAACTGCCCCTTACTTAACAG [43400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [43500]
scaffold39565_10.7_P._lessonae CCCATCAGCCACCCTTTGTGTACAGTTTTAAAGGGACAGCTACATGCACATCGCCTATAGAGAGGCCCCAACAAAGCCAGCAAATACTGACAGTTAGGCT [43500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [43600]
scaffold39565_10.7_P._lessonae CCAGGTACTTTGCAGTCACTTTCAGGGGTATCCCTTTGTTAGGAACAATGTCAAAGGAAAAGATCCATAAGCTACACATCATGAGCCAGGCCCATGTGCA [43600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [43700]
scaffold39565_10.7_P._lessonae TGAAGTGAAATGAACTGCAACCTCTGCCCAGACTCCAGCCAGACCAGGCCCTAACATGTTTGGCTCTGCCCCTTGGAGTATCATTATCTTTATGATTAAG [43700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [43800]
scaffold39565_10.7_P._lessonae TTCCAAGGGATGGAGGGAAACACGTTCGGGCGTGGCCTGGCTGGAGTCCGTGCTGAGACTGCCATTTATTTGACTTCATGTACATGAGTATGCTTAATAA [43800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [43900]
scaffold39565_10.7_P._lessonae TGTGCAGCTTATGGATCTTTTCCTTTAACATTGCTGCAGCTTGGAGCTGCGACAAACTCTCTGTCCTTGCCTGCGCTCACAGCTGTCTAGGTACCCTTAG [43900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [44000]
scaffold39565_10.7_P._lessonae AGTGGGGAAGAGAAATTTCTGCTGTTTCCAAGGAGCTAGTCTACAGTTTACTAATGAGTTTGAGGCCTGTATGGTACAGTTGAGAATGCCAGAGGCAGAT [44000]
                                                                                  (CATTG)n
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [44100]
scaffold39565_10.7_P._lessonae CCAACAAGTTCCAGCCCGCCATCACCTGAGCCTGAAGTAGCCATTGCATTGTACTCATTGTCATTGCATCAATTTCTGGGATCCTTCCTGCCTCCTTCTT [44100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [44200]
scaffold39565_10.7_P._lessonae CACGGATGTAGGAAAGCTGGTGTAGACCTTTATTAAGAATGGTTCCATACCCTATTACGATTGGTACAAAAAATTGCGATTCTTCTCTGGGAAACCTCTT [44200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [44300]
scaffold39565_10.7_P._lessonae GCTCTCATAGAGGAAGATGACTTTGACATCTGGGTCGACCAAGCTGTGCAGGCTGTTGAAGAGTGGAAAGGGGTTGACACTGTAAAGAGACAGAGAATAG [44300]
```

Table 2.4. (continued).

```
                                                                    Gypsy-24-I_XT
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [44400]
scaffold39565_10.7_P._lessonae TCGAAAGTCTATGGGCATCTGCTTCAGATGTCATCTGAAACTCACAAGGTTGCAGTGCTGCAGGATGTCTGGAAGCTCATCAAGAGTATGGAAGAGGAGA [44400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [44500]
scaffold39565_10.7_P._lessonae AAGCTGGGCAGAACGAATCTACTTATTCAAGCACACCTTTCAGGGAGAGAAGTTGTCGCCTCAAACAAAATTCTGTTGACTCATGCTTTTGAAGGGGTGT [44500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [44600]
scaffold39565_10.7_P._lessonae ATCTTCTAGATCAGAAACTCCAAACAAGAGACCACAGTAACTTGTTGACCTACTCCAAAATGATGAAAATATTCTGGGAAGAAGTGGCTTGGATCACGGC [44600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [44700]
scaffold39565_10.7_P._lessonae CAAGACACAGAAATCCAACACTTCTTAGGGACATGGGCAGGGCGAGAGTGGAGCTTCTGTGCACTGTACAGGCCATCCTGGGTGCACCAGAAGGGAAGAA [44700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [44800]
scaffold39565_10.7_P._lessonae AGCCATGTTTAATATTACCAGAATCCCTGACAAGCTAATAGGCCCTGTGTACACCCTCCCAATAAAGGGCTGCATGCGCAGGGTGCACTCAGGGACACTT [44800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [44900]
scaffold39565_10.7_P._lessonae TTGAATAGTCATTGCCAAGGGTTACCGTGAGACTTTTACTTTACGCCATTAATGCTTTCGCGGTTGATCTAGTTTTTACTAATGCTGTGTTTAATGGTGT [44900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [45000]
scaffold39565_10.7_P._lessonae TTAGCCTTATTGCGATGTAGGTAAGTGGTGGTAGGTGAGGATAACATTCCTGTTAGTTAACCCAATGTATTCTATTGTTCTGTTTATTTGTTTTATGCAA [45000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [45100]
scaffold39565_10.7_P._lessonae TGCATTTACTTACCCTTCAATAATACACTTATCCTATTAATTCTCAAGTTGCCTGTGGCCTATTTTCTGTGCATTCTTGTAGTTTGGTAACGTTTAAGTT [45100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [45200]
scaffold39565_10.7_P._lessonae ACACAGATGAGAGCGTCCTTCAGTCTATAACCAGGTGTATCAGTGGGGACTGAGCAGTGTAAGGAGTCGTGGCAGAACAGAGGACCCCTCAAACCAAGCA [45200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [45300]
scaffold39565_10.7_P._lessonae GCTCCTGTGGGGGTAGCGCTACATTAGAATAAAATTCCTAACCCGGAGATATTGAAACAGTTCTGTACAGAGAGCTCATACTTATCATGAAAAAACTAAA [45300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [45400]
scaffold39565_10.7_P._lessonae AGGGTTCATGCCCTCTGAATTAAATTGTATATAGGGGGGTATTATTTGATTAAATCCAGTGTTTACATGACTATGTATGTAAATGGACTATAAAGGAGG [45400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [45500]
scaffold39565_10.7_P._lessonae TGCAGTAAGATGAGATAACCAGAGTACTTAGTGTTGTCCCAAACTTTCAGGGAGTGAGGTATATTTGGGGTTTGCAGTCTAGGGGTTCTAATTCCATGGC [45500]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [45600]
scaffold39565_10.7_P._lessonae CTAATAGAACTCTAAGGGTTTATATTTCCATTGCCTCAATGCATGCCAGCAAAGAGCACTTAACAGTACTGTGATATTTCACCAACTGGCTAATCTTGGT [45600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [45700]
scaffold39565_10.7_P._lessonae GGCCAGATAGTACAACCTACTTTAAAAAGTTTTGAATACCTAAACCAGCCTTTTTTTCAAACGATGCAGGGACATTTTTCCTTCCAGTGACACCACCGAT [45700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [45800]
scaffold39565_10.7_P._lessonae GCAGGGGTATCTCTTTATTTTAGTGACAGGGCCAATTATTTTACCACATTGATGCTGGGGCTTTTCTTTCTGCCTGTTAGCCCCATATTTTAGTGCAGGT [45800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [45900]
scaffold39565_10.7_P._lessonae AGAATGTGTACTTATCATGTTGCACATGCATTGTTGTATGTTTTCCTTTAAATAATATCATCCTTTCTTTACTCTGTTACTCTGTAGCTAGGGAATGTAG [45900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [46000]
scaffold39565_10.7_P._lessonae TTAGTCTCAGCATTCTTTTCATGCTTATCCTCTATTTACCACATATACTGTATTTTGCTGGAGCTAAACACACTATGATTTTTTTTAAATGTCTATCTGT [46000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [46100]
scaffold39565_10.7_P._lessonae TATGATCTTCACAAGTTTTTTGATTTAGGTTTTCAACAATCTGCACAATGTAATTTGGATGAAGTCACTATTAGGCAAGCTACTAGACTGCAAGTTAACC [46100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [46200]
scaffold39565_10.7_P._lessonae ACTTAAGGATCGCCCTATAGCAGATATCCTGCACTTCTGTCTAGGAGGGGCGCACACGCACGCCACTGGATGGCTGCTTTTGCTGTGATCATTCACAGCA [46200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [46300]
scaffold39565_10.7_P._lessonae TAAGTCAATTGGCATGTGCCCGCTGACATCCATTACCCGGCACTGGCTGCCCGCCGATCAGGAAGAGACACAGAACGGAACTCTGCCTATGTAAGCAAGG [46300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [46400]
scaffold39565_10.7_P._lessonae CAGAGCTCCATTCTGACGGGGTAATCAATGAATTTGGTGCCCCTGCAAAGCAGGGAATAAAATATCTCACTTCCCTTAGTAAAAGCAGCAAGCAGTTTAC [46400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [46500]
scaffold39565_10.7_P._lessonae ACAAAAATACTGGTTAGGCACACAGTTAACCTTTTGATCGCACTAGACGTTTAACTCCTAACTCATTAGTACAGTGACAGTGCATATTTTTAGCACTGAT [46500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [46600]
scaffold39565_10.7_P._lessonae CACTTTATTAGTGTCATTGGTTCCCACAAAGTGTCAAAAGTGTCAGTTTGTGTCTGATTGCCCGCTGCAATATCCCAAATCCCCACCATTACTAGTAAAA [46600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [46700]
scaffold39565_10.7_P._lessonae AAAAAAAACTTTTGTGCAAACCAATTAATATATGCCTTTTGGGATTTTTGTTTACCAAAAAGGTGTAGCAGAATACATGTTGGCTTTAATTTTTGAAGAA [46700]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [46800]
scaffold39565_10.7_P._lessonae ATTCTTATTTTTTTCAATTTTGTTATTGGATATACCTAGTTACATAGTTAGTCAGGTTGAAAAAATACCATCTAGCTCATGTTTTAAATATTTAATAGTG [46800]
                                                                                                                      (A)n
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [46900]
scaffold39565_10.7_P._lessonae GAAAGTTAAAAATATTGCTTTTTTTATTTTTTTTTAAATTGTCAGTCTTTTTTTGTTTATGGCGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCAGAG [46900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [47000]
scaffold39565_10.7_P._lessonae GTGATCAAATACCACCAAAAGAAAGCTTTATTTGTGGGAACAGTGTTGCATGACTGCAAAATTGTCAGTTAAAGTAACACAGTTTTTTTTTTTTTAAAGC [47000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [47100]
scaffold39565_10.7_P._lessonae CCGTTTTGTGTGTGAAACTCACTCAAAAGCTACACCCGGTGCATAAAAAAAGTGCACACACACAAACGTGGGAAACACAAAAGTGCACAAGGCGTACACA [47100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [47200]
scaffold39565_10.7_P._lessonae TAGCCTTCTCCGAAGAGGGAAGGCCCTAACCCTGATCCCCCGGGGCGCAAGGCTCCTGACAGAGACTGAGGTACTTACTTGGTCCTGCCTGGCGGAAACC [47200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [47300]
scaffold39565_10.7_P._lessonae AGGCAGACCCCGTTCTCTGGGAGGACTGCCGAAACAGCCCACCCCAAGTACTAGGTGGGGCTCCCCCGAAAGGAGACCCCATGGGAGAGGGCGAACCTAG [47300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [47400]
scaffold39565_10.7_P._lessonae CCAGAACTCCATATCCACCCCCTCCCAAGACTTTCAGGGCAGGCCGGAGGACCTACGCCATACAAGTCCTGCTGTGAAAGTATACACCGCCACATAAAAA [47400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [47500]
scaffold39565_10.7_P._lessonae AGGACAAACTGTGAACACACACAACACAGAAAAGAGTGGGGAAGGGGAAGTGGAGAAGTGTGGGTAGTGTCAAAGTGCAAAACCTTGACAGGCCCCCCGG [47500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [47600]
scaffold39565_10.7_P._lessonae CCAGGAATAAAAATTCCTCTGGTGCCAGCCAAAAGGCCTGTCCCAAGAGGCAGGTGCGAAAAAAGTGTGTATGTGGTGCAGTGACCAAGGTGCCAAAAAC [47600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [47700]
scaffold39565_10.7_P._lessonae TCAAAGATGAACTGCGCCTCACCAGTGAGAATTACGGCACCCCTGAGCTGCCACCCCAGGGGCACATACACCACAGGCTTTTTTTGGTCCCAGCCTTCGG [47700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [47800]
scaffold39565_10.7_P._lessonae CCCAGACCAGTGCAGCCTATCCCTACCAGCAGACATCGGAACCTGAACAGCTTAGGGAGAGCCTACCTTCAACTGGGGACAAGCCTTTTGCAAGGCTAGA [47800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [47900]
scaffold39565_10.7_P._lessonae TTCAACCCAGGAGGAAAAGCCCTCCCATCGCCATCCCAGTTCCTCAGCCAATTACATCCAGGAGCAATACTAACCGGCCTCCAGGACAGACCGGCTTTCT [47900]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [48000]
scaffold39565_10.7_P._lessonae TGCCCCCTTCAAACTGGTAAGAACAGCTTAACCCATTCAAATCAGAAGGCGGCGGACCCTACATGCTTTCCCGGATGACCTACTCCCCATACCCCAGTGA [48000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [48100]
                                                                                                          U2
scaffold39565_10.7_P._lessonae CGTCCAGGCGCTCCGGGTTTTGGTCATACTGGTACTAGCTAAGGTCCATACCAACTGATAAGAACAGATACTACACTTGATCTTAGCCAAAAGGCAGAGA [48100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [48200]
scaffold39565_10.7_P._lessonae AGCGTTACTTTCTTTTGCAGGCCAAAAAAACGCTAAACCGCTGTCTTGGAATTAGCAGCAGAAGAGATAAAACCTTGAAGGCATGTATATTGGTAGGAAT [48200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [48300]
scaffold39565_10.7_P._lessonae GTAACATTTTAATTCCTAGCATGAATGTCAATATAAAGATAGAGTGAGATACTGGACATGTGTAAAGTGTGTATCCATGAGGGGTAATGTACGCCACCAT [48300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [48400]
scaffold39565_10.7_P._lessonae GTCATCAACTTTAGGTTGTGTTGAGTGTGTGTTAAGTCACCCAGTGTACTTTAATTACAATTTCCAGCATGCCACACTACTCTTTGTAACTGTAAATTTA [48400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [48500]
scaffold39565_10.7_P._lessonae GTTATGTGTCCCAGTAATATTTTTCCTAACCCTGTAGAGCTACAAGTTCCAGCCATTACACAGTCTGTACCAACAATCACATTCTGTGCCACATATTTTA [48500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [48600]
scaffold39565_10.7_P._lessonae GACTATTAGCCACCAAAGAAAAGAAATCCCACAAAACACGCATCATTAATCACAAAATATATATTTTATTTCTAAAAATATATTCAGTTTAGGAAAACAG [48600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [48700]
                                                                                          (AT)n
scaffold39565_10.7_P._lessonae AAAAAAACATATATATATATATATATATATATATATATATATACTGTATATATGTGTATCTATATTATATATAGATATACTGTATATATGTATGTA [48700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [48800]
scaffold39565_10.7_P._lessonae TATATCTATATAATTTTCCTTTTGTTCACCAATGTTCATATAGATTGGACAAATTAGGTTTTGTCTAATTCTACAGTTAATCAATGTTGTGTTTTAACTG [48800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [48900]
scaffold39565_10.7_P._lessonae CTTATTTCTTCGTATATGTGAAATTCAATACACTTATTAAATAAAATTGTGTGATTTGTTGAATTGAAAGTGTTTTTTCCCAATCTATATTTACACTGCT [48900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [49000]
scaffold39565_10.7_P._lessonae CAACAAACAAGCACCTTTTATAATCAATAAATACATTAGCTTACAGTCCTTAAAAAACACTTTATAGAGAGAAGGGTTAACTCTTTTCCTGCCAATGAAA [49000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [49100]
scaffold39565_10.7_P._lessonae TTTATGGTGGGTTAAACCAATATTGTTGGATGGAGAATGTGAAAAACTGGTGACAGCAAAAGGGTTAGGATGATGACAAGGTTTGCATTTGGAGTGTATA [49100]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [49200]
scaffold39565_10.7_P._lessonae ATCTTTAAAATCTCTATAACAATACATACAAAAAAAAAAAATGGTAATTCGTGTTTAAAACTGCCCTCTTATATAACAGAAAATGCTTTACAAAAGAATAA [49200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [49300]
scaffold39565_10.7_P._lessonae CATTAAAATCCAAAATGAATCAAACAATAATAATGTAGGCCAGCGTTTCTAAAAAATTTTATAGTCGGGGCATCCTTTAGAAGTACGCAAAATCTCAAAG [49300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [49400]
scaffold39565_10.7_P._lessonae CACCCCCGTGTCTAAGCTGTACAAATCACAAATATTACTTATCAATGAGAAACCTGAGCCTGGAATGATGCACAGCCTTGATGAAGTTAACTTCACCTTA [49400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [49500]
scaffold39565_10.7_P._lessonae TTGTTCCCACATCACATCAGAGGTCCCCTCATCATATCACAACCGCCCTTTAAATCAGAGACCTTTTCTTATCAGAGGTCCCCTTCATGTGGGAGTCCCC [49500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [49600]
scaffold39565_10.7_P._lessonae CCCCCCATTGCCATCAGATTGGAGTACCCCAATGACAGAGTACCCCATAACATCAGTGTCTCCCCTTCACCACAGAGTTACCCCATCATAGAGCCCCATT [49600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [49700]
scaffold39565_10.7_P._lessonae ACCGTGCCCCCCACCCTCGGTGGTAACCCAAACGGCACCCCAGTGGAGAAAAACTGATGTAGACATTTCTTTTCTTTTAATAAACTATGTTTTAACCTAT [49700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [49800]
scaffold39565_10.7_P._lessonae TACATAGATTTTAAGAATTAATACATTACTAAATAAATCACACTGCTTAGTTCTGCATCCTGAGGTACATGTGTTGTTTTTAATATAATATTCAAAGTCT [49800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [49900]
scaffold39565_10.7_P._lessonae TTCCAACTCTTATCTTCTATGGGACTCTGCTAATCAACAGTGCAGCCTCTGTAGTGACTTGAAGTGGTTGTAGAATCTTAACTCTATGCTGTTGAAATAT [49900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [50000]
scaffold39565_10.7_P._lessonae TTACTTTTGCTTCTCTTTATAAAATGTATTTAGACAGCTAAACCGTAGTCTCAGTTTTTTTAACTGTTTTCATATTCAGGTATTGAAGCATTATAGACTT [50000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [50100]
scaffold39565_10.7_P._lessonae TTCATAGATGTACCTAGAAATTAAAATAAATGAATGATACAGTCAATAAGACCTACACTACTATATCACAAGATATTATTTTTAAATCAAATGTACGTTT [50100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [50200]
scaffold39565_10.7_P._lessonae TACATCATTACCAGTACACTGCTCATATTTAACAAACTCCATATGCCGAAAGTCTGTAGTAAAACTGTGGCCAATTTATGGACATTCAAATATGTGCACA [50200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [50300]
scaffold39565_10.7_P._lessonae TACTTAACAAACAATAAAAAAAAAATGTTAAGGCCTCGTGCCCTAAAGGCTTAAAATATACTGGGCATAAAATTTCAGTTGTCATCTAAGCACCAATGCT [50300]
```

Table 2.4. (continued).

```
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [50400]
scaffold39565_10.7_P._lessonae TCTGTACCATGGTAGTCACCCACGCATACATGTATGAGGCTTTTCCCAAACTTCTGCATTCAGAAAATATGATGTACACACAGGTAACAGCCAATGCACA [50400]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [50500]
scaffold39565_10.7_P._lessonae GAAGCATCTGTGTGTATAGTCGCATAGAGGCATTGCCCTGCATCGCAGGCTGTATTCGGGACCTGAGGCTTCCCAGGCATGGGAAACCAATTGGAAATTT [50500]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [50600]
scaffold39565_10.7_P._lessonae ATGCTCAGGTTATATTCAGGCACTCACTGTCTGAGAATATATAAAAAAATCTTTAACAACTATAGTCCAGCCACAGGTGCACTTTAAGTGTAAAACATGA [50600]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [50700]
scaffold39565_10.7_P._lessonae AAACTGGATTGCTATACTTTATTGTCAAATAAACTGCTGGTACTTACTTATCCACAGTTCTCTGAATTTCCCTTTCTTCCTCCTCGTTTAACCTCTGCAA [50700]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [50800]
scaffold39565_10.7_P._lessonae TATTGTTTCTAAAAGTGGAAGACTAAACTTAATGTATTGTGCTACCTGCCAAAAGAGGAAAACAAAAAGCATATTTGAAATCTTTAAATAGCTAAGAAGT [50800]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [50900]
scaffold39565_10.7_P._lessonae AAGAACTGATGTACCAGTAAGTACTTACATCACTGCTAATCTCCTCTGCCTCTCTGTCCATGAGGAACATTCTTGCTATGCTTCCTGAAGGACCTTGTAA [50900]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [51000]
scaffold39565_10.7_P._lessonae GAGTCGCTCCCATAAGGGGCACTCTGTGTCCTTCAGCTTTTTCTTTTCTGAAAGGTAAATATATTTTAGAATTTTTATTATGTTATATATTATGTAATTT [51000]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [51100]
scaffold39565_10.7_P._lessonae AACAATGCACCAAAAAGCCTACACCATGTATCAAACCACATGCACTGAATTAATTAATTACATGGGCTGCGCTTTCACCCTAGTTAGATAATTACATAGT [51100]
                                            CR1_1a_Xt
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [51200]
scaffold39565_10.7_P._lessonae TGGTAAAGTTGAATAAAGACACTAGCCCATCCAGTTCGACCTGTGTGTGTGTGTGCATTCATGTCAAAAATCCTTTATCATATCCCTGTATACTGTGT [51200]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [51300]
scaffold39565_10.7_P._lessonae TCACTAAGATGCACATCCAAGAGTTTTTTTAAACTATTAATTTTTCCCGCTAACACTATTGATTGTGGAAGTAAATTCCACATCCTTACTGCCCTAGCAG [51300]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [51400]
scaffold39565_10.7_P._lessonae TAAAAAACCTCCTACACAGCTTAAGGTTCAACCACTTCTCCTCCAATTTTAGTGAGTGGCCCTGTGTCTTCTTACACTCCCTGAGACTGAATAGTTTTTT [51400]
U40452_P._shqipericus             ---------------------------------------------------------------------------------------------------- [51500]
scaffold39565_10.7_P._lessonae CCTATGCTAGAATCACCATTGAGGTATCTGTATATCGTTATCATATCTCCTCTCAAGCGTCTCTTCTCCAAGGAGAATACGTTTAGTGCTTGCAGTCGTT [51500]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [51600]
scaffold39565_10.7_P._lessonae CATTGTAACTAAGGTCCTCCAATTGCGTTATTCATTTTGTCACCCTTCTCTGGACTCTCTCCAGTTTCAGCACATCATTCCTGAGGATTGGTGACCAGAA [51600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [51700]
scaffold39565_10.7_P._lessonae CTGAACGGCATACTCCAGATGTGGCCCCACCAGAGTTTTATAAATTGGCAGGATATTTATCTCTGGAGGTAATTCCCTTTTTAATGCATGATAACATTCT [51700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [51800]
scaffold39565_10.7_P._lessonae GCTAGCTTTGCTTGCTGCAGCTTGACATTGCATGGCATTGCTGAGTCATCCACTATGACCCCCAGATCTTTTTTCCTCCTGAATTCCCCCTAGAGATTCT [51800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [51900]
scaffold39565_10.7_P._lessonae CCCCCTAGAGGGAAGCTTGCGCTTATATTTTAGCCCCCAAGTGTATTACTTTACATTTTTTAACATTAAACCTCATTTGCCATGTAGTTGCCCACCCCTT [51900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [52000]
scaffold39565_10.7_P._lessonae TATTTTATTAAGGTCTTCTTTCTATATCCTGCTGTGAAGTTATTGCCCTACATAGTTTTGTATGATCAGCAAAAACTAAGATTGAGCTATTTATCCCAAC [52000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [52100]
scaffold39565_10.7_P._lessonae CTCTATATCATTTATGAATAAATTAAACAGAATCGGTCCCAAGACAGATCCTTGGGGTATTCCACCTACCACTCCAGACCAGTCTGAGTACACACTATTT [52100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [52200]
scaffold39565_10.7_P._lessonae ATGACCACCCTTTGGACGTGCCCCTGTAGCCAGTTTTCTATACATAAACAAACCCAATGGTCTATGCTTACAGACCTCCATTTGTAAATTAGGCATTTAT [52200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [52300]
scaffold39565_10.7_P._lessonae GGGGGACTGTATCGAATGCTTTTGCAAAATCCAGATACACCACATCCACAGGCCTTCCTTTATCTAGATGGCAGCTCACTTCCTCGTAGAATGTTAACAG [52300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [52400]
scaffold39565_10.7_P._lessonae ATTGGTTTGTAAAGCAATGCTGATTACTACTAATTTACTGTTTTCATTGGCTAATTATTGTATATAGTCTCCTATCATCCCCTCCAAAAGTTTACATACT [52400]
                                                                               CR1-2_XT
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [52500]
scaffold39565_10.7_P._lessonae ATTGATGTTAGCCTGTAGCTTCCAGGAATAGAATAATTATCTCTTAACTTTTTAGATATTGGTACCAGGTTGGCCTTTCACCAATATAACTGGTACCATC [52500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [52600]
scaffold39565_10.7_P._lessonae TCTGTCAATATGCTGTCCTTAAAAATTAGTCTGGCTTTCACCTGACTGAGTTCTTTGAGGACTCTCGGGTGTAAGCCATCTGATCCTGGTGATTTATTTG [52600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [52700]
scaffold39565_10.7_P._lessonae TGTTAAGCTTTTCTAATTTTCTCTTCTGTTAGCTACAAGGGTACATTTTGAGATGAATTAATGGTACAGTCTTTCCTGATTACCAAATATATAACCCCCC [52700]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [52800]
scaffold39565_10.7_P._lessonae CCTCCTTCCATTGTAAAAACTGAGAAGAAGAATGCATTTAGTACAGTAGCCTTCTGCTTGCCATTTGTAACCAACTTCCCTTCATCTTCCTTTATGGGGC [52800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [52900]
scaffold39565_10.7_P._lessonae TAATGTGCTCTGAGATTGTTTTTTACTGTTAATATAAAAATGTCTTGGAATTTTCTTTTTACTCTTCTCTGCTATGTGCCTCTCGTAGTCTATTTTGGCC [52900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [53000]
scaffold39565_10.7_P._lessonae ACCTTGATTGTGTTCTTACATATCTTATTGCATTCCTTGTAGTGTTGGAATGCTGACAAACACCATTCAACTTTATATTTTTTAAAAGGCCATTTTCTTC [53000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [53100]
scaffold39565_10.7_P._lessonae TCTTTAATATGACTTTTTACTTTAAAGTTTAGACACCCAGGTTAACCCTCACTCTTTTATGTTTATTGCCTATTGGAATAATACCTTTATTTAATATGTT [53100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [53200]
scaffold39565_10.7_P._lessonae CTTTTTTTTTTTTTTGTAAATTCTTTATACAAAGGTATGCCAAAGATACATCAACTGTAATATAACATAGCATCATAGTTCGCATAACTGTTAAATATGG [53200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [53300]
scaffold39565_10.7_P._lessonae TGCTTATCTGAAGGTACACCCACGCGGGCCGATAAATATCGACCCATGCTGATCCCCCCCATCAGATCATGATTTAATATGTTCTTAAAGTACTCTCATT [53300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [53400]
scaffold39565_10.7_P._lessonae TTTCCTCAGTGTTTCAACTTTCTAGGACTTGGTCCTATTTAATACATTGTAGCATTGAATGCAATTTATAAAAGTTGGCTCTTTTGAAATTTAGTGTTCC [53400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [53500]
scaffold39565_10.7_P._lessonae TGTACTACCCTCCTATCCCCTTTTCCTATGATGTATGCTGAATGTAATAATCCTGTGATTGCTAGTTCCCAATTTGTCCTAAATTTCCACATGTGTGACC [53500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [53600]
scaffold39565_10.7_P._lessonae AGATCTGTGTTATTTGTAATTAATAGGTTTAGCAAAGCATTCTTTGTAGCCAAGGCACCCCCCAATTGGAACATGAAGTTGTCCTGTAAGGTATTTAAGA [53600]
U40452_P._shqipericus          ---------------------------------------------------CR1-2_XT----------------------------------------- [53700]
scaffold39565_10.7_P._lessonae AATGACGGGCCTTAAATGAGTGAGCTGTTCCTTCTGCCCAGTCAATATTTGGATCATTGAAGTCCTCAATTATGATGACATTGCCCTGCCTTGCCACTAT [53700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [53800]
scaffold39565_10.7_P._lessonae TTCTAACTGTGATAGGAGGTCCAATTCCTCCAAATCCTTCAGGTTAGGAGGCTTGTAGCATACACACATTATTAATTTCCCACTTTTTCCCCCCATTTGA [53800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [53900]
scaffold39565_10.7_P._lessonae AGTTCCACTCACAGGAATTCTACCTCCTCCCTTGCTCCAATTGCAATGTCATCCCTCATGTTCACTAGCAAATCATTCCTGATATACAGGCACACCCCCT [53900]
```

Table 2.4. (continued).

```
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [54000]
scaffold39565_10.7_P._lessonae CCCCATCTAGCCTCCGATACAAGGAATACTCCTGGAGAGTTGCCAGCCAGTTTTGTGAGCTGTCAAACCAGGTTTCTGATATTCCCGCAAAGTCGAGTGT [54000]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [54100]
scaffold39565_10.7_P._lessonae AATTAAAAACAGCTGACAATACTGCAGTTGACATTAAGGGGTTGATTTACTAAAAGTGGAAAGTGCAAAATCTGGTTCAACTCTGCATAGAAACCAAACA [54100]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [54200]
scaffold39565_10.7_P._lessonae GCTTCCAGGTTTTTTTTTTTTGTCAAAGCCTAATTGAACAAGATGAAATTAGAAACTGATTGGCTACCATGCACTCTCCAGTTTTAGTAAATCAACCCCT [54200]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [54300]
                                                 (ATATACA)n
scaffold39565_10.7_P._lessonae AAATGTATCCCCAAATATATATAAAATACCTATAACCAATATACAGTATACTACGCAATATACCTATTTTAGCAAATATTAATTCCCCTATATGCAAAAC [54300]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [54400]
                                                A-rich
scaffold39565_10.7_P._lessonae CTAATTTATCAGAATCAATTATAATACATCAAAATGAAAATCAAAGCAGAGGAGACAGTACATGGTGTATAAAGGCATGGATTGCAAGTGTGGTGTTCCA [54400]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [54500]
scaffold39565_10.7_P._lessonae AATACACAATATACACACAGATTTGAGTAAATGGTGGGCTGGATATAACATGTTGTAATTTATATATTCACTGACATTTATATTTTTTGGGATTTGTGTT [54500]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [54600]
scaffold39565_10.7_P._lessonae TTTTTTTTAAATTATCATTGAGAGTTTTTGCAAGTGTGGTGTTAAAAATACAAATGATGCACACGGAATTAAGTAAATGGTGGACTGGATACAGTATATT [54600]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [54700]
                                               (TATATTA)n
scaffold39565_10.7_P._lessonae ATATTTTATATACTCAGACATTTTGTTTTCATTTGTGATTTATTTTCATTTTGATGCATTATAATTTGTACTTATAGGTCTACAGCATGGCACTGTATAT [54700]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [54800]
scaffold39565_10.7_P._lessonae TCACAGTTCGATGTAGCTAGGGCCAATGAGACACAGGTATCAAGACTTTCTATATGGTACACCGGGGAACCTATTTGATCACAATTTTGTATGACCCTTG [54800]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [54900]
scaffold39565_10.7_P._lessonae TAGCTGATTATCACTTTTCCTATCCCAAAACGTGTTGCTAACAGTTCTCCCCCTTGTACAGATTGGACCTGAGTGTCAGTGGAGTTCTAGTATAATGATA [54900]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [55000]
scaffold39565_10.7_P._lessonae CTCAGCATTACATAGACAGTAGTTTCCTTTAGCTGGTTTACTGTGTACAATTTTCTCAGTAGAACAGGATATACTGTATGCACAGTATCTCACAAAAGTG [55000]
U40452_P._shqipericus            ---------------------------------------------------------------------------------------------------- [55100]
                                                 Helitron-1_DR
scaffold39565_10.7_P._lessonae AGTACAGCCCTCACATTTTTGTAAATATTTTATTATATCTTTTTATGTGACAACACTGAAGAAATGACACTTTGCTACAATGTAAAGTAGTGAGTGTACA [55100]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [55200]
scaffold39565_10.7_P._lessonae GCTTGTATAGCAGTGTATATTTGCTGTCCCCTTAAAAAAACTCAACATACAGCCATTAATGTCTAAACCTCTGGCAACAAAAGTGAGTACATCTCTAAGT [55200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [55300]
scaffold39565_10.7_P._lessonae GAAAATGTCCAAATTGTGACTTGTTAGTGTTACAAGGTCTAAGGTGTGAATGAGGAGCAGGTGTGTTAAATTTGGTGTCATCGCTCTCACTCTCTCATAC [55300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [55400]
scaffold39565_10.7_P._lessonae TGGTTATTGGAAGTTTGAAAAAAATAATTGTTGCTCTAGATAAAGATTGCCTAGGCTGTAAGAAGAATGCCAAGACCTTGAAACTGAGCTGCAGCTTAGT [55400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [55500]
scaffold39565_10.7_P._lessonae GGCCAAGACCACACAGTGGTTTAACAGGACAGGTTCCAATCAGAACAGGCCTCTCCATGGTCGACCAAAGAAGTTGAGTGCACGTGCTCAGCGTCATATC [55500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [55600]
scaffold39565_10.7_P._lessonae CAGATGTTGTCTTTGGAAAATAAACATATGAGTACTGCCAGCATTGCTGCAGAGGTTGAAGGAGTGGGGTGTCAGCCTGTCAGTGCTCAGACCATATGCC [55600]
U40452_P._shqipericus          --------------------------------------------TC1DR1-------------------------------------------------- [55700]
scaffold39565_10.7_P._lessonae GCACACTGCATCAAATTGGTCTGCAAGAAAGCCTGCAAACAGTTTGCTGAAGACAAGCAGACTAAGAACATGGATTACTGGAACCATCTCCTATGATCTG [55700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [55800]
scaffold39565_10.7_P._lessonae ATGAGACCAAGATAAACTTATTTGGTTCAGATGATGTCAAGCGTGTGTGGCGGCAACCAGGTGAGGAGTACAAAGACCAGTGTGTCTTCCCTACAGTCAA [55800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [55900]
scaffold39565_10.7_P._lessonae GCATGGTGGTGGGAGTGTCCGGATCTGGGGCTGTATAAGTGCTGCTGGCACTGGGAAGCCACAGTTCATTAAGGGAACCATGAATGCCAACATGTACTGT [55900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [56000]
scaffold39565_10.7_P._lessonae GACATACTGAAGCAAAGCATGATTCCCTCACTTCGGAGACTGGGCTCCGGGGCAGTATTCCAACATGATAATGACTCAAAACACACCTTCAAGACAACCA [56000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [56100]
scaffold39565_10.7_P._lessonae CTGCCTTGCTAAAGAAGCTGAGGGTAAAGGTGATGGACTGGCCAAGCATGTCTCCAGACCTAAAATCTATTGAGTATCTGTGGGGATCCTCAAAGGGTAG [56100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [56200]
scaffold39565_10.7_P._lessonae GTGGAGGAGTGCAAGGTCTCTAACATCCACCAGCTCCGTGATGTCGTCATGAAGGAGTAGAAGTAGACTCAAGTGGCAACCTGTGAAGTTCTGGTGAACT [56200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [56300]
scaffold39565_10.7_P._lessonae CCATGCCCGAGAGGGTTAAGGCAGTGCTGGAAAATAATGGTGGCCACAGAAAATAGTGACACTTTGGGCCCAATTTGGACATTTTCACTTAGGGGTGTAC [56300]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [56400]
scaffold39565_10.7_P._lessonae TCACTTTTGTTTCCAGCAGTTTAGACATTAATGGCTGTGTGTTGAGTTATGTTGAGGGGACAGCAAAGTTACACTGTTATACAAGCTGTACACTCACCAC [56400]
                                                                                            Helitron-1_DR
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [56500]
scaffold39565_10.7_P._lessonae TTTACATTGTAGCAAAGTGTAATTTCTTCAGTGTTGTCACATGAAAAGATATAATAAAATATTTTCAAAAATGTGAGGGGTGTACACACACTTTTGTGAG [56500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [56600]
scaffold39565_10.7_P._lessonae ATACTGTATATTCAGTGCAACATTCCACAGCTTTGGAATAAAAAACACACAGTTCAGAACTGGTCCCATCCAAGGATAGCGAGATGCAGTGGCGGCTGGT [56600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [56700]
scaffold39565_10.7_P._lessonae GCATTGGAGGCGCCGGATGCATAGAGTTCAATGGGTTTTTTTTTTTTCTGAAGCACCCGATTAGAGCCAGAGGCTCTAATAGGCTTCAGAAAAGGGTGGG [56700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [56800]
scaffold39565_10.7_P._lessonae TCCGGGGCGCAGAGCACTGCGCCCTAGCCCACCCATTTGTGTGACAATAGCGAATGAAAATTCATTATTGTTACACGGATCCTCCTCCTGGCAGATCAGG [56800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [56900]
scaffold39565_10.7_P._lessonae AAGCGGGTCCGAGACCCATTTCCTGATTGGCCGAAAGGCGAACCCATGCCATTGGCCAAGGAGGAGGCGGGAGGACTTGAGGAGACGCAGGGAGACGCGG [56900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [57000]
scaffold39565_10.7_P._lessonae GGGACTGAGGAGAAGCCACCACTGCAAATCAGGTAAGTGCACTGGTCACTCTGCAGTGAAGGGGGCACAATGGTCTCTCTGCATTGAAGGGGACACGCTG [57000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [57100]
scaffold39565_10.7_P._lessonae GTCACTCTGCATTGAAGGGGGCACGCTGGTCTCT?????????????????????????????????????????????????????????????????? [57100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [57200]
scaffold39565_10.7_P._lessonae ???????????????????????????????????????????????????????????????????????????????????????????????????? [57200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [57300]
scaffold39565_10.7_P._lessonae ???????????????????????????????????????????????????????????????????????????????????????????????????? [57300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [57400]
scaffold39565_10.7_P._lessonae ???????????????????????????????????????????????????????????????????????????????????????????????????? [57400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [57500]
scaffold39565_10.7_P._lessonae ?????????????????????????????????????CAAAGCAATGCCTATTCCATTTTTCTGTTTGCGCCCCCCAACCCCAAAAAAATTTTGAGCACC [57500]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [57600]
scaffold39565_10.7_P._lessonae AGCCGTCACTGGCGAGATGGAGAAGGGGGGTCTCGGCTCCTCTCAGGTGTTACAGAGTGGTGTCCTTCCATTGATGAGTGTTTTAAACCCCTTCTTATGT [57600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [57700]
scaffold39565_10.7_P._lessonae GAGCTGCCTACTATGTGTGAATAAATGTTTCATCTTAATACTAGACTGAGATTGTGCTTTTCTCCTTTCTTCTTCATGGTCTTTATTGCAGTGATTACAT [57700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [57800]
scaffold39565_10.7_P._lessonae CCAGCTCTCAGGAACGAGCAGCCATGAGTGGACATTGGACTTTTATTGTCTATAAATATTTCCTCAAGAGACTTTTTGTTCTTTGGTGCGCCGTTCTCTT [57800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [57900]
scaffold39565_10.7_P._lessonae TTTCTCACCCCACATGCACCCCTCAGTATAGGCCCACACTACTCCTTCATCTTGCCTTCTTTTTCATCTCACACACAACTCTGCTCTGCCCCTGTGAGAA [57900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [58000]
scaffold39565_10.7_P._lessonae AATAAAACTCTTCCGATAGTAACCCCTTCTTACAGACTGGATCATTTGGAGAGAAGGATGACGCCATCAACCCAGTGTAAGCTTCAAAACCACCAAACAT [58000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [58100]
scaffold39565_10.7_P._lessonae GAAGCTTACACATGCTTAGGACTGAAGAGCAATTGAGCAGCAGGAGAGCATGGGGAAAGTGAGTATTTGGGCGTACATTGTATGCACCCCTGCTTTATGG [58100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [58200]
scaffold39565_10.7_P._lessonae ATGAAATTGCCAATACCAGCTTTTATCAGTTTTACAGACAGATGCTGCTCTGTGTTTCAGGAGGGTTAAAGTGGTAGTAAACTCTAAAATTTCAATTCTA [58200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [58300]
scaffold39565_10.7_P._lessonae CTCATTTAAATAATCAACACATACTGTGCAACTCACTGTCTTTAGAGCTCTTCTATCCTACTTACTTTTCTTGCAATCCGTCACGTTTACGGCACATTTC [58300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [58400]
scaffold39565_10.7_P._lessonae CTCTGCTGTTAGTCCTTGCAATAACATGCCGTGCCTCGCTCACAGCCTCTCTGTGGCAATGCTCCACAATTCCACAAGAGCATGAGCTCAATTGGGAATT [58400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [58500]
scaffold39565_10.7_P._lessonae TTGCGATGCCAGACAGGGTTGCCATAGTAATCACAATGAAAATAAGGCTTGGCTACAAACTCACTGTGAATGCATGAGATTACGGCAGTGAGAATTAGAA [58500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [58600]
scaffold39565_10.7_P._lessonae AGGGCGCGGTGAAAATGGAAGATAATACTCAACATGGCACCGGCTTCAGATGAGGAGGAACAAATTACAAACTGCAGCAAATACAAGAGACATCACAAGG [58600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [58700]
                                                                   Penelope-5_XT
scaffold39565_10.7_P._lessonae GGTTACAACTATCCCTAAAGAAGCTTGGGGCTCCTAAACACCATCGGTTACCCATAACATGGTGTCTTAACATATTTGCTGCAGTAGTTTGACAACTATT [58700]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [58800]
scaffold39565_10.7_P._lessonae ACCTTAAATATTTAACACCAGCTCCAGGTGTCATGGTACCATGGTGAATGTATTATGAATATTGGAACATGGTGGTTTTCTTGTTCAATATTTTTATTAA [58800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [58900]
scaffold39565_10.7_P._lessonae GATTCAAGCAAGCAAAAGTCAGAAATACAATTATCTCTGGTTTGTAGAACTTAGCAAGGTGTATGCAACGCACCAAAAAAAAAAAAAAAACAGGGATCAC [58900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [59000]
scaffold39565_10.7_P._lessonae ATTGCATTGCTCAGGGCTTTTTTTCACTTGGAACTTGGTGGAACTTAGTTCCACCACCTCTGGCTCAGGCCCTCTGCTCCCTGCTCACACTATCACTTGA [59000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [59100]
scaffold39565_10.7_P._lessonae AAACCCAGAAGTCCAGCTTCTTGGTTTACAAGTGACAGCTTGTCTCCCAATGGCTGCCACAGATATGATCTCCTGAGCAGCTCTTATTGAGTGCAGGATG [59100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [59200]
scaffold39565_10.7_P._lessonae GGGACAAGGGGGATGCAGGTGCCGTGCGGATGCTGACACCCCCACTGGATAATCTCCCTGCAAGTGAGAGAGTCGGAGCCACCTACATTGTGGTCGTGGT [59200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [59300]
scaffold39565_10.7_P._lessonae TGAGTTCCTGCCCCTATTTTCTGAGAAAAAATAGCCCTGGCATTGCTAATATATACAATTATTTTGTCAGTTGCCAAGAAAAATACCTAAGCACAGTAAC [59300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [59400]
scaffold39565_10.7_P._lessonae ATTCGTGACTGACCTTAGCAACCAAGAACAGAGTCTATAAAATGAAGGGGTCAGGTGTGATAAGCCGGTGTTCTAAAATTTAGTCGGACCCGTGAAAATT [59400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [59500]
scaffold39565_10.7_P._lessonae CCGGACCCTCATCACTTCCGGTCACTTCCGGTGATACTACGTCACCACCAGCTGGAGCGACAGCTGTTGCGAGCCCCGGTGCGCATGCGCACAAGAAATT [59500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [59600]
scaffold39565_10.7_P._lessonae TTCCAGGTCCGATGAGATTTTAAGACTTTGCTAACAGCTGACTGAGAGGAGGAGGAGGGGCTGAGGTAGGACGACAACACCGCCGCGGGAAAATTTTACA [59600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [59700]
scaffold39565_10.7_P._lessonae ACACCGTCGCATCATCGAGCAAGGAAAATGTCTTGTGCGCATGCGCACCGGGGCTCGCAACAGCTGTGGTGGTGACGTAGCGTCACCGGAAGTGACGAGG [59700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [59800]
scaffold39565_10.7_P._lessonae GTCTGGAATTTTCAGGGGGCCGATGAAATTTTACAACACCGGCGCACACATCAACATCAGTCAGTGGTGAGCAACAAGAAGAAACGAAGGGAAGGATTTA [59800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [59900]
scaffold39565_10.7_P._lessonae CTAAAACTGGAGTACACAGAATCTGGTGCAGCTGTGCATGGCGGATACCAGATTTTACTGTTAGCCTAGGTTTGCACTGCCGTAACTTCAAGGTCGCGTG [59900]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [60000]
scaffold39565_10.7_P._lessonae ACTTTCGTGTGACTTTGAATCTGGCATCCCTGTGTGACTTCATCGCGGCTTGCATGCAAATTCTTTAACAGAAGTCAAATGCAAATCATATTGAAGTCGC [60000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [60100]
scaffold39565_10.7_P._lessonae ACCTAAAGTAGTGCAGGAACCTTTTCTAAGTCTGAGCGACTTGAGTCACACCGATTAGAACAGTTCCATTTCAGGTAATGGGGGCGTGACTTTTCATGTG [60100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [60200]
scaffold39565_10.7_P._lessonae ACTTTGAACTCTGTCACATGACAAGTCACGGCAGTGTGAACCGGGGCTAAAAGCTTAATTGAACAAACTGAAGTTTAAAGCAGATTGGTTCCTATGCACA [60200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [60300]
                                                                                                                     A-rich
scaffold39565_10.7_P._lessonae GCTGCACCAGATTTAGTGTGCTCTAGTTTTGGTAAATCAACACCCTAGTGTCAAGCGTGTAAAGAGAGTAGAAACATAAGAAAGGAAGGGAGAAGGAAAG [60300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [60400]
scaffold39565_10.7_P._lessonae TAAGGGGAAGGGGTTCTGGGAAAAAGAAGAGGAGAGTAAAGTGGAGAACATGGTGCTTTTAAGAAAATTTAAGATCCCTGTCACATTCTTGCACAATCAA [60400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [60500]
scaffold39565_10.7_P._lessonae CATTTGCCTTGACACATGACACCATGGTGATTGGATTATGACTACTGAGGTACCCGTGGGCTATAACTGCTGAGGTATGTTGCCATCACTCATTAGAACC [60500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [60600]
scaffold39565_10.7_P._lessonae AAGGAAGCCATTTGGACAGGTGCTGGAGAAGTCTGCAGCAGTGACTAACTACTACGAACAAACATTGGAGTTACATTTCAAAAGTGTTTGCTATATGTTG [60600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [60700]
scaffold39565_10.7_P._lessonae GAGCTTTTCACACTATAACAAGTAACACTATTTGTGAGACTCATGCATGCTTACCTCCTGATGCATGAATAATATATAGTGCAAATTCATTTGAGCTATT [60700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [60800]
scaffold39565_10.7_P._lessonae TTCAATCTGTGAGAAAAAAAAAAAGAAATATTTAATTTCATAGGTAACACAATATAGCATTAAAAGCTTTCTTCACTCTACCTATGATTCTCCTATAATTG [60800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [60900]
scaffold39565_10.7_P._lessonae GCACAACATCAGCATTACTGGGCTTTGTGCTCCCTACCTTTATAAATGCCAATAGAATTAGTATACCACTACTACTTATGTGGATGAGTAAAAGCAGGAG [60900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [61000]
scaffold39565_10.7_P._lessonae AGATGCATCACTATGATCTTACATTCTTTTCCATATCTAAAAAGGTGTAGTTATTTTATTATTTTAGCAAAATGGTAATAGGCCAAATATTTTCATAGCT [61000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [61100]
scaffold39565_10.7_P._lessonae TGCTCCTTTCTCACAGTGCCCTGCATTTCCTTCATTTTGGATATCATTCGGCTGTCAACGTGTCTGGTATGGCTTCTCTGTTCTTAACCGCTAGCTAGAG [61100]
```

Table 2.4. (continued).

```
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [61200]
scaffold39565_10.7_P._lessonae TACTAGCCTACATTATCCCATCATTACCAAGCCATTTTTCAGTTTCAATTATTGTGATACTTTGGCAGACAATTACTCTGTCATGAAACACTGTACAAAT [61200]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [61300]
scaffold39565_10.7_P._lessonae ATAAATTTTATGACTTTTTTGGAGCCAGATAAAGCTGATATTTTATCTTTTAGTATACATGGGAAAAAAGACAAACATATTAAAAAACAACTTGTTTCCT [61300]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [61400]
scaffold39565_10.7_P._lessonae TTAATCTCCGTTAAAAAAAAGAAAAATGCCATTACAGTGTAAATATCCCAAAAATTACCCATTTTTGAAAGTAGACACCACAATGTGATCACGTTTCTTT [61400]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [61500]
scaffold39565_10.7_P._lessonae TTGCCACAATTTTTTGGAAATTAAGAAATATGCTGGTATTAATGTAGTGAAGACATGAAGCTTGGTAATGGTCCACTAGATACAGTGCACTGGTAATAAA [61500]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [61600]
scaffold39565_10.7_P._lessonae CAGAGGGAGGAGATGGTGAAGGGGTTAATGCAGGGGTCTCAAAAAGGTGGCCCTCCAGCTGTTGCAGAACTACAATTCCCATGTGGCATTGCAAGGCTGA [61600]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [61700]
scaffold39565_10.7_P._lessonae CAGTTACAAGCATGACTCCCATAGGCAAAGTCATGATTGGACTTGTAGTGCTGCAACAGCTGGTGGGTGGCAAGTTTGAGACCCCTGGGTTAATGTAAAG [61700]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [61800]
scaffold39565_10.7_P._lessonae AGTACATACAGTGGGAGGACTTAGGGGGCTTAATGTGCAGATGCCCAGGATAAAGGAGGTGAAGGGTTAAAAAACAGGTCACAGGAGGGAGGGTAAAAGG [61800]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [61900]
scaffold39565_10.7_P._lessonae GTAAAAAAAAAAAAAAACTTTATTGGAATTCGCTGCTGATGTGATATGTACAGTGATCTGGATCGAAAGAATGACTTATTAATTCATTAGTTGCTCTTCC [61900]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [62000]
scaffold39565_10.7_P._lessonae CTCTCCTACTTCCATTGTGAGAGAAGGGGAGGGCACACTACACTGTTTACATACATATGTTATCAATTTGATGGGTCTCCCTTTGAATAAACACAGCGAT [62000]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [62100]
scaffold39565_10.7_P._lessonae CCCAATGGTATAGAGATGCTTCAATTGGCTCTGTACGATTTCCATAGAAAGCCCAATGTTTTTTTTTTTTTTTGTAGTGGCATTTACGTATAAACATCAC [62100]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [62200]
                                                                                      hAT-N33_CPB
scaffold39565_10.7_P._lessonae TGCAGAAATAAGTGTCCACTACTTTTCTGTTTAAAGACATACAGCCAGGGCCGGTGCTTCCACTAGGCAAACTAGGCAGCCGCCTAGGGCGCATTGCCAC [62200]
U40452_P._shqipericus           ---------------------------------------------------------------------------------------------------- [62300]
scaffold39565_10.7_P._lessonae CTAGGGGCGCAGCCATGAGTCGGCACTCTCTCGCCATCATTAATGATCCTTGTGAGCTGAGGGGAGAGGCGGCAGTGGGCAAGGAAGAAGGGACAGAGGA [62300]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [62400]
scaffold39565_10.7_P._lessonae AGATAATAGGTGTCTGGGGCAGTGGCAGAACTACCAGGCCTTGGCTTTCCACCGCTGTTTGGGGGGGC???????????????????????????????? [62400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [62500]
scaffold39565_10.7_P._lessonae ???????????????????????????????????????????????????????????????????????????????????????????????????? [62500]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [62600]
scaffold39565_10.7_P._lessonae ???????????????????????????????????????????????????????????????????????????????????????????????????? [62600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [62700]
scaffold39565_10.7_P._lessonae ???????????????????????????????????????????????????????????????????????????????????????????????????? [62700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [62800]
scaffold39565_10.7_P._lessonae ???????????????????????????????????????????????????????????????????????????????????????????????????? [62800]
                                                                                        hAT-N33_CPB
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [62900]
scaffold39565_10.7_P._lessonae ??????????????????????????????????CAAGTAGCTGGTCTTGCCTAGGGCGTAAAATAGTCTAGCACCGGCCCTGCATACAGCAGTAGATAA [62900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [63000]
scaffold39565_10.7_P._lessonae GAGGTTAAGGTATATCTAAAGCCAAATCTTTTTCTTTTGTTTTTTTGCCATCTGAAGAGGGGGTATTCTGTCCACTTTCTATACTGCAGACTCAACAGGA [63000]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [63100]
scaffold39565_10.7_P._lessonae ATTTAGAGGATATCTTTCCAATTTGAGGGAAATCCCACTAACAGGGACACAGACAGCAAGGCAAATCTGTGGTATTAACTCCTCACCATCATATCCACAT [63100]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [63200]
scaffold39565_10.7_P._lessonae ATTTTAAAAAGTTGTGTCCTTTGTTAGGATTTAAACACACATTTACTCTTCTAGTCTCGGTTTGCTTCTATATGTTCTTGTTATCTAATATTTCTTAAAG [63200]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [63300]
scaffold39565_10.7_P._lessonae TTATTGTCAGTGTAGTTTTAAAGCAGTCTATTCTAACCATTTTGAGTAAGGTAATAAGTTGCAGCAGTAACATATATATATACACAGTACAGACCAAAAG [63300]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [63400]
scaffold39565_10.7_P._lessonae TTTGGACACACCTTCTCATTCAAAGAGTTTTCTTTATTTTCATGACTATGAAAATTGTAGAGTCACACTTCAAGAGGAAGTCACCTGAAATGTTTTTCAC [63400]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [63500]
scaffold39565_10.7_P._lessonae TTCACAGGTGTGCCCTGTCAGGTTTAATAAGTGTGATTTCTTGCCTTATAAATGGGGTTGGGACCATCAGTTGTGTTGCGCAGAAGTCAGGTGGATACAC [63500]
```

Table 2.4. (continued).

```
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [63600]
scaffold39565_10.7_P._lessonae AGCTGATAGTCCTACTCAATAGACTGTTAGAATTTGTATTATGGCAAGAAAAAAGCAGCTAAGTACAGGAAAACGAGTGGCCATCATTACTTTAAGAAAT [63600]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [63700]
scaffold39565_10.7_P._lessonae GAAGGTCAGTCAGTCCGAAAAATTGGGAAAACTTTGAAAGTGTCCCCAAGTGCAGTCACAAAAAACATCAAGCGCTACAAAGAAACTGGCTCACATGCGG [63700]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [63800]
scaffold39565_10.7_P._lessonae ACCGCCCCAGGAAAGGAAGACCAAGAGTCACCTCTGCTGCGGAGGATAAGTTCATCCGAGTCACCAGCCTCAGAAATCGCAGGTAAACAGCAGCTCAGAT [63800]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [63900]
scaffold39565_10.7_P._lessonae TAGAGACCAGGTCAATGGCACACGGAGTTCTAGCAGCAGACACATCTCTAGAACAACTGTTAAGAGGAGACTGTGTGAATCAGGCCTTCGTGGTAGAATA [63900]
U40452_P._shqipericus          ---------------------------------------------------------------------------------------------------- [64000]
scaffold39565_10.7_P._lessonae TCTGCTAGGAAACCACTGCTAAAGAAAGGCAACAAGCAGAAGAGACTTGTTTGGGCAAAAGAACACAAGGAATGGACATTGGACCAATGGAAATCTGTGT [64000]
U40452_P._shqipericus          ----------------------------------------------------------------------------------- [64083]
scaffold39565_10.7_P._lessonae TTTGGTCTAATGAGTCCAAATTTGAGACCTTTGGTTCCAACCACCGTGTCTTCGTGCGACGCAGAAAAGGTGAACGG------ [64083]
```

Table 2.5. Calculation of the number of nucleotide differences (lower diagonal) and uncorrected p distance (upper diagonal) and their standart deviations among western Palearctic water frog species and outgroups on the basis of nucleotide sequence of the serum albumin protein coding exons.

	Species	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
1	***P. lessonae***		0,019 ±0,003	0,021 ±0,003	0,019 ±0,003	0,004 ±0,001	0,021 ±0,003	0,136 ±0,008	0,137 ±0,008	0,458 ±0,011	0,469 ±0,010
2	***P. ridibundus***	38 ±6,065		0,006 ±0,002	0,012 ±0,003	0,017 ±0,003	0,006 ±0,002	0,136 ±0,008	0,137 ±0,008	0,455 ±0,011	0,464 ±0,010
3	***P. cf.bedriagae***	40 ±6,123	11 ±3,417		0,014 ±0,003	0,020 ±0,003	0,010 ±0,002	0,139 ±0,008	0,140 ±0,008	0,459 ±0,011	0,468 ±0,010
4	***P. shqipericus***	39 ±6,160	23 ±4,955	27 ±5,589		0,019 ±0,003	0,012 ±0,003	0,138 ±0,008	0,139 ±0,008	0,458 ±0,011	0,467 ±0,010
5	***P. bergeri***	8 ±2,702	34 ±5,910	38 ±6,417	37 ±6,446		0,020 ±0,003	0,136 ±0,007	0,137 ±0,007	0,461 ±0,011	0,471 ±0,010
6	***P. epeiroticus***	37 ±5,849	11 ±3,060	17 ±3,755	21 ±4,876	34 ±5,849		0,142 ±0,009	0,143 ±0,008	0,451 ±0,012	0,462 ±0,011
7	***R. chensinensis***	268 ±14,746	268 ±14,847	268 ±14,778	270 ±14,907	265 ±14,382	247 ±14,987		0,003 ±0,001	0,477 ±0,010	0,481 ±0,010
8	***R. kukunoris***	270 ±14,589	270 ±14,695	270 ± 14,595	272 ±14,745	267 ±14,220	249 ±14,739	5 ±2,284		0,479 ±0,010	0,483 ±0,010
9	***X. laevis***	887 ±22,641	881 ±22,564	868 ±22,491	884 ±22,634	886 ±22,297	770 ±21,711	927 ±20,822	931 ±20,882		0,123 ±0,007
10	***S. tropicalis***	907 ±21,166	897 ±20,953	884 ±20,738	901 ±21,124	904 ±20,785	788 ±20,667	935 ±20,247	938 ±20,203	243 ±14,193	

Table 2.6. Calculation of the number of aa differences (lower diagonal) and uncorrected p distance (upper diagonal) and their standart deviations among western Palearctic water frog species and outgroups on the basis of aa sequence of the serum albumin protein coding exons.

		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
1	***P.lessonae***		0,048 ±0,008	0,058 ±0,010	0,045 ±0,008	0,011 ±0,004	0,055 ±0,011	0,237 ±0,016	0,24 ±0,016	0,624 ±0,020	0,636 ±0,020
2	***P.ridibundus***	29 ±5,072		0,016 ±0,005	0,02 ±0,006	0,047 ±0,009	0,003 ±0,002	0,233 ±0,016	0,237 ±0,016	0,622 ±0,020	0,629 ±0,020
3	***P.shqipericus***	27 ±4,901	12 ±3,419		0,034 ±0,008	0,056 ±0,009	0,020 ±0,007	0,251 ±0,017	0,255 ± 0,018	0,616 ±0,020	0,629 ±0,020
4	***P.cf.bedriagae***	32 ±5,161	9 ±2,823	19 ±4,125		0,045 ±0,009	0,023 ±0,008	0,237 ±0,016	0,24 ±0,016	0,625 ±0,020	0,634 ±0,020
5	***P.bergeri***	6 ±2,370	26 ±4,807	25 ±4,685	31 ±5,108		0,053 ±0,011	0,241 ±0,017	0,244 ±0,017	0,616 ± 0,021	0,629 ±0,021
6	***P.epeiroticus***	22 ±4,256	1 ±0,956	9 ±3,028	8 ±2,648	21 ±4,211		0,271 ±0,021	0,273 ±0,024	0,607 ±0,024	0,622 ±0,024
7	***R.chensinensis***	143 ±9,859	141 ±9,471	143 ±9,500	139 ±9,720	133 ±9,729	108 ±8,829		0,005 ±0,003	0,651 ±0,019	0,658 ±0,019
8	***R.kukunoris***	145 ±9,934	143 ±9,557	145 ±9,570	141 ±9,810	135 ±9,837	109 ±8,832	3 ±1,686		0,652 ±0,019	0,658 ±0,019
9	***X.laevis***	376 ±12,351	375 ±12,232	377 ±12,180	340 ±12,370	340 ±12,556	242 ±11,923	393 ±11,458	394 ±11,452		0,179 ±0,015
10	***S.tropicalis***	384 ±12,166	380 ±12,130	383 ±12,126	348 ±12,376	348 ±12,557	248 ±12,113	398 ±11,370	398 ±11,370	109 ±9,163	

CHAPTER 3

MANUSCRIPT 2: DISCORDANCE BETWEEN MITOCHONDRIAL AND NUCLEAR PHYLOGEOGRAPHY IN WATER FROG (*PELOPHYLAX*) COMPLEX OF THE EASTERN MEDITERRANEAN REGION

Çiğdem Akın Pekşen, C. Can Bilgin, Peter Beerli, Rob Westaway, Robert Schreiber, Glib Mazepa, Gaston-Denis Guex, Thomas Uzzell, Jörg Plötner

3.1. Introduction

Terrestrial environments in the eastern Mediterranean region, including Anatolia, has experienced high rates of crustal deformation for many millions of years. Significant events (cf. Steininger and Rögl, 1984) include: the closure of Tethys Sea linking the Mediterranean and the Indian Ocean as a result of uplift of the Arabian Platform; the isolation of the Paratethys Sea from the Global Ocean and its evolution into separate basins, including the modern Black and Caspian seas; the deformation of mountain ranges (e.g., the Pontides, Caucasus and Taurus); and the onset of the Messinian Salinity Crisis (MSC) caused by interruption of the marine connection between the Atlantic Ocean and the Mediterranean Sea. Seyrek et al. (2014) provided an up-to-date synthesis of the crustal deformation since the Late Miocene in a major part of the study region. In addition to geological processes, climatic changes modifying terrestrial environments include significant global cooling and the formation of ice sheets during the Pliocene and Pleistocene periods (e.g., Ehlers and Gibbard, 2007) and an increase in topographic relief as a consequence of climate change through erosional unloading of the Earth's crust caused uplift (Westaway et al., 2009a) have also caused significant changes in terrestrial environments.

To study how such geological and climatic events have affected species distribution, diversity, and genomes, a variety of mitochondrial and nuclear genetic markers have been used. Although the genome of an organism is subjected to common historical processes, molecular markers do not respond in the same way, resulting in discordance in tree topologies, branch lengths due to heterogeneities (Edward, 2009), times of divergences and phylogeographical patterns among genes. This is not surprising because each type of marker has a specific characteristics such as their inheritance mechanism, effective population size, recombination and mutation rate (Avise, 1994; Ballard and Whitlock, 2004; Currat et al., 2008; Leache, 2009; Petit and Excoffier, 2009).

Many potential mechanisms have been suggested to explain observed discordant patterns in both tree topologies and phylogeographic patterns in natural populations; these include incomplete lineage sorting, gene duplication, horizontal gene transfer, recombination, introgression (Degnan and Rosenberg, 2009), adaptive processes (Plötner et al. 2008), and sex-biased asymmetries (Coyne and Orr, 2004; Maroja et al., 2009,). In this paper we discuss the four most common drivers: incomplete lineage sorting, introgression, adaptive processes and sex-biased asymmetries. Incomplete lineage sorting is the retention and stochastic sorting of ancestral polymorphism, whereby some alleles, more closely related in the gene tree than is expected given the species tree, suggest paraphyletic and misleading relationships among lineages and unpredictable biogeographic patterns among mtDNA and nuDNA markers (Funk and Omland, 2003; Ballard and Whitlock, 2004; Maddison and Knowles, 2006).

The next most frequently observed driver introgressive hybridization, has been defined as exchange of genes between distinct evolutionary lineages (Seehausen, 2004). It has obvious impact on adaptive radiations such as Darwin's finches and African cichlid fish (Freeland and Boag, 1999; Salzburger et al., 2002) and on the formation of new species as seen in *Heliconius* butterflies (Mavarez et al., 2006). In particular, in evolutionary lineages that have diverged for long periods of time and have then come into secondary contact, for example as a result of range expansion from glacial refugia following the last glacial event.

The mode of introgression and its interaction with adaptive and sex-biased processes generally results in asymmetric introgression, which can form the last pattern of biogeographic discordance between mitochondrial and nuclear markers (Toews and Brelsford, 2012). Sex-biased processes include male-biased dispersal, as in *Pelophylax ridibundus* (Holenweg Peter, 2001); female-biased, a fitness loss in hybrids particularly the heterogametic sex when interbreeding occurs between divergent species, for example in eastern Palearctic water frogs, *P. nigromaculatus* and *P. plancyi* (Liu et al., 2010); or selection on genes playing a role in mating behaviour, for instance in field crickets, *Gryllus firmus* and *G. pennsyllvanicus* (Maroja et al., 2009). In adaptive processes, selection can also favour one group of mitochondrial haplotypes over another in a particular geographic region due to fitness advantage of its own distinct nuclear background. For example, Plötner et al. (2008) showed that, in northern Europe, *P.ridibundus* with the *P. lessonae*-specific mt haplotype have a fitness advantage over those with *ridibundus* mitochondria, being less sensitive to oxygen deficiency. All these sex-biased and adaptive processes lead to asymmetric mitochondrial introgression, resulting in a discordant pattern among mtDNA and nuDNA markers.

Water frogs (genus *Pelopyhylax*) in the eastern Mediterranean region represent a genetically and phylogenetically diverse group, made up of lineages of both older origin such as the Middle or Upper Miocene and others with a more recent origin in the Pliocene and Pleistocene (Plötner et al., 2009, Akın et al., 2010b). Although they are found in all types of freshwater environments, their skin physiology makes them highly sensitive to environmental changes caused by climate change, crustal deformation, and regional scale vertical motions that result in a loss or gain of surface waters needed for their survival and reproduction. Their populations tend to be highly structured genetically and to preserve signals of historical responses to geological and climatic changes (Akın et al., 2010b). They are thus an almost ideal group to study of the effect of geological and climatic processes on patterns of phylogeography and on the molecular evolution of protein coding (mitochondrial) and non-coding (nuclear) genes (Beerli et al, 1996, Plötner et al. 2010, Akın et al., 2010b).

Recent phylogeographic study of eastern Mediterranean water frogs (Akın et al., 2010b) revealed extensive genetic diversity in mtDNA, separated into six main haplogroups (MHGs). Three MHGs exist in Anatolia, the most widespread being distributed from western Anatolia to central Russia; the other two Anatolian MHGs are restricted exclusively to the areas west (the Cilician Plain) and east of the Amanos Mountains. The other three MHGs occur in the Levant, on Cyprus and in Europe. Estimates of divergence times of these groups showed that their separations were well correlated with geological events. How nuDNA reacted during these geological processes is, however, not known. Furthermore, it is not easy to identify any nuDNA marker that reflects true phylogenetic signals. In this study, the composite serum albumin intron-1+RanaCR1 (SAI-1+RanaCR1) was used as a nuDNA marker. It supports some aspects previously identified using mtDNA, including the sister group relationship between *P. perezi* and *P. saharicus*, and their joint sister group relationship to other western Palearctic water frogs, and the monophyly of the *P. lessonae* and the Anatolian populations (Plötner et al., 2009). It also indicates that the Anatolian water frogs consist of two distinct groups, and frogs from Cyprus represent a distinct evolutionary species *(P. cypriensis* Plötner et al., 2012).

Herein, we present a large mtDNA and nuDNA dataset, collected from eastern Mediterranean region especially Anatolia and neighbouring regions. These data reveal that the markers show discordances in the tree topology, the number of distinct genetic stocks, the levels of genetic differentiation, the times of divergence and the patterns of geographic distribution. Our observations suggest that inconsistency between the two marker sets can be explained by distinct processes, including incomplete lineage sorting and retention of ancestral polymorphism because of large effective population size of nuDNA; and introgression after secondary contact acting with sex-biased or adaptive processes linked to the inheritance pattern of mtDNA.

3.2. Material and Methods

3.2.1. Field Trips, Locality Selection and Sampling

Field trips in Turkey (2010-2011) were planned based on distributions of distinct mitochondrial haplogroups (MHG), broadly known from previous findings. Some regions, especially south-western Anatolia, have been well sampled while eastern Anatolia has been represented by samples from few localities (Akın et al., 2010a; 2010b). Because the study area consists of an extensive geographical region, locality selection was conducted in a way that should adequately reveal distributions of genetic lineages. Our main target for locality selection has been sampling river systems homogeneously throughout Turkey.

A total of 1500 tissue samples from 285 distinct localities at altitudes from 0 m to 2276 m were collected from within Turkey. 111 additional samples from 32 distinct localities from Kazakhstan, Armenia, Ukraine, Iran, Jordan, Poland and Germany were also included. Moreover, a total of 691 samples from previous studies (Plötner et al., 2001; 2008; 2009; 2012; Sumida et al., 2001; Akın et al., 2010a; 2010b) were combined for analysis to reveal the distribution pattern genetic markers distribution of water frogs in the eastern Mediterranean region (Appendices 3.1 and 3.2).

3.2.2. PCR and Sequencing of Mitochondrial and Nuclear Genes

DNA isolation was carried as described by Akın et al. (2010b). The procedure for amplification of two mitochondrial genes (NADH dehydrogenase subunit 2, ND2, 1038 bp; and NADH dehydrogenase subunit 3, ND3, 340 bp) were given by Plötner et al. (2008). For amplification of the nuclear serum albumin intron 1 (SAI-1), including the non-long terminal repeat (non-LTR) retrotranposon *Rana*CR1, the primer set Ex1-F5 (forward) and Ex2-R2 (reverse) were used following the method described by Plötner et al. (2009). Two additional internal (Int) primers were designed based on the complete sequences of SAI-1 obtained from homozygous individuals, to read the second part of the gene in heterozygous individuals after positions of G or CA repeats where length polymorphism can start. After G repeats, the 630 bp region of the SAI-1 gene was amplified using primer sets Int1F: 5`- CACTCAC**T**AAAA**CA**AGAAGAAAAGC – 3‘ or Int1Fv2: 5`- CACTCAC**G**AAAA**TT**AGAAGAAAAGC – 3‘ and Int1R: 5`- TTCAACAG-CTGGTT-TTCCCAC – 3‘. The 410 bp region of SAI-1 after CA repeats was also amplified by primer set Int2F: 5`- GGTTGAACTGGATGGACGGA – 3‘ and Int2R: 5`- CAACAGCTGGTTTTCCCACTG – 3‘. Amplification of these partial segments of SAI-1 involved an initial incubation at 96 ^{o}C for 3 min, followed by 35 cycles of 94 ^{o}C for 1 min, 60 ^{o}C for 1 min, 72 ^{o}C for 1 min, then a final 5 min extension at 72 ^{o}C. Using PCR primers and BigDye terminator chemistry on a 3130XL or 3730XL Genetic Analyzer (Applied Biosystems), PCR products of both the mitochondrial ND2 and ND3 genes and the nuclear SAI-1 gene were directly sequenced by Services in Molecular Biology GmbH (Berlin, Germany) and Mclab (California, United States) respectively. Sequences corresponding to new mitochondrial ND2 and ND3 haplotypes and nuclear SAI-1 alleles have been deposited in the EMBL Nucleotide Sequence Database under the accession numbers listed in Appendices 2.1 and 2.2.

3.2.3. Sequence Alignment and Grouping

All sequence alignments were performed using the CLUSTALW algorithm in MEGA 5.10 (Tamura et al., 2011). Alignments were then checked by eye, and corrected manually. Because of the length polymorphism in the nuclear SAI-1 marker among distinct lineages, several gaps were added to adjust length of sequences. In the *Pelophylax shqipericus* lineage, an additional 353 bp fragment within the retroelement *Rana*CR1 was recognized. After searching the RepeatMasker database (Institute for Systems Biology; http://www.systemsbiology.org; with the options: search engine=cross match; speed/sensitivity=slow; DNA source=vertebrate), it was determined that this fragment consists of simple repeats (GGTAC) and a member of DNA transposon family (TDR22) (Jurka and Drazkiewicz, 2002). This part of the sequence was therefore removed from all genetic and phylogenetic analysis.

For mitochondrial genes, each sequence was blasted against the GenBank database to establish to which main haplogroup it belongs. For the nuclear marker, the sequences of each individual were grouped according to genotypes as either homozygotes or heterozygotes. Two peaks in the chromatograms at corresponding positions were accepted as heterozygotes. Because there were enough homozygote individuals (nearly 500), we did not clone any nuclear sequences. Instead, nuclear allele phasing or allelic composition of a genotype was estimated on the basis of alleles derived from homozygotes (i.e. known phases) and internal primer pairs that specifically amplified one member of the allele pair within each genotypes becaused by polymorphism at the primer binding site. The resulting alignment of albumin intron alleles was subjected to a test for recombination using the Recombination Detection Program RDP 3.44 (Martin et al., 2010).

3.2.4. Phylogenetic Analysis

Calculation of haplotype and genotype frequency, haplotype diversity (h) and gene diversity (H), expected/observed heterozygosity, and nucleotide diversity (π) (Nei, 1987) were implemented in software ARLEQUIN version 3.5.1.2 (Excoffier and Lischer, 2010). Estimation of model of sequence evolution for both data types was conducted in MEGA 5.10 based on the Bayesian Information Criterion (BIC, Swarz, 1978). The best-fit molecular evolution model for the complete mitochondrial ND2+ND3 (328 sequences) was the general time-reversible model (GTR) with gamma-shaped rate variation (G = 1.046) and a fraction of invariant sites (I=39%) (ln L=-12585.68, BIC=33328.34); the best-fit model for the nuclear SAI-1 + *Rana*CR1 (145 sequences) was the Tamura-3-parameter (T92) model (Tamura, 1992) with a gamma-distributed shape parameter G = 0.622 (ln L=-6794.10, BIC=17040.46). Because the GTR model is not available in MEGA for genetic distance calculation, the second best-fit model, the Tamura-Nei (TrN) model (Tamura and Nei, 1993) with a gamma-shaped rate variation (G=0.325) and (ln L=-12638.43, BIC=33381.97) was used to calculate genetic distance among distinct mitochondrial groups.

Bayesian phylogenetic analysis and divergence time estimation of mitochondrial and nuclear data sets were performed in the program BEAST version 1.7.5 (Drummond et al., 2012). The data sets were prepared using the BEAST assistance program BEAUTI 1.7.5. For the mtDNA data set, Bayesian analysis was initiated from the UPGMA starting tree general time-reversible mutation model (GTR) with gamma-shaped rate variation, using 4 discrete mutation classes, and a percentage of invariant sites (GTR+G+I) (Huelsenbeck and Rannala, 2004). For the nuDNA dataset, the Hasegawa-Kishino-Yano (HKY) mutation model (Hasegawa et al., 1985) with gamma distributed site rate variation, using 4 discrete mutation classes, and a percentage of invariant sites (HKY+G+I), was set to run using a random starting tree. For the nuDNA data set, a relaxed molecular clock (Drummond et al., 2006) was used, whereas for mtDNA data set, a strict clock was estimated using an uncorrelated lognormal prior and the Yule model as a tree prior. To calculate posterior distribution parameters, the MCMC was run for 100,000,000 steps and sampled every 10,000 steps. The first recorded 1000 trees were discarded as burn-in. The effective sample sizes for posterior probability were evaluated from the logfiles in TRACER 1.5 (Rambaut and Drummond, 2009). Additionally, *P. nigromaculatus* (North Korea), *P. saharicus* (north-western Africa), *P. perezi* (Iberian Peninsula*)*, *P. lessonae* (Central Europe), *P. bergeri* (Apennine Peninsula), *P. shqipericus* (western coast of Balkan Peninsula), and *P. cretensis* (Crete) were included as outgroup comparisons in this study (Appendices 1 and 2).

To reveal evolutionary relationships and current mutational variations and probable ancestral connections among mitochondrial haplotypes and nuclear alleles, median-joining networks (Bandelt et al., 1999) were constructed using the program NETWORK 4.6.1.1. For haplotype phylogeny 1817 ND3 haplotypes and for nuclear phylogeny 1369 SAI-1+RanaCR1 alleles were used. Outgroup sequences were excluded from the network analysis for both mitochondrial and nuclear datasets.

Bayesian tree topologies, numbers of mutational connections and branching patterns among haplotypes and alleles, using TrN+G genetic distance on the basis of joint ND2+ND3 sequences (as suggested by Akın et al., 2010b) and T92 + G genetic distances among SAI-1+RanaCR1 alleles, were accepted as parameters to define the MHGs, the main allele groups (MAGs), subgroups, and allele groups. In addition to these, unique variations such as transitions, transversions, and insertions and deletions (indels) within the SAI-1+*Rana*CR1 marker were used to define allele groups, because when programs calculate genetic distance from a dataset including indels as well as substitutions they generally underestimate genetic distance among lineages.

Divergence times for both mtDNA and nuDNA datasets were calculated by applying two distinct methods. The first was a simple linear regression model as used by Akın et al. (2010b). For mtDNA, pairwise TrN+G genetic distance was divided by two constant evolutionary rates (1.4 and 1.5% per Myr) calculated using as a calibration point two distinct divergence times (5.3 and 5.5 Ma) between Cyprian and Anatolian water frog populations. For nuDNA, pairwise T92 + G genetic distance was divided by two evolutionary rates (0.69 and 0.72% per Myr) calculated using the same two putative divergence times (5.3 and 5.5 Ma) between Cyprian and Anatolian water frog populations. Second, a Bayesian method was applied, using the software BEAST (Drummond and Rambout, 2012).

3.3. Results

3.3.1. Molecular Diversity

In total, 568 ND2 and 1821 ND3 sequences from Turkey, the Middle East, Central Asia, the Levant, Cyprus, Central Europe and Eastern Europe were used in the analysis (Appendix 3.1). The ND2 sequences were represented by 242 distinct haplotypes with $h=0.98\pm0.002$ and $\pi=2.76\pm1.34\%$, while the ND3 sequences defined 182 distinct haplotypes with $h=0.93\pm0.004$ and $\pi=3.03\pm1.53\%$. The joint sequences (ND2+ND3; N=328) including outgroups contained 663 variable sites (48.1%) of which 606 (44%) were parsimony-informative. The nuclear marker analysis for SAI-1+*Rana*CR1 yielded sequences for 1369 individuals from the same spread of regions (Appendix 3.2). They were represented by 295 distinct genotypes of which 863 were heterozygous and 506 were homozygous with expected heterozygosity=0.9314 and observed heterozygosity=0.6304. These genotypes were formed by 114 unique alleles with gene diversity $H=0.92\pm0.003$ and $\pi=2.05\pm1.00\%$. The unique alleles and outgroup sequences (N=145) contained 268 variable sites (23.1%) of which 190 (16.4%)

were parsimony-informative. No evidence for recombination of nuclear serum albumin alleles was found.

3.3.2. Phylogenetic Relationships, Genetic Divergence, and Geographical Pattern of Mitochondrial Haplogroups

The Bayesian tree topology, from joint analysis of ND2+ND3 genes (Fig. 3.2), the median-joining network (Fig. 3.3), the geographical pattern of ND3 haplotypes (Fig 3.1) and pairwise TrN+G among ND2+ND3 sequences (Appendix 3.3) indicate eight well differentiated MHGs as shown by Akın et al., (2010b). The mean TrN+G distances (G=0.325) between these eight MHGs varies from 0.032 (MHG6-MHG7) to 0.102 (MHG1-MHG8) while mean distance values within each MHG was ≤ 0.014.

MHG1 includes specific haplotypes of European *P. ridibundus*, ranging from France (throughout Europe) to Central Russia, and haplotypes of Balkan lake frogs, *P. kurtmuelleri* (Akın et al., 2010b). MHG2 consists of characteristic haplotypes of *P. bedriagae*, found in Jordan, western Syria and the Nile delta of Egypt. Even though this group has been sampled only to a limited extent, it reveals a high diversity (π=1.0±0.59%), and has been divided into two subgroups. MHG2a was found only in Jordan and As Suwayda in southern Syria whereas MHG2b was recorded in Egypt and elsewhere in Syria. The actual geographic patterns of these subgroups are not known, however, beacuse of limited sampling. MHG3 represents characteristic haplotypes of the recently described species *P. cypriensis* (Plötner et al., 2012) in Cyprus. Sister groups MHG4 (Cilician West) and MHG5 (Cilician East) were found mainly in the Cilician plain sympatrically, but the frequency of MHG5 is higher in the eastern part of the Amanos mountains (Akın et al., 2010b; Fig 3.1. and Appendix 3.1).

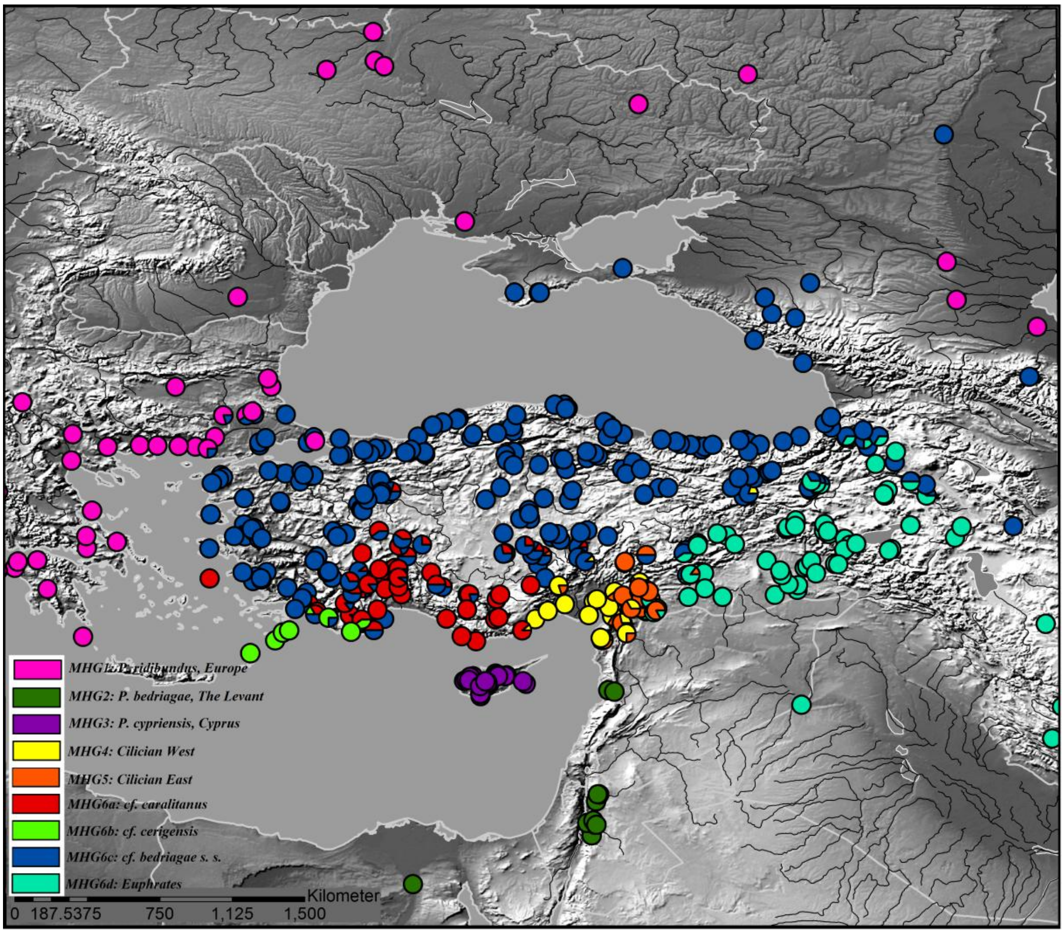


Figure 3.1. Distribution of main mitochondrial haplogroups (MHG1-6) and subgroups (MHG6a-d) in the eastern Mediterranean region water frog complex (genus *Pelophylax*).

MHG6 (cf. *bedriagae*, Anatolia) is the most diverse group (haplotype diversity, h=0.89±0.01 and nucleotide diversity, π=1.6±0.09). It consists of four subgroups (a-d), between which the mean genetic distance ranges from 0.017 to 0.027. MHG6a (cf. *caralitanus*) was mainly found in south-western Turkey (the Anatolian Lake District and Konya plain). It coexists with haplotypes of MHG4 and 5 in the eastern border of Konya plain. MHG6b (cf. *cerigensis*) was locally distributed in the region between Antalya and Muğla on the Mediterranean coast of south-western Turkey, also in Rhodos and Karpathos islands. MHG6c (cf. *bedriagae*) is the most widely distributed subgroup, ranging from western

Anatolia, including the Aegean islands of Samos, Lesvos and Chios, to central Russia and to the northern shore of the Caspian Sea (type locality of *P. ridibundus*). MHG6d (Euphrates) was found in the catchments of Euphrates and Tigris rivers (Akın et al., 2010b) in eastern Anatolia. It overlaps with haplotypes of MHG6c in the valleys of the Aras and Kura rivers in northeastern Anatolia and western Iran (Fig.3.1).

MHG7 (Central Asia 1) corresponds to characteristic haplotypes of *P. terentievi,* distributed to the south and east of the Caspian Sea in Iran, Turkmenistan and Uzbekistan. MHG8 (Central Asia 2) represents characteristic haplotypes of the undescribed species, *P. sp. novum,* found in Kyrgyzstan, Kazakhstan and western Tajikistan. It coexists with haplotypes of MHG7 on the river Zeravshan, which is north-east of the river Amu Darya (unpublished data).

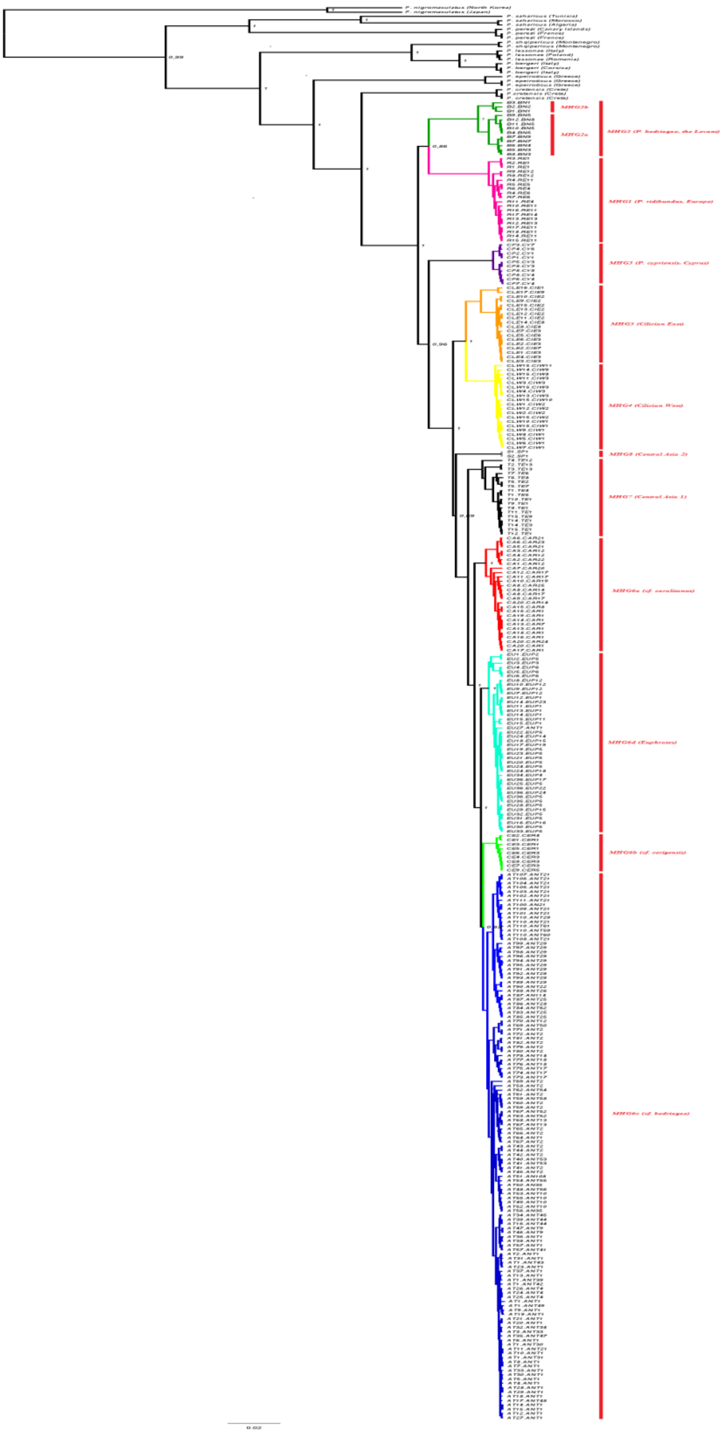


Figure 3.2. Maximum clade credibility tree calculated on the basis of Bayesian phylogenetic analysis of the joint ND2+ND3 mtDNA haplotypes (1378 bp) from Western Palearctic and eastern species of eastern Palearctic water frogs (genus *Pelophylax*). Values at nodes are posterior probabilities. The branch labels are haplotype IDs of ND2 and ND3 combinations given in Appendix 3.1.

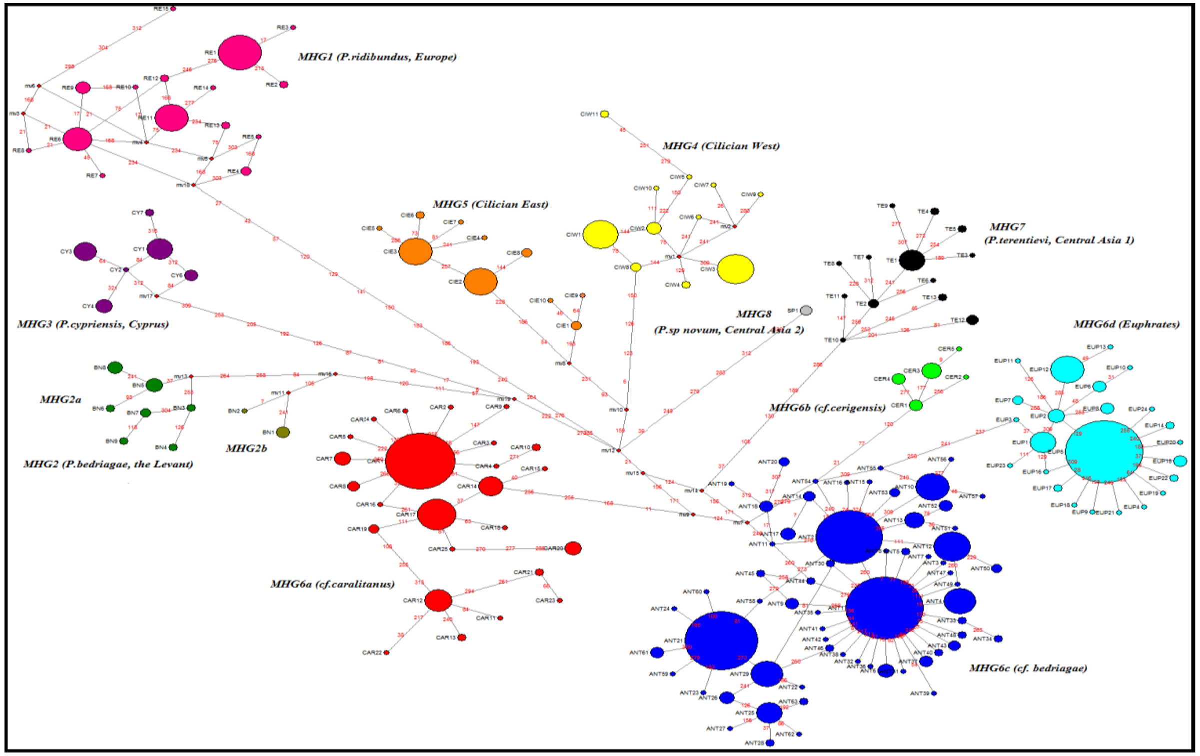


Figure 3.3. Median joining network of mitochondrial ND3 haplotypes constructed by NETWORK 4.6.1.1 (Bandelt et al., 1999) showing genealogical relationships among main haplogroups (MHG1-8) and subgroups (MHG6a-6d and MHG2a-2b). The sizes of the circles represent haplotype frequency; median vectors (mv) indicate ancestral haplotypes that were not observed in the data set. Numbers on lines show mutational changes from one haplotype to next one in the ND3 alignment.

3.3.3. Phylogenetic Relationships, Genetic Divergence, Geographical Pattern of Nuclear Allele Groups and Their Relationships with Mitochondrial Haplogroups

The Bayesian tree topologies (Fig. 3.4), the median-joining network of the nuclear SAI-1+RanaCR1 alleles (Fig. 3.6), the geographic pattern of nuclear alleles (Fig. 3.5a,b,c), the pairwise T92+G genetic distance (Appendix 3.4) and unique molecular variations among albumin alleles, particularly for subdivision of subgroups and allele groups (Appendix 3.5), reveal five distinct MAGs: MAG1 (Anatolia), MAG2 (Asia), MAG3 (Ridibundus), MAG4 (Levant; BED2) and MAG5 (Cyprus). The mean T92+G distance (G=0.622) between these MAGs ranged from 0.013 (MAG2-MAG3) to 0.050 (MAG1-MAG5); the mean distance values among MAG1, MAG2 and MAG3s were ≤ 0.010.

The Anatolia MAG1 is the most widespread and well differentiated monophyletic group within the eastern Mediterranean water frog complex, with five allele subgroups (a-e; Fig. 3.4), some widely distributed, others geographically restricted. The mean distance values between the five subgroups are 0.005-0.018. Each of these subgroups in turn consists of one or more allele groups. MAG1 has variations in G repeats (3-5) at positions between 514 and 518 within the *Rana*CR1 element and in T repeats at positions 1135-1140 at the end of the intron.

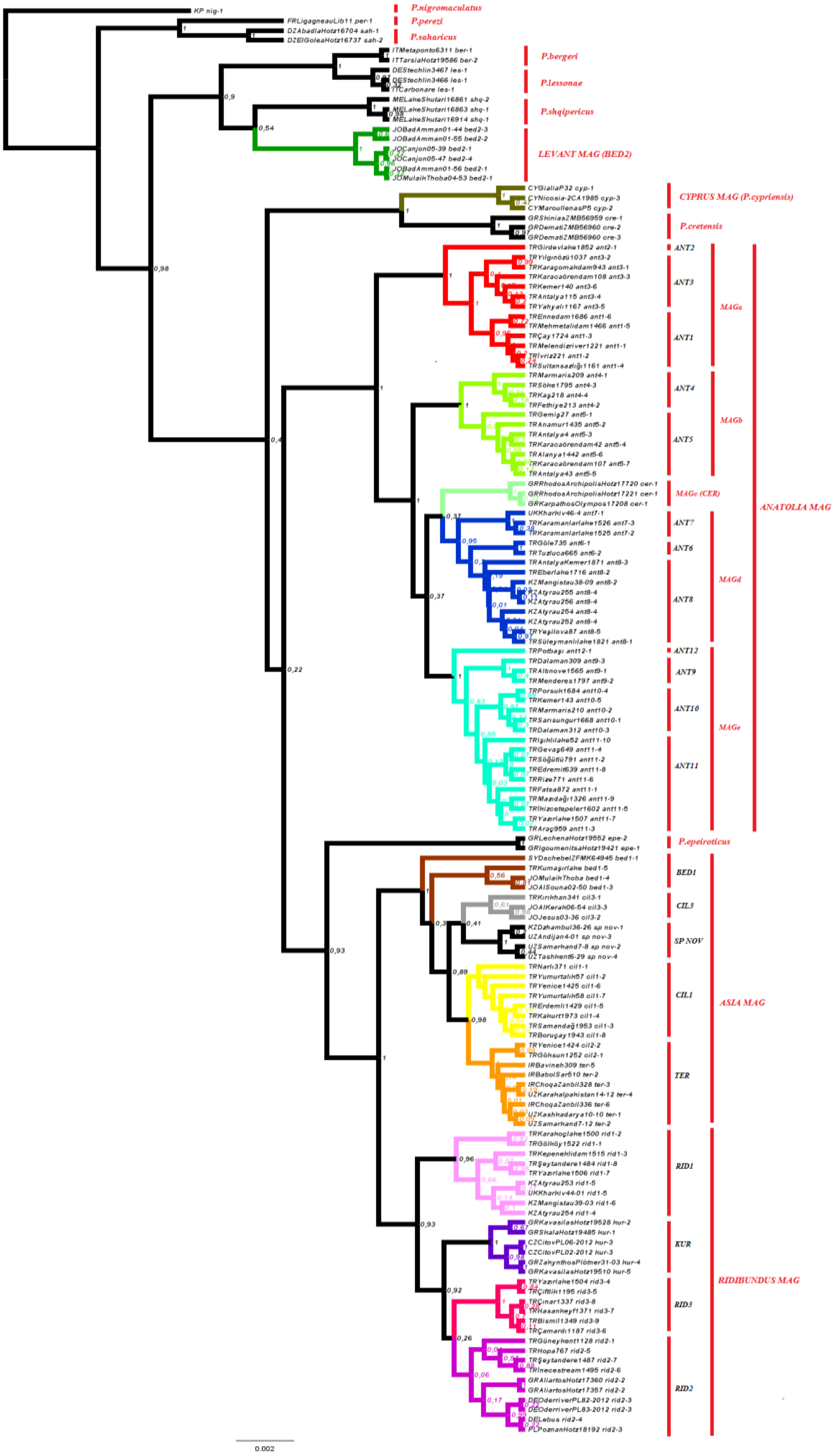


Figure 3.4. Maximum clade credibility tree constructed using Bayesian phylogenetic analysis of nuclear SAI-1 + RanaCR1 alleles from western Palearctic and eastern taxa of Eastern Palearctic water frogs (genus *Pelophylax*). Values at nodes indicates posterior probabilities. The branch labels are names of alleles given in Appendix 3.2.

MAG1a has three allele groups: ANT1, ANT2 and ANT3. Alleles of ANT1 (ant1-1 - ant1-6) were found only in the closed Konya basin (most frequently, including the type locality of *P. cf caralitanus*), in Kayseri-Sultansazlığı and Akşehir-Eber lakes (Isparta province), and in Işıklı lake (Kütahya and Uşak provinces). Except for Kütahya and Uşak, haplotypes characteristic of MHG6a (cf. *caraliranus)* were also found at all of these localities. The ANT2 allele (ant2-1) was most frequently recorded in the Anatolian Lake District region except in a few localities (Afyon and İzmir Çandarlı) where individuals had mostly cf. *caralitanus* specific haplotypes (MHG6a). In contrast, alleles of ANT3 (ant3-1 - ant3-6) were distributed in most parts of Turkey except western Anatolia. Its distribution, therefore, covers not only the cf. *caralitanus* subgroup (MHG6a) but also other mitochondrial haplogroups (Fig. 3.1).

MAG1b has two geographically restricted allele groups: ANT4 and ANT5. Alleles of ANT4 (ant4-1 - ant4-4) were frequently found in the Mediterranean coastal region of SW Anatolia between Antalya and Muğla where haplotypes specific for cf. *cerigensis* (MHG6b) occurred. They were also found in the Lake District region where cf. *caralitanus* specific haplotypes (MHG6a) were found, and less frequently in the catchment of the Büyük Menderes River where haplotypes specific of cf. *bedriagae* (MHG6c) were present. In contrast, alleles of ANT5 (ant5-1 - ant5-7) were predominantly recorded farther east along the Mediterranean coast of Anatolia between Antalya and Mersin where haplotypes specific for cf. *caralitanus* (MHG6a) occurred. The MAG1c (cer1-1) allele was only found on the islands of Rhodos and Karpathos, where only *cf. cerigensis* specific haplotypes (MHG6b) have been reported.

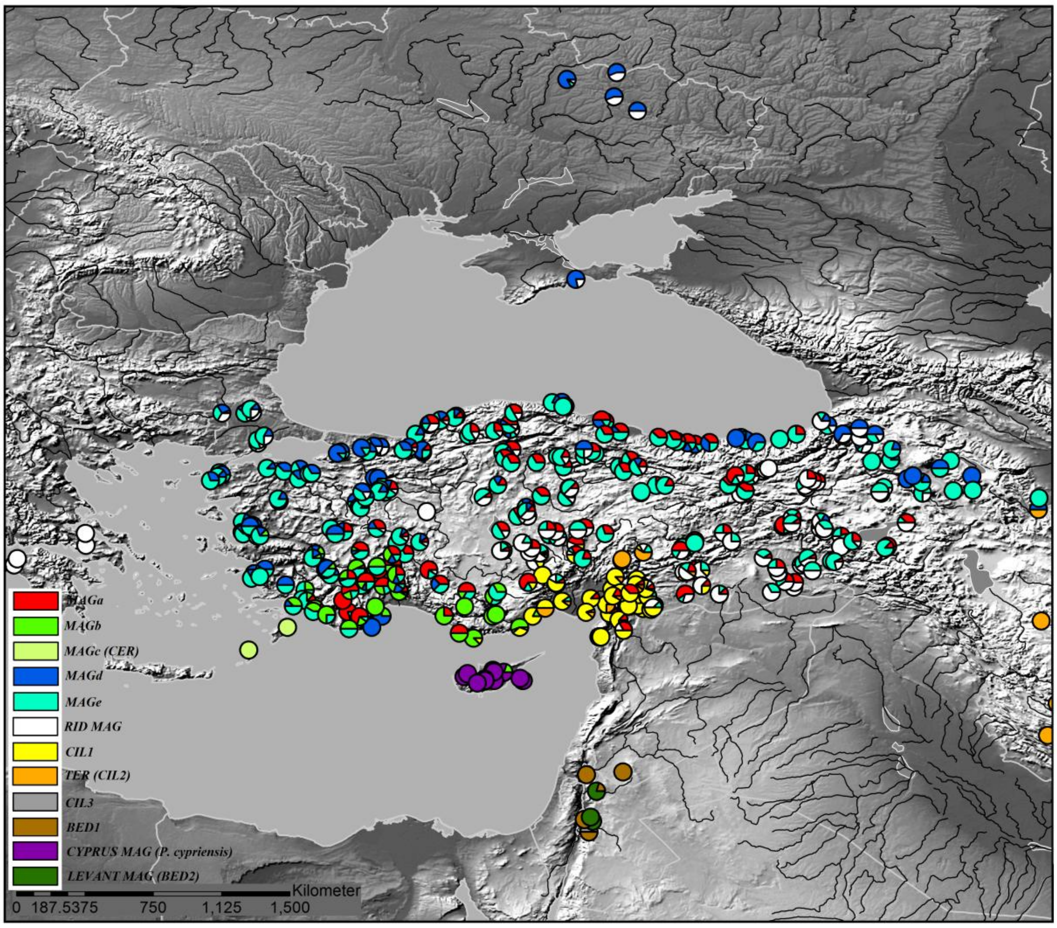


Figure 3.5a. Distribution of allele groups of the Anatolia main allele group (MAG1a-e), Asia (MAG2: CIL1, TER, CIL3, BED1), Cyprus (MAG5) and Levant (MAG4: BED2). Distribution of RID (MAG3) is shown on this map without giving group divisions.

MAG1d has three allele groups: ANT6, ANT7 and ANT8. Alleles of ANT6 (ant6-1 - ant6-2) were found between north-eastern Anatolia, Ukraine and Kazakhstan, including throughout the Caucasus. Alleles of ANT7 (ant7-1 - ant7-3) had the widest distribution, including western and central Anatolia, western and central parts of the Black Sea region (but not the eastern Black Sea region), and Thracia, Ukraine and Kazakhstan. The absence of this allele group from the eastern Black Sea region indicates that it probably spread over Thracia and the western Black Sea region from Anatolia to eastern Europe. ANT8 includes several rare alleles (ant8-1, 8-4 and 8-5), found in a few localities, as well as common alleles ant8-3 (in western Anatolia) and ant8-2 (several localities in Ukraine, Kazakhstan but only one locality in Turkey, Akşehir-Eber lake), which suggests that they occurred frequently in Anatolia in the past, but later they were lost or became rare. The distribution of this MAGd shows a similar pattern to haplotype MHG6c (cf. *bedriagae*; Fig. 3.1).

MAG1e has four allele groups, ANT9, ANT10, ANT11 and ANT12. Alleles of ANT9 (ant9-1 - ant9-3) were only found in south-western Anatolia. Alleles of ANT10 (ant10-1 - ant10-5) were distributed in south-western, western, and central Anatolia, the western Black Sea region and Thracia. Alleles of ANT11 (ant11-1 - ant11-10) were found throughout Turkey except for southern Mediterranean coastal localities.

The Asia MAG2 is probably the most interesting group, consisting of geographically overlapping or adjacent western Asian allele groups (CIL1, CIL3, and BED1) and adjacent Central Asian allele groups (TER and SP NOV); the mean distance values between these being 0.004-0.011. Within MAG2, there are variations in the number of CA microsatellite repeats (4-6) at the 3' UTR region of the *Rana*CR1 retrotransposon, and all share a 25 bp deletion at position 1051-1075 (Plötner et al., 2012).

Alleles of CIL1 (cil1-1 - cil1-8) occur in the Cilician and Narlı plains on both the western and eastern sides of the Amanos Mountains. At the boundaries of these plains, several heterozygous individuals, carrying alleles of the CIL-1 subgroup and either MAG1 or MAG3 groups were found.

Alleles of CIL3 (cil3-1 - cil3-3) were interestingly found in the eastern Amanos mountains in a few localities (Kırıkhan in Hatay province and Lake Kumaşır in Kahramanmaraş province) and in Jordan (Al Kerak and near Jesus where individuals were heterozygous with an allele of BED1). Alleles of BED1 (bed1-3, bed1-3 - bed1-5) were also recorded in Jordan, Syria and one locality in Turkey (Lake Kumaşır, where one individual was heterozygous carrying alleles of CIL1 and BED1 groups). There may, however, well be individuals carrying alleles belonging to CIL3 and BED1 in the region between Hatay in Turkey and Jordan particularly throughout the catchment of the River Orontes. No field studies have so far been carried out in this region; sampling there (which will only be possible when the political situation in Syria and Lebanon improves) could make clear both the phylogenetic positions of these groups and their relationships to the CIL1 group, which are now only supported by a low posterior probability value, 0.3 (Fig. 3.5). In respect of mtDNA, central southern Turkey includes the Cilician West (MHG4) haplotype (west of the Amanos Mountains) and Cilician East (MHG5) haplotype (east of the Amanos Mountains), with haplotypes of *P. bedriagae* (MHG2) distributed in Syria and Jordan (Fig. 3.1). Just as for the nuDNA data, the haplotype pattern is not known in the catchment of the River Orontes between Hatay and Syria.

The TER group (alleles cil2-1, cil2-2, ter1-ter6), one of the Central Asian groups of MAG2, was mostly found to the south and east of the Caspian Sea, in Iran, Turkmenistan and Uzbekistan. The distribution of these alleles overlaps with that of haplotypes specific for *P. terentievi* (unpublished data). It is difficult to explain why two alleles, cil2-1 and cil2-2, were only found in central-southern Turkey, forming a clade within the TER group, not the CIL1 group. Individuals carrying these two alleles, have haplotypes from distinct groups (MHG4 and 5 and MHG6c and d), depending on the locality. Alleles of the other Central Asian group, SP NOV, were found in Kyrgyzstan, Kazakhstan and western Tajikistan, coincident with haplotypes specific for *P. sp nov.* (unpublished data).

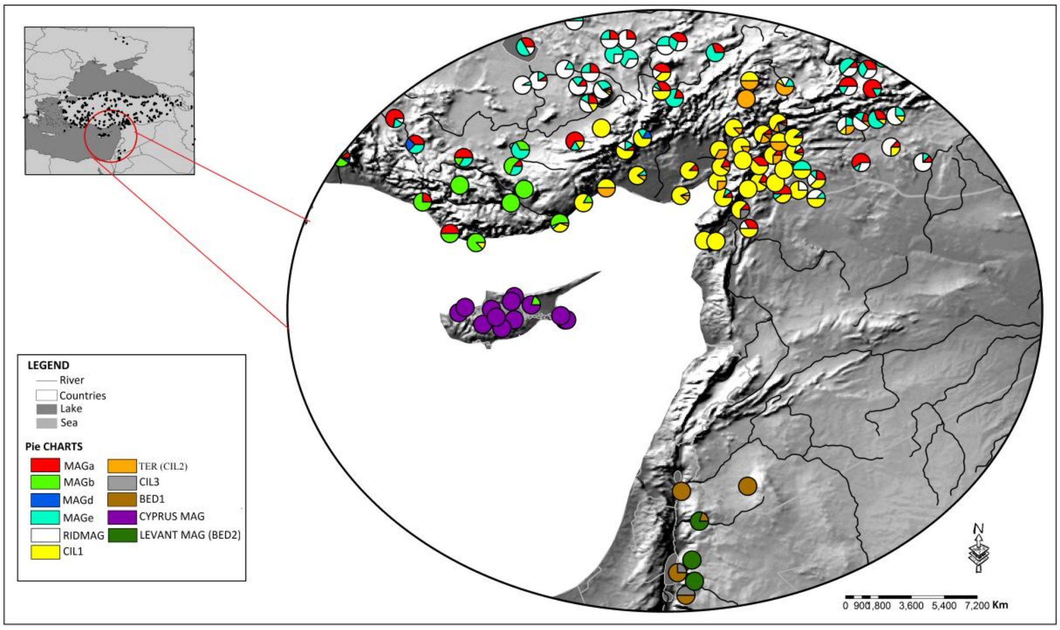


Figure 3.5b. Distribution of allele groups in central-southern Turkey (MAG1a, MAG1b, MAG1d, MAG1e, RID MAG3, Asia MAG4 (CIL1, CIL2=TER, CIL3, BED1) and the Levant (Levant MAG-BED2, BED1 and CIL3).

The Ridibundus MAG is widely distributed. It shows variations in CA microsatellite repeats (5-10) at the 3' UTR region of the *Rana*CR1 retrotransposon within SAI-1 and T repeats (5-6) at the end of the intron (positions 1135-1140). It consists of four allele groups (RID1-RID3 and KUR); mean distance values between these are 0.005-0.013. Alleles of RID1 are mainly distributed in the European part of Turkey, the western Black Sea region, Kazakhstan (including the allele rid1-5, found at the type locality of *R. ridibundus*) and Ukraine (Fig 3.4b), where some individuals were heterozygous for one allele from the RID1 group, the other allele from the Anatolia MAG1d or the MAG1e subgroups. This sympatric distribution of RID1 and ANT allele groups is also supported by the overlapping distribution of mtDNA haplotypes belonging to MHGc (cf. *bedriagae*) and MHG1 (*P. ridibundus*) in these regions, except in the western Black Sea where haplotypes of cf. *bedriagae* type were only recorded but no *ridibundus* specific haplotypes.

RID2 includes Central European specific *ridibundus* alleles (rid2-3 and 2-4). RID2 also includes one of the most common *ridibundus* alleles (rid2-1) in Central Anatolia and the Black Sea region, as well as rid2-6 and 2-7 (unique to the European part of Turkey) and rid2-5 (a common allele in north-eastern Anatolia). Relationships between these last three alleles and the others are, however, not clear. Alleles of RID2 in Turkey were carried as homozygotes or heterozygotes in individuals with alleles from other ANT or RID groups. Except in Central Europe and the European part of Turkey, the haplotype pattern of Central Anatolia, the Black Sea Region and north-eastern Anatolia (where the haplotype specific for *cf. bedriagae* was present), was not concordant with the distribution of nuclear alleles of RID2 group, since no *ridibundus* haplotypes were found in these regions.

RID3, the most frequent rid allele group in Turkey, includes alleles specifically distributed in the eastern Anatolia (rid3-7, 3-8 and 3-9), the rid3-5 allele found in some localities near the Tuz Gölü salt lake in central Anatolia, in the European part of Turkey and in south-eastern Anatolia, and the rid3-6 allele recorded only at a few localities near the Tuz Gölü. Individuals were either homozygote, especially in eastern and central Anatolia, or heterozygote with alleles from the ANT, CIL and RID groups. The RID3 group probably reveals the most discordant haplotype pattern; the region where alleles of this group are found is dominated by haplotypes of the cf. *caralitanus*, cf. *bedriagae* or Euphrates haplogroups (Akın et al., 2010b). Except in the European part of Turkey, none of haplotypes of the *ridibundus* MHG were found in these regions.

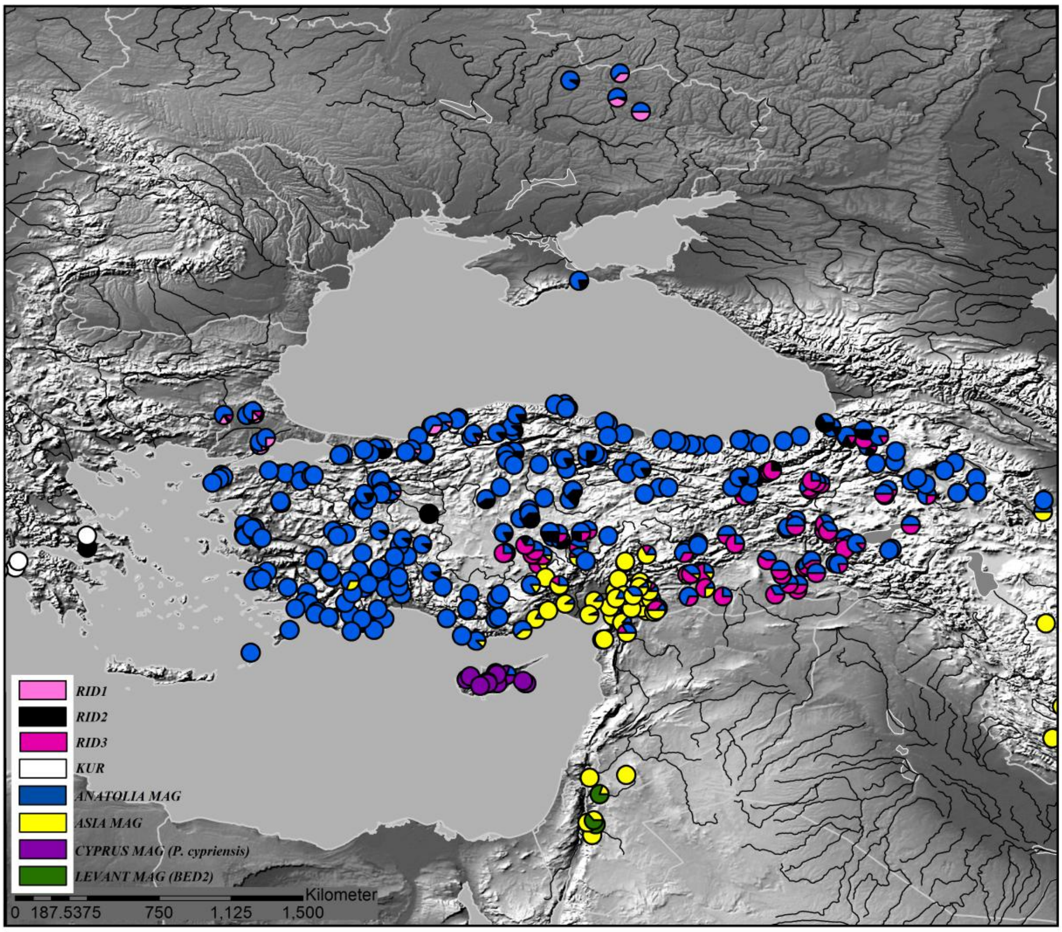


Figure 3.5c. Distribution of allele groups of RID MAG3 (RID1, RID2, RID3 and KUR). Distributions of other MAGs, including Anatolia, Asia, Cyprus and Levant are shown only without group divisions.

Group KUR contains alleles characteristic of Balkan lake frogs, *P. kurtmuelleri*. It is well resolved from the other RID allele groups by the high posterior probability value of 0.93, the number of mutational connections in the median-joining network and several unique mutations within the SAI-1+RanaCR1 marker, including a 124 bp deletion starting after the CA repeats at positions 758-890 (Plötner et al., 2009). The distribution of alleles of this group is concordant with the haplotype pattern specific for *P. kurtmuelleri*. Its complete distribution and its relationships with other European water frogs are not known.

The Levant MAG4 (BED2) is the other group that carries *P. bedriagae* specific haplotypes. In contrast to the BED1 group, which is closely related to Cilician and other Central Asian groups, BED2 forms a clade among outgroup species. It seems to have sister relationships with *P. shqipericus*, *P. lessonae and P. bergeri*, although, this conclusion is supported by a low posterior probability value (Fig. 3.5). Alleles of this group share with the Asia MAG2 a 25 bp deletion at positions 1051-1075, but also has a 7 bp deletion at positions 758-764 and several unique transitions and transversions. Alleles of this group were found in Jordan, but its actual distribution is not known because of sampling deficiency. Finally, the Cyprus MAG5 has alleles characteristic of the recently described Cyprus water frog species, *P. cypriensis* (Plötner et al., 2012) and it carries haplotypes specific of this species.

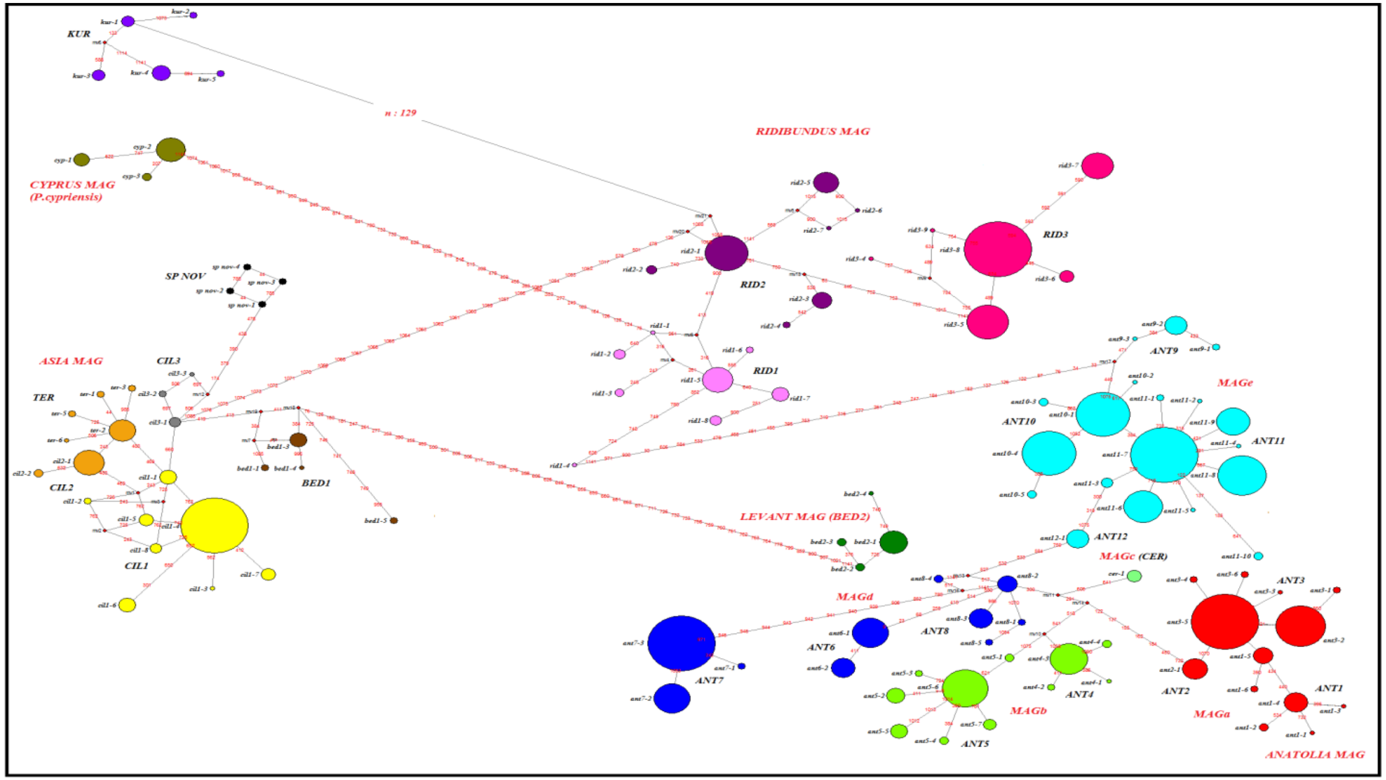
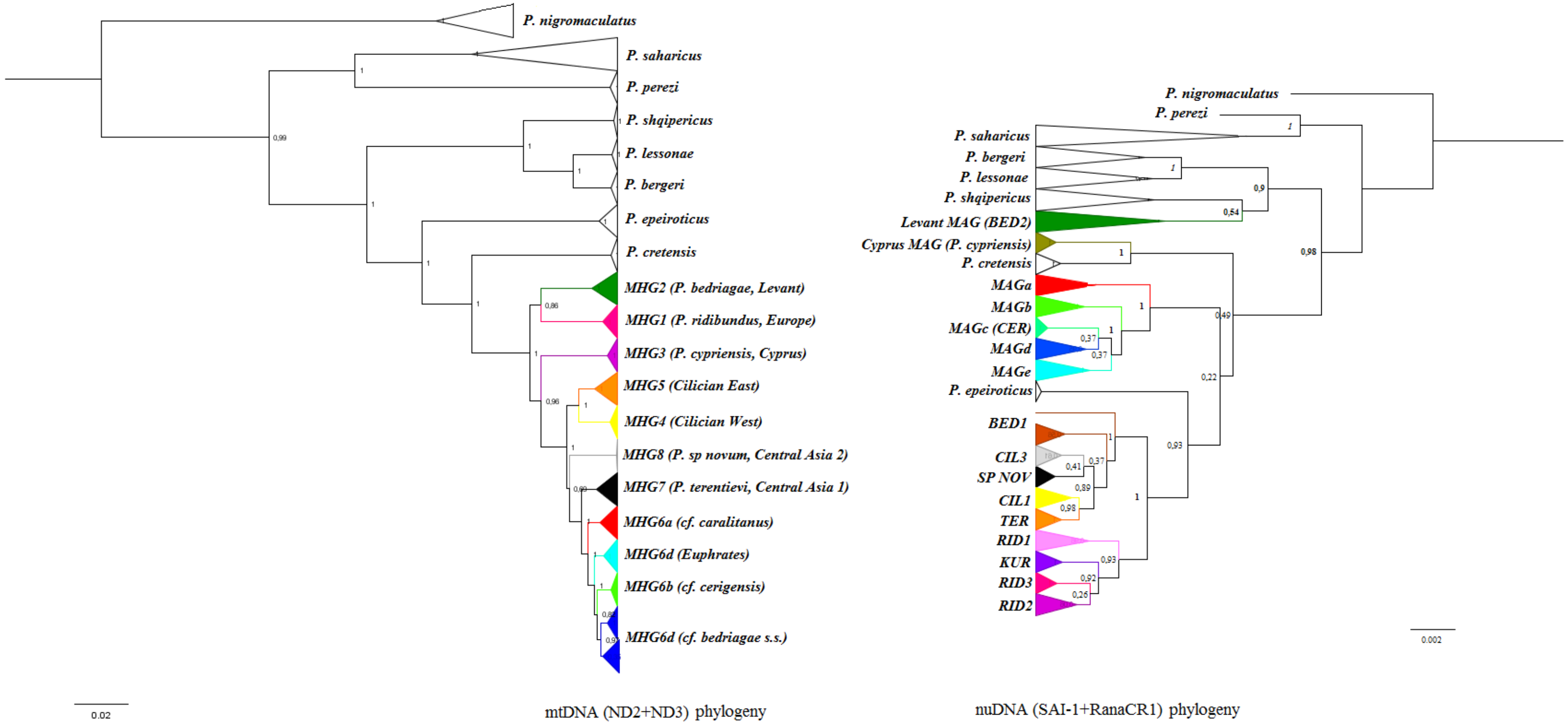


Figure 3.6. Median joining network of nuclear SAI-1+RanaCR1 alleles constructed by NETWORK 4.6.1.1 (Bandelt et al., 1999) demonstrating phylogenetic relationships among main allele groups (MAG1 and subgroups MAG1a-e, Anatolia; MAG3, Ridibundus; and MAG2, Asia). The sizes of the circles indicate allele frequency; median vectors (mv) represent ancestral alleles that were not found in the dataset. Numbers on lines show mutational changes (substitutions and indels) from one allele to next in the SAI-1+RanaCR1 alignment.

3.3.4. Comparison of mtDNA and nuDNA Tree Topologies and Estimation of Times of Divergence

Our Bayesian phylogenetic results reveal clear discrepancies between the mitochondrial and nuclear gene trees (Fig. 3.7). The topology obtained from mitochondrial genes consists of several reciprocally monophyletic groups, supported by high posterior probabilities. In contrast, the topology based on the nuclear marker contains both weakly supported groups, some of which showed paraphyletic relationships; and some well supported clades. Thus, for example, in the mtDNA tree, *P. bedriagae* (MHG2) represents an ingroup species, clustering with *P. ridibundus* (MHG1) as a sister group, whereas in the nuDNA tree it (Levant MAG5) forms a clade within the outgroup species *P. shqipericus/P. lessonae/ P. bergeri*. *P. epeiroticus* split off before *P. cretensis/P. cypriensis* in the mtDNA tree, but in the nuDNA tree seems more closely related with the Anatolia and Asia/Rid MAGs. *P. cretensis* diverges earlier than *P. cypriensis* in the mtDNA tree, but these two form sister species in the nuDNA tree (Plötner et al., 2012). *P. ridibundus* in the mtDNA tree forms a sister group with *P. bedriagae* from the Levant whereas in the nuDNA tree it clusters with the Asia MAG2, including groups from Central Asia, central-southern Turkey and the Levant (BED1). In contrast to the well characterized Cilician (MHG4 and 5) and Central Asia (MHG7 and 8) monophyletic groups in the mtDNA tree, their relationships within the Asian MAG2 are not fully resolved; some clades within this group were indeed only weakly supported.



mtDNA (ND2+ND3) phylogeny

nuDNA (SAI-1+RanaCR1) phylogeny

Figure 3.7. Bayesian phylogenetic tree topologies of mtDNA (ND2 + ND3 genes) on the left and nuDNA (SAI-1 + RanaCR1) on the right. Tree topologies include only main groups (MHG or MAG) and subgroups without showing haplotype and allele names.

The two methods for estimating divergence times, a simple linear regression model and analysis using BEAST, provided similar results within a data type (Table 3.1). As already noted, for both mtDNA and nuDNA, divergence times between the Cyprian and Anatolian water frog populations (5.3 and 5.5 Ma) were used as a calibration points, based on the idea that these populations became separated around the end of the MSC when the Mediterranean Sea reverted to being a marine basin (Akın et al., 2010b). Using these calibration points, however, there are discrepancies between mtDNA and nuDNA for some groups or species. Thus, for example, the estimated rate for mtDNA evolution indicates that *P. cretensis* diverged before 9 Ma, whereas the estimated rate for nuDNA evolution indicates that its divergence occurred around the same time as that of *P. cypriensis*, about 6-5 Ma. mtDNA indicates a deep divergence (about 3.5-4.5 Ma) between Cilician groups (MHG4 and 5) and Central Asian groups (MHG7 and 8) whereas nuDNA results indicate a very shallow divergence among these groups (CIL1 and 3-TER and SP NOV), diversifying about 1.5-0.5 Ma. Similarly, in contrast to the mtDNA results, divergence between the RID MAG3 and the Asian MAG2 seems very recent in the nuDNA results (~2.0-1.7 Ma).

Table 3.1. Estimates of divergence times for mtDNA and nuDNA markers. Divergence times calculated between mitochondrial groups (MHGs) and subgroups on the basis of TrN+G distances and between nuclear groups (MAGs) and subgroups on the basis of T92+G distances. An evolutionary rate for mtDNA was estimated by dividing genetic distance between MHG3 and MHGs 4, 5, and 6 (0.077) by the two divergence times (5.3 and 5.5 Ma), giving rates of 1.45% Myr^{-}1 and 1.4% Myr^{-}1 respectively. For nuDNA, the T92+G distance between the Cyprus MAG5 and subgroups CIL1, CIL3, and BED1 of Anatolian MAG1 (0.038) was divided by the same two time estimates, yielding rates of 0.72% Myr^{-}1 and 0.69 Myr^{-}1 respectively. Using BEAST, divergence times were estimated using the calibration point *P. cypriensis* - sister clade (Anatolian populations) at 5.3 ± 1.0 Ma. The tree prior was a birth-death process.

		Divergence Time Estimates (Ma)		
			BEAST	
Group Comparisons	TrN + G	Regression Model	Mean	95% credibility
MHG1/2-MHG3-8	0.082	5.47		
MHG1-MHG2	0.079	5.27	5.1	2.38-6.81
MHG3-MHG4/5/6	0.077	5.3***		
MHG8-MHG6/7	0.052	3.47		
MHG4/5-MHG6/7/8	0.047	3.13		
MHG4-MHG5	0.041	2.73		
MHG6-MHG7	0.032	2.13	4.27	2.12-5.49
MHG6a-MHG6b/c/d	0.021	1.40	3.87	1.9-4.96
MHG6d-MHG6b/c	0.018	1.20	3.42	1.6-4.31
MHG6b-MHG6c	0.017	1.13	3.12	1.36-3.88
P. cretensis-MHG1-8	0.176	11.73	7.52	4.02-10.42
Anatolia MAG - Ridibundus/Asia MAGs	0.040	5.56		
Cyprus - Anatolia MAG/CIL1/CIL3/BED1	0.038	5.3***	4.76	2.85-6.59
MAGa-MAGb/c/d/e	0.015	2.08	3.3	1.57-5.21
MAGe-MAGb/c/d	0.010	1.39	2.2	1.1-3.56
MAGb-MAGc/d	0.007	0.97	1.89	
MAGc-MAGd	0.005	0.69	1.66	
Ridibundus MAG-Asia MAG	0.013	1.81	3.4	1.69-5.48
RID1-KUR/RID2/RID3	0.008	1.11	2.24	1.04-3.74
KUR-RID2/RID3	0.010	1.39	1.55	0.72-2.67
RID2-RID3	0.005	0.69	0.92	0.32-1.69
BED1-SP NOV/CIL3/TER/CIL1	0.008	1.11	1.68	
SP NOV-TER/CIL1	0.010	1.39	1.28	
TER-CIL1	0.005	0.69	0.96	0.42-1.67
BED2-Anatolia/Asia/Ridibundus	0.048	6.67	7.94	4.07-12.36
P.cretensis-Anatolia/Ridibundus/Asia MAG	0.035	4.86		

3.4. Discussion

Our analysis of both mtDNA and nuDNA markers in the eastern Mediterranean water frog complex has uncovered several striking discordances. The evolutionary rate estimated for two genomes is different, with the mitochondrial rate (~0.7% Myr^{-1}) nearly twice the nuclear rate (1.4% Myr^{-1}). Six major discordant groups and their probable causes are discussed below.

3.4.1. Potential Mechanisms Causing Phylogeographic Discordance among mtDNA and nuDNA markers

3.4.1.1. *P. cypriensis* versus *P. cretensis*

3.4.1.1.1. Isolation of Cyprus

We have used as a calibration point the isolation of Cyprus from Anatolia at ~5.5-5.3 Ma based on the palaeogeography of the region at the time of the MSC (Plötner et al., 2010; Akın et al., 2010b). Phylogenetic results for mtDNA, constrained such that Cyprian water frogs became isolated from the mainland after the MSC, indicated that populations on Crete diverged ~10-9 Ma, before the MSC (Plötner et al., 2010; Akın et al., 2010b). In contrast, our new results for the nuDNA marker (Fig. 3.7) indicate that both the Cyprian and Cretan populations diverged from the mainland at the end of the MSC and are a sister species.

Plötner et al. (2010) and Akın et al. (2010b) envisaged that during the latter stages of the MSC, when the Mediterranean basin had partially re-flooded, a land bridge linked Cyprus to Anatolia, allowing exchange of frog populations. This land bridge became flooded and the frog populations became isolated when the Mediterranean Sea rose to its present level at the end of the MSC and the start of the Pliocene. A more recent synthesis of the palaeogeography and palaeoenvironments in the Mediterranean region during the MSC (Bache et al., 2012) agrees that the MSC began about ~6 Ma when uplift of Spain and Morocco restricted the connections between the Mediterranean Sea and the Atlantic Ocean (cf Krijgsman et al., 1999a;b), resulting in the desiccation of the Mediterranean basin; and also agrees that the ending of the MSC involved partial re-flooding of the basin, at which point the sea surface was ~650 m below its present level. Subsequent re-flooding to the present sea-level occurred at an orbitally-tuned age of 5.46 Ma. This is the best current estimate for the timing of the end of the MSC.

At present, Cyprus and Anatolia are separated by a seaway that in places is ~750 m deep. The present sea floor does not mark the sea floor at the end of the MSC, however, because it is underlain by Pliocene and Pleistocene sediment; between Cyprus and NW Syria, up to 2500 m of post-Messinian sediments have been deposited (Hall et al., 2005). Loading by this sediment can be expected to have depressed the adjoining crust, such that prior to the end of the MSC the land surface may well have been above the contemporaneous (low) sea level. The sea-floor in this region has experienced significant crustal deformation since the Messinian (Hall et al. 2005; Seyrek et al., 2014); it forms part of a major active fault zone, the Misis-Kyrenia Fault Zone. The palaeogeography at the time of partial re-flooding near the end of the MSC, depicted by Bache et al. (2012: Fig. 16), shows a ~20 km wide palaeo-strait separating Cyprus and Anatolia. This illustration has, however, not been corrected for the effects of post-Messinian sediment loading and other crustal deformation. We therefore continue to regard as reasonable the assumption that the frog populations in Cyprus and Anatolia became isolated at the start of the Pliocene; hence its continued use in the present study. No land bridge between Cyprus and Anatolia is plausible since then (cf. Hadjisterkotis *et al*. 2000).

3.4.1.1.2 Isolation of Crete

The palaeogeographic history of Crete has been rather different, being related primarily to the development of the Hellenic subduction zone, along which the leading edge of the African plate has plunged beneath Eurasia during the Cenozoic. The dynamics of the subduction process have affected the stress field, causing extension within the overriding plate, which has resulted in significant change in its shape and, consequently, significant relative movements between Crete, the Peloponnese to the west, and western Anatolia to the east. The palaeoenvironmental changes associated with the MSC have been superimposed onto the effects of these processes. It should be noted, however, that the palaeogeographic maps published by Bache et al. (2012) illustrating conditions during the MSC do not take account of subsequent changes in the shape of the region (i.e., are non-palinspastic) and should be viewed in the context of dynamic reconstructions. Recent syntheses of the evolution of this subduction-related system include works by Ring et al. (2010) and Royden and Papanikolaou (2011). These reconstructions are, however, subject to some uncertainty, because the magnitude of the subduction-related extension has been inferred largely from cooling histories, but these histories will in turn be affected by changes to the geometry of the subduction (Westaway, 2006).

Royden and Papanikolaou (2011) estimated that since the subduction began at ~40 Ma this part of the African plate has moved northward relative to Eurasia by ~1000 km, but the Eurasian crust has extended by ~100 km north of the Peloponnesos and by ~250 km north of Crete; Crete has thus moved ~150 km southward relative to the Peloponnesos. Furthermore, the southern margin of Eurasia was initially almost straight and oriented west-east, but has evolved (as an example of ‘oroclinal bending’) to its present strongly curved shape as a result of forces associated with the subduction. Crete thus has also experienced components of east-west separation relative to both the Peloponnesos and Anatolia. Western Crete is currently ~120 km from the Peloponnesos and ~230 km from SW Anatolia but reconstructions by Royden and Papanikolaou (2011) show that these distances were smaller at earlier periods (~80 km and ~150 km at 4 Ma and <20 km and ~80 km at 15 Ma).

During the Middle Miocene the entire modern Aegean region is thought to have been subaerial (e.g., Rögl, 1999), so no isolation of frog populations would be expected. During the Tortonian stage of the Late Miocene (~11-7 Ma), a marine transgression entered the Aegean region from the south (e.g., Rögl, 1999), forming an elongated north-south marine embayment that may have been no more than ~100 km wide (e.g., Popov et al., 2006). This was evidently a time of complex changes to marine and terrestrial environments, as discussed for example by Köhler et al. (2010), Krijgsman et al. (2010) and Vasiliev et al. (2011); it is unclear whether the marine connection at this time between the Mediterranean and the Aegean was located to the west or to the east of Crete.

During the peak of the MSC (~5.6 Ma) lake basins developed in parts of the central Aegean Sea (e.g., Anastasakis et al., 2006). These received sediment input from adjoining areas of land (e.g., Hejl et al., 2008). There is no evidence, however, that these lacustrine environments reached as far south as Crete. At this time, what is now Crete can be envisaged as an upland rising kilometres above the playas that occupied the desiccated Mediterranean and southern Aegean basins. The heights of the lowest cols separating Crete from Anatolia or the Peloponnesos are unclear, however, making it difficult to form any conclusion from the geological evidence as to whether the frog populations on Crete were isolated or not. The partial marine flooding that occurred late in the MSC is, however, envisaged (Bache et al., 2012) as isolating Crete from any adjoining land areas. Nonetheless, much of present area of the central and northern Aegean Sea remained land for much of the Pliocene (e.g., Anastasakis et al., 2006; Hejl et al., 2008); the progressive subsidence that has widened this sea to its present dimensions has presumably involved outward flow of mobile lower-crustal material and is coupled to the uplift of the adjoining land areas (cf. Westaway et al., 2009).

The complexity of the above-mentioned geological history makes clear that it is unwise to use any inferred timing of the ‘separation’ of Crete to calibrate our records; basing the calibration on Cyprus is evidently preferable.

3.4.1.1.3 Possible Explanations for the Discrepancy

In principle, the inconsistency between our mtDNA and nuDNA markers for the divergence time of *P. cretensis* could be explained in two ways. First, the divergence time from the nuDNA is correct, in which case the freshwater environments that existed in the central Aegean Sea during the MSC somehow enabled linkage between the Cretan and Anatolian frog populations. It would, however, be difficult to test this hypothesis. Second, the divergence time from the mtDNA is correct, in which case Crete became isolated from Anatolia at ~9 Ma, as a result of the partial marine inundation of the Aegean basin early in the Late Miocene. This seems more plausible since distinct selective constrains on both mitochondrial and nuclear genes and lineages could result in distinct evolutionary rates. An important precaution in the analysing biogeographic data is that a lineage divergence and the formation of a geographic barrier may not be consistent with each other. It is also possible that large differences among mtDNA genes and rate heterogeneties between lineages and within a lineages over time are too large for molecular clock calibrations (Heads, 2005).

3.4.1.2. The Levant (*P. bedriagae*)

Another striking discordance between results for mtDNA and nuDNA arises for the Levant group of frog populations, including *P. bedriagae*. mtDNA markers indicate an ingroup relationship of this group with other eastern Mediterranean water frog groups, which form a sister group with *P. ridibundus* from Europe. On the other hand, the nuDNA marker places it as an outgroup to all other members of the *P. ridibundus* group on the phylogenetic tree, indicating a time of divergence rather older than MSC. Moreover, the geographic distribution of the two markers (Figs. 3.4 and 3.7) reveals a complex pattern that is difficult to interpret. According to mtDNA, the Levant, including the Nile delta, the Jordan valley and upper reaches of the River Orontes, are occupied exclusively by *P. bedriagae* specific haplotypes. In contrast, the nuDNA reveals the existence of two divergent groups, Levant (BED2) and Asia (CIL3 and BED1), in the Levant region (Fig 3.5).

The present configuration of the Levant began to develop circa 15 Ma, when uplift of the northern Arabian Platform closed the former east-west oriented Tethys Seaway, forming a narrow land bridge between Africa and Eurasia in the vicinity of Gaziantep and Aleppo (e.g., Steininger and Rögl, 1984; Rögl, 1999). This region has since become transected by the Dead Sea Fault Zone (DSFZ), the boundary between the African and Arabian plates, which has had major effects on both topography and drainage (e.g., Westaway, 2004; Seyrek et al., 2014). The southern DSFZ, which has existed since the Middle Miocene (e.g., Garfunkel, 1981), is drained by the southward-flowing River Jordan, which has headwaters in southern Lebanon. The northern DSFZ, which may have developed as recently as the latter part of the Late Miocene (~6 Ma; e.g., Seyrek et al., 2014), is drained primarily by the River Orontes, which has its headwaters in northern Lebanon and flows northward across NW Syria to the Mediterranean coast in central-southern Turkey. The headwaters of the Jordan and Orontes rivers are ~80 km apart, the region in between being drained by the River Litani, which flows southward along the DSFZ then westward to the Mediterranean coast in southern Lebanon. Various hypotheses have been proposed for significant drainage changes in this region; for example, Horowitz (2001) proposed that the Orontes headwaters formerly drained southward into the Jordan, perhaps as recently as the Early Pliocene, whereas Butler et al. (1998) envisaged a succession of diversions of the Litani as active faulting has progressed. In contrast, Bridgland et al. (2012) envisaged that the Orontes catchment has remained constant since ~6-5 Ma, with no evidence of capture of the former headwaters of the Jordan. On the other hand, Bridgland et al. (2012) noted two major gorges along the Orontes, upstream and downstream of the Ghab Basin in NW Syria. Either or both might act to isolate frog populations, as has evidently occurred as a result of the development of the Berke Gorge on the River Ceyhan through the Amanos Mountains in central-southern Turkey, isolating the MHG4 and MHG5 frog populations (Fig. 3.4). At this stage, however, the lack of sampling in Syria and Lebanon makes it impossible to say what effect these gorges and/or putative drainage diversions might have had on isolation of frog populations.

Our mtDNA results indicate that the separation of *P. bedriagae* occurred during the MSC (~6-5 Ma), but nuDNA indicates that it was earlier. This discordance between mtDNA and nuDNA markers could be explained by recent introgression, male-biased dispersal during Pleistocene, or more recently at ~70 ka which was the last wet phase, by a large salty lake that covered the central Jordan Valley (Horowitz, 2001). Thus, although no samples are available from the Nile delta, Israel, Lebanon or the Upper and Middle reaches of the River Orontes, the pattern suggests male mediated gene flow, facilitating connectivity between these two lineages. Male-biased dispersal was shown in the closely related species *Pelophylax ridibundus* (Holenweg Peter, 2001). The distribution of mtDNA haplogroups reveals that females seem to show a strong philopatry. It is hypothesized that males from the Asia group (CIL3, BED1) may have dispersed into the Jordan valley from the Orontes catchment and mated with females of the BED2 group, acquiring their mtDNA. Another possible explanation is that the dispersal has not been sex-biased, but results from coalescence time differences between the different markers caused by effective population size differences between them; mtDNA rapidly coalescences and sorts among lineages before historical signs of introgression disappear in nuDNA.

3.4.1.3. Cilician versus Central Asia Group

The relationships between Cilician and Central Asia groups are probably the most complicated. Although both markers support close relationships among these groups, the mtDNA topology indicates clear monophyletic groups (MHG4/5 and MHG7/8), whereas topological relationships within the Asia MAG are not resolved by nuDNA. In particular, two alleles found exclusively in the Cilician and Narlı plains form a clade within the TER group, one of the Central Asia groups. It is not clear how such geographically distant groups that have developed in allopatry with no geographical connection, share these alleles. A second issue relating to these groups concerns how their genetic distance could have remained so shallow in nuDNA (Asia MAG), whereas the genetic distance from the mtDNA (MHG4/5 and MHG7/8) increases with geographic distance, indicating the expected deep divergence. Possibly these aspects result from incomplete lineage sorting and retention of ancestral alleles in the populations and pattern of inheritance differences between nuDNA and mtDNA markers (Funk and Omland, 2003; Ballard and Whitlock, 2004; Maddison and Knowles, 2006). Thus, these two groups were probably connected in the distant past, but were later completely isolated from each other. Some alleles, such as TER specific alleles, may have remained in the Cilician population as a relict. In contrast, lineage sorting of nuclear genes takes longer than for mtDNA because of the large effective population size and recombination. When nuDNA still harbours imprints of past polymorphism, mtDNA quickly evolves and differentiates into distinct lineages, erasing the ancestral history especially in the case of strong female philopatry.

3.4.1.4. Discordance within the Cilician Groups

The other prominent discordance within the Cilician groups is that mtDNA reveals two deeply divergent monophyletic groups (MHG4 in both Cilician and Narlı plains and MHG5 in mostly Narlı plain about 3.8 Ma) but nuDNA does not support such a divergence and the pattern of geographic distribution. The main barrier between the Cilician and Narlı plain, probably separating MHG4 and MHG5, is the Amanos mountain range. It has developed recently (about 3.7-3.6 Ma) as a result of the modern pattern of plate motions (Seyrek et al., 2007; 2008). This mountain range possibly become a significant geographic barrier to gene flow within a few hundred thousand years; the development of two distinct mitochondrial DNA haplogroups due to a high mutation rate and small effective population size. Unlike mtDNA, nuDNA has a relatively slow evolutionary rate and a large effective population size, so that this mountain range has not been an effective barrier enough to prevent gene flow. Particulary, in the northern part of the range, upper reaches of rivers in the Cilician plain and Narlı plains are present in the close proximity, which could make gene flow among water frog populations a possible. Moreover, recent dispersal of water frogs by human is possible because water frog collecting is very widespread in the Cilician and Narlı plains (Akın & Bilgin, 2010). This might increase genetic mixture among mitochondrial haplogroups and nuclear alleles.

3.4.1.5. *Ridibundus* versus Anatolia groups

Discordance between the Ridibundus group and the Anatolia groups is evident from the geographic pattern of mtDNA and nuDNA markers in central and eastern Anatolia. mtDNA data reveal only haplotypes specific to MHG6 (cf. *bedriagae*; Anatolia group) in these regions, whereas nuDNA data also document the existence of allele groups (RID2 and RID3) from the Ridibundus MAG. Very deep divergence between these two groups is supported by both markers, their estimated divergence time corresponding to the MSC (~6-5 Ma).

As near the Mediterranean Sea, dramatic environmental changes have also occurred farther north and east. The region extending west-east from the Vienna area of Austria to Kazakhstan and Turkmenistan and north-south from central

Ukraine to the modern Black Sea coast of Turkey was formerly covered by a vast water body known as the Paratethys Sea (see, e.g., Rögl, 1999, or Popov et al., 2006, for detailed documentation and palaeogeographic maps). Around 12 Ma this become isolated from the Mediterranean Sea as a result of uplift of intervening barriers, and subsequently developed into a reduced salinity environment. The Paratethys included the modern Black and Caspian Sea basins and other lowlands farther west such as the Hungarian Plain and the Vienna Basin. Subsequent vertical crustal motions, both uplift and subsidence, have subdivided the Paratethys region into these distinct basins that are now separated by uplands or by mountain ranges such as Greater and Lesser Caucasus ranges (Popov et al., 2006). During the peak of the MSC the Black Sea basin, then apparently isolated from both the Mediterranean Sea and the inflow from the River Danube, experienced a significant fall in water level, as is illuatrated in the sequence of palaeogeographic maps by Bache et al. (2012); this event is known as the Pontian desiccation. Fluctuations in the level of the Black and Caspian seas have continued during the Pliocenne and Quaternary, a notable instamce being the transition in the Caspian basin from the Kimmerian lowstand to the Akchagyl highstand in the Middle Pliocene, although there is uncertainty in the timing of this event (e.g., ~4.2 Ma, Steininger et al., 1996; ~3.4 Ma; Hall et al., 2009; ~3.2 Ma, Van Baak et al., 2013). Following the mid-Pliocene climatic optimum, when conditions in the study region were warmer and wetter than at present (e.g., Haywood et al., 2000), the climate has become cooler and more arid, and has fluctuated as a result of Milankovitch forcing in response to variations in the Earth's orbit (e.g., Rohling and Hilgen, 1991; Ehlers and Gibbard, 2007). The transition from the Early Pleistocene to the Middle Pleistocene, circa 800 ka, involved a switch from dominance of the climate by shorter-period fluctuations to a predominant 100 kyr periodicity, known as the Mid-Pleistocene Revolution (MPR), which has been associated with even colder and more arid conditions during the cold stages (e.g., Maslin and Ridgewell, 2005; Head et al., 2008). Associated feedbacks, whereby reduced vegetation cover at these times of harsh climate results in faster erosion, have resulted in increased rates of vertical crustal motion at this time, contributing to the development of topographic relief (e.g., Westaway et al., 2009). During the Late Pleistocene to Holocene transition, the Black Sea was isolated from the global marine environment and was a fresh to brackish water lake, in part because of the melt water entering its via the River Danube, from the Alpine ice sheet, and from Scandinavian ice sheet, via the River Dnieper (e.g., Chepalyga, 2007). This period ended around 9.4 ka with the incursion of Mediterranean water over the Bosphorus sill, creating the modern marine-connected Black Sea (e.g., Ryan et al., 2003; Hiscott et al., 2007).

We infer that this combination of effects of climate change and crustal deformation affecting the Black Sea and its surroundings around the time of the MSC resulted in the primary divergence between the Ridibundus group and Anatolia groups. However, the geographical pattern of both mtDNA and nuDNA data suggests that these two groups may have come into secondary contact as recently as the latest Pleistocene or earliest Holocene, possibly during the period of lacustrine isolation noted above. Thus, introgression might have occurred between these groups (both in northern Turkey and in eastern Europe), until the more saline conditions created by the marine reconnection during the Holocene reduced the distribution of both groups (which both occur in Ukraine according to both mtDNA and nuDNA data). In contrast, evidence of introgression is only supported by nuDNA, not mtDNA, in Central to Eastern Anatolia. This could be explained by male-biased dispersal of the Ridibundus group into Anatolia during low-salinity conditions of Black Sea (Holenweg Peter, 2001). In the course of time, gene flow among the high density of local Anatolia females and the less frequent invading *ridibundus* males would result in individuals carrying the haplotype specific for Anatolia but their genotypes would be heterozygous alleles from both Anatolia and Ridibundus groups. It follows that repeated backcrossing throughout several generations could produce several combinations of heterozygous and homozygous individuals in each of the groups. The geographic patterns of mtDNA and nuDNA in central and eastern Anatolia might thus be explained.

3.4.1.6. Discordance Patterns within the Anatolia MAG

As in the groups already discussed, although mtDNA results support well separated monophyletic groups, nuDNA reveals unresolved relationships among some clades (MAGc, d and e) within the Anatolia MAG. Thus, mtDNA subgroups indicate divergence times of 1.5-1.0 Ma, reflecting the MPR, whereas time estimates of nuDNA subgroups indicate 2.1-0.8 Ma (as a result of divergence of MAGa earlier than the rest), covering both the Pliocene-Pleistocene boundary and the MPR, thus indicating spans of time when significant global coolings have occurred (e.g., Ehlers and Gibbard, 2007).

The first discordant pattern is caused by the caralitanus-related group (MAGa in nuDNA, MAGa (cf. *caralitanus)* in mtDNA): cf. *caralitanus*, recognized from mtDNA, only occurs in the south-western Anatolia, whereas the MAGa allele group, recognized from nuDNA, occurs throughout the Black Sea region and eastern and south-eastern Anatolia, as well as south-western Anatolia. Both the mtDNA and nuDNA markers indicate that these *caralitanus* specific groups may well be the oldest group within the Anatolia MAG. Decades ago, Kosswig (1955) proposed that much of the biogeography of Anatolia is explicable in terms of the existence of the ‘Central Anatolian Lake System’, a vast, interconnected wetland environment that extended across much of Anatolia, which he believed existed in the Pliocene. One of course has to be extremely careful with old concepts such as this, because the chronologies of the ‘continental’ and ‘marine’ Pliocene were not standardized and much of the stratigraphic record that was then thought to be ‘continental Pliocene’ subsequently turned out to be Late Miocene (e.g., Berggren and Van Couvering, 1974, pp. 37-56). Nonetheless, this idea is consistent with the wet climate now evident in Anatolia during the Pliocene (e.g., Haywood et al., 2000), and with the much lower relief that existed then compared with at present, prior to phases of post-Pliocene uplift that are estimated as several hundred metres in western Anatolia, rising eastward significantly towards eastern Anatolia, and the many sites where large lakes can be reconstructed and dated to the Pliocene (e.g., Westaway et al., 2006; Seyrek et al., 2008; Demir et al., 2009). We therefore suggest that a widespread Pliocene lacustrine environment, as envisaged by Kosswig (1955), made possible the dispersal across most of Anatolia of the caralitanus-related allele group MAGa that is now evident from the nuDNA records as the retention of ancestral polymorphism in populations.

The second inconsistency between the mtDNA and nuDNA markers occurs in the cf. *cerigensis* group, which has been described as a new species, *P. cerigensis*, in Rhodos and Karpathos islands (Beerli et al., 1994). mtDNA data indicate that both islands and the adjacent mainland (Anatolia) have identical mtDNA haplotypes, whereas nuDNA indicates that alleles of islands (MAGc) was distinct from the mainland. This inconsistency could be as a result of migration of few individuals versus genetic drift.

3.4.2. Systematic Implications

For a long time, Anatolian water frogs have been designated as *P. cf. bedriagae.* Notwithstanding the extensive overlapping and mixing distribution of distinct genetic lineages evident from both nuDNA and mtDNA markers, which occur not only in transition zones but also across wider geographic regions, Anatolian water frogs clearly consist of two distinct genetic lineages. The first and larger group is the Anatolia group (Anatolia MAG, nuDNA; MHG6, mtDNA), consisting of several subgroups as previously discussed (Figs 3.4 and 3.7). The second and geographically more restricted group is the Cilician group (CIL1, CIL3, and BED1, nuDNA; MHG4 and MHG5, mtDNA), likewise including several subgroups (Figs 3.4 and 3.7). The extent of its distribution southward and its relationship with the Levant group are, however, unclear because of the lack of samples from Syria and Lebanon. These results indicate that Anatolian water frogs are conspecific neither with *P. ridibundus* (Europe) nor with *P. bedriagae* (the Levant); they therefore warrant species status and the names of these two new species should be clarified. This study revealed the possibility of an extensive gene flow among several genetically distinct water frog lineages despite biological species concept. Several recent studies, however, showed that speciation can be possible with ongoing gene flow (Nosil, 2008; Feder et al., 2012).

3.5. References

Akın, Ç., Bilgin, M., Bilgin, C.C. (2010a) Discordance between ventral colour and mtDNA haplotype in the water frog Rana (ridibunda) caralitana, 1988 Arıkan. *Amphibia-Reptilia* 31: 9–20.

Akın, Ç., Bilgin, C.C., Beerli, P., Westaway, R., Ohst, T., Litvinchuk, S.N., et al. (2010b) Phylogeographic patterns of genetic diversity in eastern Mediterranean water frogs were determined by geological processes and climate change in the Late Cenozoic. *J Biogeogr* 37: 211–2124.

Akın, Ç. and Bilgin, C.C. (2010) Türkiye'de Su Kurbağalarının Toplanması, İşlenmesi ve İhracatına İlişkin Ön Rapor (KKGM'ye sunulmuştur). ODTÜ, Ankara, 10 pages.

Anastasakis, G., Piper, D.J.W., Dermitzakis, M.D., Karakitsios, V., (2006) Upper Cenozoic stratigraphy and paleogeographic evolution of Myrtoon and adjacent basins, Aegean Sea, Greece. *Mar Petrol Geol* 23: 353-369.

Avise, J.C., (1994) Molecular Markers, Natural History, and Evolution. Chapman & Hall, New York.

Bache, F., Popescu, S.-M., Rabineau, M. et al. (2012) A two-step process for the reflooding of the Mediterranean after the Messinian Salinity Crisis. *Basin Res* 24: 125-153.

Ballard, J., Whitlock, M. (2004) The incomplete natural history of mitochondria. *Molecular Ecol* 13: 729-744.

Bandelt, H. J., Forster, P., Röhl, A. (1999) Median-joining networks for inferring intraspecific phylogenies. *Mol Biol Evol* 16: 37-48.

Beerli, P., Hotz, H., Tunner, H., Heppich, S., Uzzell, T. (1994) Two new water frog species from the Aegean islands Crete and Karpathos (Amphibia, Salientia, Ranidae). *Notulae Naturae, Academy of Natural Sciences of Philadelphia* 470:1-9.

Beerli, P., Hotz, H., Uzzell, T. (1996) Geologically dated sea barriers calibrate a protein clock for Aegean water frogs. *Evolution* 50: 1676–1687.

Berggren, W.A., Van Couvering, J.A., (1974) The Late Neogene: Biostratigraphy, geochronology and paleoclimatology of the last 15 million years in marine and continental sequences. Developments in Palaeontology and Stratigraphy, 2. Elsevier, Amsterdam, 215 pp.

Bridgland, D.R., Westaway, R., Romieh, M.A., Candy, I. et al. (2012) The River Orontes in Syria and Turkey: Downstream variation of fluvial archives in different crustal blocks. *Geomorphology* 165-66: 25-49.

Butler, R.W.H., Spencer, S., Griffiths, H.M., (1998) The structural response to evolving plate kinematics during transpression: evolution of the Lebanese restraining bend of the Dead Sea Transform. In: Dewey, J.F., Holdsworth, R.E., Strachan, R.A. (eds.), Transpression and transtension zones. Geological Society, London, Special Publications, 135, 81-106.

Chepalyga, A.L. (2007) The late glacial great flood in the Ponto-Caspian basin. In: Yanko-Hombach, V.V., Gilbert, A.S., Panin, N., Dolukhanov, P.M. (Eds.), The Black Sea Flood Question: Changes in Coastline, Climate and Human Settlement. Springer, New York.

Cosentino, D., Gliozzi, E., Pipponzi, G. (2007) The late Messinian lago-mare episode in the Mediterranean basin: preliminary report on the occurrence of Paratethyan ostracod fauna from central Crete (Greece). *Geobios* 40: 339-349.

Coyne, J.A., Orr, H.A. (2004) Speciation. Sinauer Associates, Sunderland, MA. 545 pp.

Currat, M., Ruedi, M., Petit, R.J., Excoffier, L., (2008) The hidden side of invasions: massive introgression by local genes. *Evolution* 62: 1908–1920.

Degnan, J.H., Rosenberg, N.A. (2009) Gene tree discordance, phylogenetic inference and the multispecies coalescent. *Trends Ecol Evol* 24: 332-340.

Demir, T., Seyrek, A., Guillou, H., Scaillet, S., Westaway, R., Bridgland, D., (2009) Preservation by basalt of a staircase of latest Pliocene terraces of the River Murat in eastern Turkey: evidence for rapid uplift of the eastern Anatolian Plateau. *Global Planet Change* 68: 254-269.

Dermitzakis, M. (1990) Paleogeography, geodynamics processes and event stratigraphy during the Late Cenozoic of the Aegean area. International symposium on: biogeographical aspect of insularity, Roma 1987. *Accad Naz Lincei* 85: 263-288.

Dermitzakis, M., Papanikolaou, D.J. (1981) Paleogeography and geodynamics of the Aegean region during the neogene. *Ann Geol Pays Hellen* 20: 245-289.

Drummond, A. J., Ho, S. Y. W., Phillips, M. J., Rambaut, A. (2006) Relaxed phylogenetics and dating with confidence. *PLoS Biol* 4: E88.

Drummond, A. J., Suchard, M. A., Xie, D., Rambaut, A. (2012) Bayesian phylogenetics with BEAUti and the BEAST 1.7. *Mol Biol Evol* DOI: 10.1093/molbev/mss075.

Ehlers, J., Gibbard, P.L. (2007) The extent and chronology of Cenozoic global glaciation. *Quatern Int* 164–165: 6–20.

Edwards, S.V. (2009) Is a new and general theory of molecular systematics emerging? *Evolution* 63: 1-19.

Feder, J., Egan, S., Nosil, P. (2012) The genomics of speciation-with-gene flow. *Trends Genet* 28:342–350.

Freeand, J.R., Boag, P.T (1999) The mitochondrial and nuclear genetic homogeneity of the phenotypically diverse Darwin's ground finches. *Evolution* 53: 1553-1563.

Funk, D.J., Omland, K.E. (2003) Species-level paraphyly and polyphyly: frequency, causes and consequences with insights from animal mitochondrial DNA. *Ann Rev Ecol Evol Syst* 34: 397-423.

Excoffier, L., Lischer H.E.L. (2010) Arlequin suite ver 3.5: A new series of programs to perform population genetics analyses under Linux and Windows. *Mol Ecol Resour* 10: 564-567.

Garfunkel, Z., (1981) Internal structure of the Dead Sea leaky transform (rift) in relation to plate kinematics: *Tectonophysics* 80: 81-108.

Garfunkel Z. (1988) The pre-Quaternary geology of Israel. In: Yom-Tov Y, Tchernov E, eds. *The zoogeography of Israel*. Dordrecht: Dr Junk, 7–34.

Götz, L.-G. (1996) Beschreibung und Vergleich der Tektonik pazifischer und mediterraner Backarc-Becken hergeleitet aus echographischen und bathymetrischen Vermessungen. Ber. Zentrum Meeres- Klimaforschung, Reihe C: *Geophysik* 9: 1–165.

Hadjisterkotis, E., Masala, B., Reese. D.S. (2000) The origin and extinction of the large endemic Pleistocene mammals of Cyprus. *Biogeographia* 21: 593-606.

Hall, J., Aksu, A.E., Calon, T.J., Yaşar, D. (2005) Varying tectonic control on basin development at an active microplate margin: Latakia Basin, Eastern Mediterranean. *Mar Geol* 221: 15–60.

Hasegawa, M., Kishino, H., Yano, T.A. (1985) Dating the human-ape splitting by a molecular clock of mitochondrial DNA. *J Mol Evol* 22: 160-174.

Haywood, A.M., Sellwood, B.W., Valdes, P.J. (2000) Regional warming: Pliocene (3 Ma) paleoclimate of Europe and the Mediterranean. *Geology* 28: 1063-1066.

Heads, M. (2005) Dating nodes on molecular phylogenies: a critique of molecular biogeography. *Cladistics* 21: 62–78.

Head, M.J., Pillans, B., Farquhar, S.A. (2008) The Early–Middle Pleistocene Transition: characterization and proposed guide for the defining boundary. *Episodes* 31: 255-259.

Hejl, E., Grave, J.D., Riedl, H., Weingartner, H., Haute, P.V.D. (2008) Fission-track thermochronology of the Middle Aegean Island Bridge - implications for Neogene geomorphology and palaeogeography. *Zeitschrift der Deutschen Gesellschaft für Geowissenschaften* 159: 495-512.

Hiscott, R.N., Aksu, A.E., Muddie, P.J., Marret, F., Abrajano, T., Kaminski, MA., Evans, J., Çakıroğlu, A.I., Yaşar, D. (2007) A gradual drowning of the southwestern Black Sea shelf: evidence for a progressive rather than abrupt Holocene reconnection with the eastern Mediterranean Sea through the Marmara Sea Gateway. *Quatern Int* 167-168: 9-34.

Holenweg Peter, A.-K. (2001) Dispersal rates and distances in adult water frogs, *Rana lessonae, R. ridibunda*, and their hybridogenetic associate *R. esculenta*. *Herpetologica* 57 (4): 449-460.

Horowitz, A. (2001) The Jordan Rift Valley. Lisse, Netherlands: A.A. Balkema.

Huelsenbeck, J.P., Rannala, B. (2004) Frequentist properties of Bayesian posterior probabilities of phylogenetic trees under simple and complex substitution models. *Systematic Biol* 53: 904–913.

Jurka, J., Drazkiewicz, A. (2002) TDR22: a putative non-autonomous DNA transposon from Danio rerio. *Repbase Reports* 2(3): 15-15.

Kissel, C., C. Laj. (1988) The Tertiary geodynamical evolution of the Aegean arc: a paleomagnetic reconstruction. *Tectonophysics* 146: 183–201.

Kosswig, C. (1955) Zoogeography of the Near East. Syst Zool 4: 49-73.

Köhler, C.M., Heslop, D., Krijgsman, W., Dekkers, M.J. (2010) Late Miocene paleoenvironmental changes in North Africa and the Mediterranean recorded by geochemical proxies (Monte Gibliscemi section, Sicily) *Palaeogeogr Palaeocl* 285: 66-73.

Krijgsman, W. (2002) The Mediterranean: mare nostrum of earth sciences. *Earth Planet Sci Lett* 205: 1-12.

Krijgsman, W., Hilgen, F.J., Raffi, I., Sierro, F.J. Wilson, D.S. (1999a) Chronology, causes and progression of the Messinian salinity crisis. *Nature* 400: 652–655.

Krijgsman, W., Langereis, C.G., Zachariasse, W.J., Boccaletti, M., Moratti, G., Gelati, R., Iaccarino, S., Papani, G. Villa, G. (1999b) Late Neogene evolution of the Taza- Guercif Basin (Rifian Corridor, Morocco) and implications for the Messinian salinity crisis. *Mar Geol* 153: 147–160.

Krijgsman, W., Stoica, M., Vasiliev, I., Popov, V.V. (2010) Rise and fall of the Paratethys Sea during the Messinian Salinity Crisis. *Earth Planet Sc Lett* 290: 183-191.

Leaché, A.D. (2009) Species tree discordance traces to phylogeographic clade boundaries in North American Fence lizards (Sceloporus). *Syst Biol* 58: 547–559.

Liu, K., Wang, F., Chen, W., et al. (2010) Rampant historical mitochondrial genome introgression between two species of green pond frogs, *Pelophylax nigromaculatus* and *P. plancyi*. *BMC Evol Biol* 10: 1-14.

Maddison, W.P., Knowles, L.L. (2006) Inferring phylogeny despite incomplete linaege sorting. *Syst Biol* 55(1): 21-30.

Maroja, L.S., Andres, J.A., Walters, J.R., Harrison, R.G. (2009) Multiple barriers to gene exchange in a field cricket hybridzone. *Biol J Linn Soc* 97: 390–402.

Martin, D.P., Lemey, P., Lott, M., Moulton, V., Posada, D., Lefeuvre, P. (2010) RDP3: a flexible and fast computer program for analyzing recombination. *Bioinformatics* 26: 2462-2463.

Maslin, M.A., Ridgwell, A.J. (2005) Mid-Pleistocene revolution and the ‘eccentricity myth’. In: M.J. Head and P.L. Gibbard (Editors), Early–Middle Pleistocene transitions: the land–ocean evidence: *Geological Society of London Special Publication* 247: pp. 19–34.

Mavarez, J., Salazar, C., Bermingham, E., Salcedo, C., Jiggins, C.D., Linares, M. (2006) Speciation by hybridization in Heliconius butterflies. *Nature* 441:868–871

Nei, M. (1987) Molecular evolutionary genetics. Columbia University Press, New York.

Nosil, P. (2008) Speciation with gene flow could be common. Mol Ecol 17(9): 2103-2106.

Petit, R.J., Excoffier, L. (2009) Gene flow and species delimitation. *Trends Ecol Evol* 24: 386–393.

Plötner, J., Ohst, T., Böhme, W., Schreiber, R. (2001) Divergence in mitochondrial DNA of Near Eastern water frogs with special reference to the systematic status of Cypriote and Anatolian populations (Anura, Ranidae). *Amphibia-Reptilia* 22: 397–412.

Plötner, J., Uzzell, T., Beerli, P., Spolsky, C., Ohst, T., Litvinchuk, S. N., Guex, G.-D., Reyer, H.-U., Hotz, H. (2008) Widespread unidirectional transfer of mitochondrial DNA: a case in western Palearctic water frogs. *J. Evol Biol* 21: 668–681.

Plötner, J., Köhler, F., Uzzell, T., Beerli, P., Schreiber, R., Guex, G.-D. & Hotz, H. (2009) Evolution of serum albumin intron-1 is shaped by a 5' truncated non-long terminal repeat retrotransposon in western Palearctic water frogs (Neobatrachia). *Mol Phylogenet Evol* 53: 784–791.

Plötner, J., Uzzell, T., Beerli, P., Akın, Ç., Bilgin, C.C., Haefeli, C., Ohst, T., Köhler, F., Schreiber, R., Guex, G.-D., Litvinchuk, A. N., Westaway, R., Reyer, H.-U. & Hotz, H. (2010) Genetic divergence and evolution of reproductive isolation in eastern Mediterranean water frogs. Evolution in action. Case studies in adaptive radiation and the origin of biodiversity. Special volume from the SPP 1127 ‘Radiations – Genesis of Biological diversity’ of the DFG (ed. by M. Glaubrecht), pp. 373–403. Springer, Heidelberg, Berlin.

Plötner, J., Baier, F., Akın, Ç., Mazepa, G., Schreiber, R., Beerli, P., Litvinchuk, S.N., Bilgin, C.C., Borkin, L., Uzzell, T. (2012) Genetic data reveal that water frogs of Cyprus (genus Pelophylax) are an endemic species of Messinian origin. *Zoosyst Evol* 88: 261-283.

Popov, S.V., Shcherba, I.G., Ilyina, L.B., Nevesskaya, L.A., Paramonova, N.P., Khondkarian, S.O., Maygar, I. (2006) Late Miocene to Pliocene palaeogeography of the Paratethys and its relation to the Mediterranean. *Palaeogeog Palaeocl* 238: 91-106.

Rambaut, A., Drummond, A.J. (2009) *Tracer v1.5*. Available at http://beast.bio.ed.ac.uk/Tracer (last accessed 04 March 2012).

Ring, U., Glodny, J., Will, T.M., Thompson, S.N. (2010) The retreating Hellenic subduction system: high-pressure metamorphism, exhumation, normal faulting and large-scale extension. Annu Rev Earth Pl Sc 38: 45-76.

Rohling E.F, Hilgen, F.J. (1991) The eastern Mediterranean climate at times of sapropel formation: a review. *Geol Mijnbouw* 70: 253-264.

Royden, L.H., D.J. Papanikolaou (2011) Slab segmentation and Late Cenozoic disruption of the Hellenic Arc. *Geochem Geophy Geosy* 12: Q03010, 24 pp., doi: 10.1029/2010GC003280.

Rögl, F. (1999) Mediterranean and Paratethys. Facts and hypotheses of an Oligocene to Miocene paleogeography (short overview). *Geol Carpath* 50: 339-349.

Ryan, W.B.F., Major, C.O., Lericolais, G., Goldstein, S.L. (2003) Catastrophic flooding of the Black Sea. *Annu Rev Earth Pl Sc* 31: 525-554.

Salzburger, W., Baric, S., Sturmbauer, C. (2002) Speciation via introgressive hybridization in east African cichlids? *Mol Ecol* 11: 619-625.

Schwarz, G. (1978). Estimating the dimension of a model. *Ann Stat* 6 (2): 461-464.

Seehausen, O. (2004) Hybridization and adaptive radiation. *TRENDS Ecol Evol* 4(19): 198-207.

Seyrek, A., Demir, T., Pringle, M.S., Yurtmen, S., Westaway,R., Beck, A., Rowbotham, G., (2007) Kinematics of the Amanos Fault, southern Turkey, from Ar/Ar dating of offset Pleistocene basalt flows: Transpression between the African and Arabian plates. *Geological Society, Special Publications,* 290: London, pp. 255–284.

Seyrek, A., Westaway, R., Pringle, M., Yurtmen, S., Demir, T., Rowbotham, G., (2008) Timing of the Quaternary Elazığ volcanism, eastern Turkey, and its significance for constraining landscape evolution and surface uplift. *Turk J Earth Sci* 17: 497-541.

Seyrek, A., Demir, T., Westaway, R., Guillou, H., Scaillet, S., White, T.S., Bridgland, D.R. (2014) The kinematics of central-southern Turkey and northwest Syria revisited. *Tectonophysics* in press (online preprint available).

Steininger, F.F., Rögl, F. (1984) Paleogeography and palinspastic reconstruction of the Neogene of the Mediterranean and Paratethys. In: Dixon JE, Robertson AHF (eds), The Geological Evolution of the Eastern Mediterranean. *Geological Society London SpecialPublications* 17: 659-668 (reprinted 1996).

Steininger, F.F., Berggren, W.A., Kent, D.V., Bernor, R.L., Sen, S., Agustí, J., (1996) Circum-Mediterranean Neogene (Miocene and Pliocene) marine-continental chronologic correlations of European mammal units. In: Bernor, R.L., Fahlbusch, V., Mittmann, H.-W. (Eds), The Evolution of Western Eurasian Neogene Mammal Faunas. Columbia Univ Press, New York, pp. 7-46.

Sumida, M., Kanamori, Y., Kaneda, H., Kato, Y., Nishioka, M., Hasegawa, M., Yonekawa, H. (2001) Complete nucleotide sequence and gene rearrangement of the mitochondrial genome of the Japanese pond frog *Rana nigromaculata*. *Genes Genet Syst* 76: 311–325.

Tamura, K. (1992) Estimation of the number of nucleotide substitutions when there are strong transition-transversion and G + C-content biases. *Mol Biol Evol* 9: 678-687.

Tamura, K., Nei, M. (1993) Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. Molecular Biology and Evolution, 10: 512–526.

Tamura, K,, Peterson, D., Peterson, N., Stecher, G., Nei, M., Kumar, S. (2011) MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. *Mol Biol Evol* 28: 2731-2739.

Toews D.P.L., Brelsford, A. (2012) The biogeography of mitochondrial and nuclear discordance in animals. *Mol Ecol* 21: 3907-3930.

Van Baak, C.G.C., Vasiliev, I., Stoica, M., Kuiper, K.F., Forte, A.M., Aliyeva, E., Krijgsman, W. (2013) Paleomagnetic A magnetostratigraphic time frame for Plio-Pleistocene transgressions in the South Caspian Basin, Azerbaijan. *Global Planet Change* 103: 119–134.

Vasiliev, I., Iosifidi, A.G., Khramov, A.N., Krijgsman, W., Kuiper, K., Langereis, C.G., Popov, V.V., Stoica, M., Tomsha, V.A., Yudin, S.V. (2011) Magnetostratigraphy and radio-isotope dating of upper Miocene-lower Pliocene sedimentary successions of the Black Sea (Taman Peninsula, Russia). *Palaeogeography, Palaeoclimatology, Palaeoecology* 310(3-4): 163-175.

Westaway, R. (2004) Kinematic consistency between the Dead Sea Fault Zone and the Neogene and Quaternary left-lateral faulting in SE Turkey. *Tectonophysics* **391**: 203–237.

Westaway, R. (2006) Cenozoic cooling histories in the Menderes Massif, western Turkey, may be caused by erosion and flat subduction, not low-angle normal faulting. *Tectonophysics* 412: 1-25.

Westaway, R., Guillou, H., Yurtmen, S., Beck, A., Bridgland, D., Demir, T., Scaillet, S., Rowbotham, G., (2006) Late Cenozoic uplift of western Turkey: Improved dating of the Kula Quaternary volcanic field and numerical modelling of the Gediz river terrace staircase. *Global Planet Change* 51: 131-171.

Westaway, R., Bridgland, D. R., Sinha, R., Demir, T. (2009) Fluvial sequences as evidence for landscape and climatic evolution in the Late Cenozoic: a synthesis of data from IGCP 518. *Global Planet Change* 68: 237–253.

3.6. Appendices

Table 3.2. Locality information for mitochondrial ND2 and ND3 haplotypes. This table gives details of localities, collection or laboratory IDs, and old and new haplotype IDs for the investigated individuals. Since several additional new haplotypes have been included for Anatolian groups (MHG4, 5 and 6), a new haplotype abbrevation system is used to enable the distribution of haplotypes to be easily followed. Samples used for the first time in this study are marked with a grey background, while samples taken from previous studies are listed with white backgrounds. Accession numbers starting with AB, AJ, AM, GQ and GU were taken from the EMBL database. They correspond to the publications of Sumida et al., (2001), Plötner et al., (2001, 2008, 2009), and Akın et al., (2010a,b). Abbreviations denote: MHG, main haplogroup; ND2, mitochondrial gene for NADH dehydrogenase subunit 2; ND3, mitochondrial gene for NADH dehydrogenase subunit 3; ZFMK, Zoologisches Forschungsmuseum und Alexander Koenig, Bonn; ZISP, Zoological Institute St. Petersburg; and ZMB, Zoologisches Museum Berlin.

Country	**Locality**	**Lat**	**Long**		**Haplotype ID (old)**		**Haplotype ID (new)**		**Accession Number**		**MHG/ Species**
				Collection/ Laboratory ID	**ND2**	**ND3**	**ND2**	**ND3**	**ND2**	**ND3**	
Albania	Durrës	41.3247	19.4268	-		RE4				AJ310330	MHG1
				-	R11	RE4			AM749704	AJ310330	
Armenia	Megri	38.9135	46.2340	ZISP.-Sp.308		AN41		ANT16		GU812198	MHG6c
Bulgaria	Alepu swamps near Sozopol	42.3995	27.6930	ZMB47094	R1	RE1			AM900661	AJ310338	MHG1
	Kazanlak	42.4006	25.3010	Hotz17994		RE1				AJ310338	MHG1
				Hotz17995		RE1				AJ310338	
				Hotz17996		RE1				AJ310338	
				Hotz17997		RE1				AJ310338	
	Nessebar	42.6054	27.6062	ZMB51288	R2	RE1			AM749712	AJ310338	MHG1
Cyprus	Northern Cyprus	35.1855	33.5674	Hotz19410	A1	AN12	CA1	CAR12	GU812088	GQ902088	MHG6a
				Hotz19411	CP6	CY4			HE820104	HE861955	MHG3
				Hotz19412	CP6	CY4			HE820104	HE861955	
				Hotz19413	CP6	CY4			HE820104	HE861955	
				Hotz19416	A1	AN12	CA1	CAR12	GU812088	GQ902088	MHG6a

Table 3.2. (continued).

.

Cyprus	Argaka reservoir	35.047	32.506	ZFMK48755		CY7				HE861948	MHG3
	Potamos tis Ezousas near Episkopi	34.671	32.916	ZFMK48757		CY1				HE861949	MHG3
	Cape Greco (water reservoir in the west)	34.9794	34.0548	P21	CP8	CY3			HE820092	GU812161	MHG3
				P22	CP8	CY3			HE820093	GU812161	
				P23	CP8	CY3			HE820094	GU812161	
				P24	CP8	CY3			HE820095	GU812161	
				P25	CP5	CY3			HE820096	GU812161	
	Stream close to Gialia	35.0769	32.5690	P32	CP4	CY6			HE820097	HE861950	MHG3
				P33	CP4	CY6			HE820098	HE861951	
	Gönyeli dam	35.2332	33.2937	P3	CP8	CY3			HE820099	GU812161	MHG3
	Lefkosa (stream system of the Pediaios)	35.2017	33.3522	P2	CP8	CY3			HE820100	GU812161	MHG3
	Maroullenas-1	35.0084	33.1477	P5	CP8	CY4			HE820101	HE861952	MHG3
	Maroullenas-2	34.9996	33.1423	P6	CP8	CY4			HE820102	HE861953	MHG3
	Maroullenas-3	35.0054	33.1453	P7	CP8	CY4			HE820103	HE861954	MHG3
				P8	CP6	CY4			HE820104	HE861955	
	Nicosia-1	35.1682	33.5273	-	CP1	CY1			GU812078	AJ310334	MHG3
				-	CP1	CY1			GU812078	AJ310334	
				ZFMK48760		CY1				AJ310334	
	Nicosia-2	35.1951	33.3189	DB238		CY2				GU812160	MHG3
				DB239		CY3				GU812161	
				DB240		CY3				GU812161	
	Nicosia (channel in the forest part)	35.1707	33.3567	P15	CP8	CY3			HE820105	GU812161	MHG3
				P16	CP8	CY3			HE820106	GU812161	
				P17	CP8	CY3			HE820107	GU812161	
				P18	CP7	C74			HE820108	HE861956	

Table 3.2. (continued).

.

Cyprus	Nicosia (channel in the forest part)	35.1707	33.3567	P19	CP8	CY3			HE820109	GU812161	MHG3
	2 km southwest of Palaichhori	34.9140	33.0681	P1	CP1	CY1			GU812078	AJ310334	MHG3
	Panagia (forest station at stream Peristerona)	35.0156	33.0833	P4	CP1	CY1			GU812078	AJ310334	MHG3
	Lake Paralimni	35.0358	33.9753	P20	CP8	CY3			HE820110	GU812161	MHG3
	Peristerona-1	34.9770	33.0912	P34	CP1	CY1			GU812078	AJ310334	MHG3
				P35	CP1	CY1			GU812078	AJ310334	
	Peristerona-2 (headwater)	34.9953	33.0926	P26	CP1	CY1			GU812078	AJ310334	MHG3
				P27	CP1	CY1			GU812078	AJ310334	
				P28	CP1	CY1			GU812078	AJ310334	
				P29	CP1	CY1			GU812078	AJ310334	
				P30	CP1	CY1			GU812078	AJ310334	
				P31	CP1	CY1			GU812078	AJ310334	
	Potamos tou Limniti, north of Stavros	35.161	32.734	ZFMK48758		CY7				HE820111	MHG3
	Pyrgos Dam	35.1495	32.6549	P9	CP4	CY6			HE820112	HE861957	MHG3
				P12	CP3	CY7			HE820113	HE861958	
				P13	CP4	CY6			HE820114	HE861959	
	near Stavros	35.0673	32.6310	P14	CP4	CY6			HE820115	HE861960	MHG3
	Troodos-1	34.7269	32.9095	ZFMK59099	CP2	CY1			GU812079	AJ310334	MHG3
				ZFMK590100		CY1				AJ310334	
				ZFMK590102		CY1				AJ310334	
	Troodos-2	34.9161	32.9003	ZMB77443	CP8	CY8			HE820116	HE861961	MHG3
				ZISP10531	CP8	CY8			HE820117	HE861962	

Table 3.2. (continued).

Cyprus	Lake Xyliatos	35.0375	33.0381		CP1	CY1					MHG3
					CP1	CY1					
Egypt	Cairo	29.9638	31.2289	Hotz16375	B1	BN1			GU812072	AJ310322	MHG2
				Hotz16376	B1	BN1			GU812072	AJ310322	
				Hotz16377		BN1				AJ310322	
France	Aramon	43.8967	46.827	-	R4	RE6			AM900652	AM900653	MHG1
	St. Étienne du Gres	43.7786	4.6533	-	R1	RE1			AM900661	AJ310338	MHG1
Georgia	Batumi	41.6420	41.6800	ZMB47390	A25	AN26	AT30	ANT1	GU812112	AJ310337	MHG6c
				ZMB47490	A33	AN42	AT75	ANT17	GU812119	GU812199	
	Sukhumi	42.9970	40.9825	ZMB44562	A34	AN42	AT73	ANT17	GU812120	GU812199	MHG6c
				ZMB44563	A35	AN42	AT74	ANT17	GU812121	GU812199	
Greece	Aliartos	38.3688	23.0841	Hotz17357	R5	RE5			AM749705	AM749705	MHG1
				Hotz17359	R8	RE12			AM749709	AM749709	
				Hotz17360	R9	RE12			AM749710	AM749709	
	Apolakkia/Rhodos	36.0592	27.7876	Hotz18167	A8	AN24	CE2	CER4	GU812095	GU812183	MHG6b
	Apollona/Rhodos	36.2543	27.9779	-		AN24		CER4		GU812183	MHG6b
	Archipolis/Rhodos	36.3117	28.1360	Hotz18164		AN24		CER4		GU812183	MHG6b
Greece	Archipolis/Rhodos	36.3117	28.1360	Hotz17218	A8	AN24	CE2	CER4	GU812095	GU812183	MHG6b
				-		AN24		CER4		GU812183	
	Chios	38.3568	26.1433	Ploetner137.03	A15	AN54	AT99	ANT29	GU812102	GU812209	MHG6c
				Ploetner138.03	A15	AN54	AT99	ANT29	GU812102	GU812209	
				Ploetner143.03	A15	AN54	AT99	ANT29	GU812102	GU812209	
	Dadia	41.1419	26.2846	Hotz22714		RE1				AJ310338	MHG1
				Hotz22717		RE1				AJ310338	
	Ikaria	37.6075	26.1521	Hotz17325	A3	AN19	CA10	CAR19	GU812090	GU812180	MHG6a
				Hotz17327	A3	AN19	CA10	CAR19	GU812090	GU812180	

Table 3.2. (continued).

Greece	Ikaria	37.6075	26.1521	Hotz17329	A3	AN19	CA10	CAR19	GU812090	GU812180	MHG6a
	Ivira	40.9004	23.6005	Hotz17979		RE7				GU812153	MHG1
				Hotz17984		RE6				AM900653	
	Kalanistra	38.0633	21.8485	ZMB49804	R17	RE11			AM900644	AJ310329	MHG1
	Kaminia	39.7653	20.8678	ZMB49822	R14	RE11			AM749699	AJ310329	MHG1
	Kavasilas	37.8762	21.2854	Hotz19510	R12	RE13			AM749702	AM749702	MHG1
				Hotz19528	R17	RE14			AM900644	AM749697	
	Keramoti	40.9351	24.4038	Hotz17412		RE1				AJ310338	MHG1
				Hotz17413		RE2				GU812151	
	Kymina	40.5565	22.7005	Hotz17986		RE6				AM900653	MHG1
				Hotz17988		RE6				AM900653	
	Kythira	36.1530	22.9871	Hotz17408	R15	RE11			AM900646	AJ310329	MHG1
				Hotz17409	R15	RE11			AM900646	AJ310329	
				Hotz17424	R15	RE11			AM900646	AJ310329	
	Lefkes	40.9015	25.8001	Hotz17430		RE1				AJ310338	MHG1
	Lesvos	39.2103	26.1787	Ploetner145.03	A13	AN54	AT92	ANT29	GU812100	GU812209	MHG6c
				Ploetner146.03	A12	AN54	AT93	ANT29	GU812099	GU812209	
				Ploetner182.03	A14	AN54	AT91	ANT29	GU812101	GU812209	
				ZMB56920	A12	AN54	AT93	ANT29	GU812099	GU812209	
	Mangana	40.9289	24.8456	Hotz22721		RE1				AJ310338	MHG1
				Hotz22723		RE6				AM900653	
				Hotz22724		RE6				AM900653	
				Hotz22725		RE1				AJ310338	
	Mistros	38.5228	23.8325	Hotz17341	R7	RE6			AM900653	AM900653	MHG1
				Hotz17342	R6	RE4			AM749706	AJ310330	
				Hotz17343	R7	RE6			AM900653	AM900653	

Table 3.2. (continued).

Greece	Monastiraki	40.8515	26.1026	Hotz17365		RE1				AJ310338	MHG1
				Hotz17366		RE1				AJ310338	
				Hotz17367		AN38		ANT13		GU812195	MHG6c
				Hotz17368		RE1				AJ310338	MHG1
	Nea Manolada	38.0316	21.3611	Hotz19532	R17	RE11			AM900644	AJ310329	MHG1
				Hotz19533		RE11				AJ310329	
				Hotz19548	R13	RE13			AM749703	AM749702	
	Olympos/Karpathos	35.7427	27.1685	Hotz17207	A6	AN21	CE1	CER1	GU812093	GU812181	MHG6b
				Hotz17208	A6	AN21	CE1	CER1	GU812093	GU812181	
				Hotz17420	A6	AN21	CE1	CER1	GU812093	GU812181	
	Pagouria	40.9164	25.3780	Hotz17446		RE1				AJ310338	MHG1
	Paradisos	39.2993	23.2110	Hotz12923	R3	RE1			AM749713	AJ310338	MHG1
				Hotz12926		RE1				AJ310338	
				Hotz12927		RE6				AM900653	
				Hotz12928		RE1				AJ310338	
				Hotz12931		RE2				GU812151	
				Hotz12932		RE1				AJ310338	
				Hotz12933		RE6				AM900653	
				Hotz12934		RE8				GU812154	
				Hotz12935		RE1				AJ310338	
	Samos	37.7641	26.9750	Hotz17322	A18	AN54	AT89	ANT29	GU812105	GU812209	MHG6c
				Hotz17323	A19	AN47	AT90	ANT22	GU812106	GU812203	
	Skala	38.6675	23.0712	Hotz19483	R10	RE11			AM900662	AJ310329	MHG1
				Hotz19500	R10	RE11			AM900662	AJ310329	
	Lake Stimfalias/ Peloponnese	37.3452	22.1026	ZMB49267	R17	RE11			AM900644	AJ310329	MHG1
				ZMB49820	R17	RE11			AM900644	AJ310329	

Table 3.2. (continued).

Greece	Zakynthos	37.8052	20.8627	ZMB56972	R17	RE11			AM900644	AJ310329	MHG1
				Ploetner29.03	R16	RE11			AM749698	AJ310329	
				Ploetner30.03	R18	RE11			AM900639	AJ310329	
				Ploetner31.03	R18	RE11			AM900639	AJ310329	
				Ploetner32.03	R18	RE11			AM900639	AJ310329	
Hungary	Budapest	47.5325	19.0333	ZMB44447		RE1				AJ310338	MHG1
	Kis Balaton	48.0992	20.3171	ZMB44490		RE1				AJ310338	MHG1
Iran	Phalet village			AMPH\IRA\536		AN60	EU4	EUP6			MHG6d
	Babol Sar	36.6803	52.6357	AMPH\IRA\508			T7	TE6	ACC	GU812222	MHG7
				AMPH\IRA\509			T15	TE1	ACC	GU812218	
				AMPH\IRA\510			T15	TE1	ACC	GU812218	
				AMPH\IRA\511			T15	TE1	ACC	GU812218	
				AMPH\IRA\512			T5	TE2	ACC	GU812219	
	Badal	38.6336	44.7720	AMPH\IRA\351		AN59	EU22	EUP5	ACC	AJ310312	MHG6d
	Bastan	38.9046	44.9386	AMPH\IRA\301		AN59	EU23	EUP5	ACC	AJ310312	MHG6d
	Bavineh	33.6042	47.2026	AMPH\IRA\338		AN56	EU1	EUP2	ACC	GU812210	MHG6d
	Bisotun	34.4038	47.4483	AMPH\IRA\307		AN56	EU1	EUP2	ACC	GU812210	MHG6d
				AMPH\IRA\308		AN60	EU5	EUP6	ACC	GU812213	
				AMPH\IRA\309		AN60	EU6	EUP6	ACC	GU812213	
				AMPH\IRA\310		AN64		EUP10		GU812216	
				AMPH\IRA\311		AN56		EUP2		GU812210	
	Choplu	36.4739	47.0393	AMPH\IRA\302		AN65	EU15	EUP11	ACC	GU812217	MHG6d
	Choqa Zanbil	32.0177	48.5451	AMPH\IRA\327		AN56		EUP2		GU812210	MHG6d
				AMPH\IRA\328		AN61		EUP7		GU812214	
				AMPH\IRA\329		AN61		EUP7		GU812214	
				AMPH\IRA\330		AN62		EUP8		GU812215	

Table 3.2. (continued).

Iran	Choqa Zanbil	32.0177	48.5451	AMPH\IRA\331		AN62		EUP8		GU812215	MHG6d
				AMPH\IRA\332		AN62		EUP8		GU812215	
				AMPH\IRA\333		AN56		EUP2		GU812210	
				AMPH\IRA\334		AN62		EUP8		GU812215	
				AMPH\IRA\335		AN62		EUP8		GU812215	
				AMPH\IRA\336		AN56		EUP2		GU812210	
	Galugan	37.5171	49.3091	AMPH\IRA\523			T10	TE1	ACC	GU812218	MHG7
				AMPH\IRA\524			T9	TE1	ACC	GU812218	
	Jeiugir	32.9873	47.8106	AMPH\IRA\313		AN59	EU2	EUP5	ACC	AJ310312	MHG6d
	Kenar Darya	36.8472	53.3131	AMPH\IRA\117			T12	TE1	ACC	GU812218	MHG7
				AMPH\IRA\118			T15	TE1	ACC	GU812218	
				AMPH\IRA\119			T8	TE1	ACC	GU812218	
				AMPH\IRA\120			T15	TE9	ACC	GU812225	
				AMPH\IRA\121			T1	TE4	ACC	GU812221	
				AMPH\IRA\122			T5	TE2	ACC	GU812219	
				AMPH\IRA\123			T15	TE1	ACC	GU812218	
	Lendj Abad	33.4511	49.0293	AMPH\IRA\312		AN60		EUP6		GU812213	MHG6d
	Mangol	36.2505	52.3563	AMPH\IRA\112			T15	TE1	ACC	GU812218	MHG7
				AMPH\IRA\113			T5	TE7	ACC	GU812223	
				AMPH\IRA\114			T6	TE8	ACC	GU812224	
	Marrave Tappe	37.7266	55.9071	AMPH\IRA\521			T1	TE4	ACC	GU812221	MHG7
	Now Kandeh	36.7154	53.8836	AMPH\IRA\513			T15	TE1	ACC	GU812218	MHG7
				AMPH\IRA\514			T14	TE1	ACC	GU812218	
				AMPH\IRA\515			T5	TE2	ACC	GU812219	
				AMPH\IRA\516			T11	TE1	ACC	GU812218	

Table 3.2. (continued).

Iran	Now Kandeh	36.7154	53.8836	AMPH\IRA\517			T15	TE1	ACC	GU812218	MHG7
				AMPH\IRA\518			T15	TE1	ACC	GU812218	
				AMPH\IRA\520			T15	TE1	ACC	GU812218	
				AMPH\IRA\115			T14	TE3	ACC	GU812220	
				AMPH\IRA\116			T15	TE1	ACC	GU812218	
	Khuzestan Kuli-Ali Reza	31.2499	49.6501	AMPH\IRA\530			T4	TE12	ACC	GU812228	MHG7
	Simili	31.7108	49.4057	AMPH\IRA\316				TE12		GU812228	MHG7
				AMPH\IRA\317				TE10		GU812226	
				AMPH\IRA\318				TE11		GU812227	
				AMPH\IRA\319				TE12		GU812228	
				AMPH\IRA\320				TE12		GU812228	
	Sorkheh Dizaj	38.8278	48.8247	AMPH\IRA\124		AN56	EU1	EUP2	ACC	GU812210	MHG6d
				AMPH\IRA\125		AN56	EU1	EUP2	ACC	GU812210	
				AMPH\IRA\126		AN57	EU3	EUP3	ACC	GU812211	
	Zanjan Ab Kenar	37.4474	49.3215	AMPH\IRA\501			T9	TE1	ACC	GU812218	
Jordan	Al Kerak	31.1833	35.7000	J-06-54	B12	BN8			ACC	ACC	MHG2
	Amman	32.0334	35.8091	ZFMK63535	B5	BN3			GU812076	AJ310321	MHG2
	Bab Amman	32.2042	35.8867	J-01-44	B11	BN5			ACC	GU812158	MHG2
				J-01-55	B11	BN5			ACC	GU812158	
				J-01-56		BN5				GU812158	
				J-01-57	B8	BN3			ACC	AJ310321	
	Canyon near Wadi Mujib	31.4492	35.7892	J-05-39		BN7				ACC	MHG2
				J-05-45	B7	BN9			ACC	ACC	
				J-05-46	B7	BN9			ACC	ACC	
				J-05-47	B7	BN7			ACC	ACC	
				J-05-48	B7	BN7			ACC	ACC	

Table 3.2. (continued).

Jordan	16 km southward from Jesus Baptisizing site	31.4939	35.5861	J-03-35		BN4				AJ310319	MHG2
				J-03-36	B9	BN5			ACC	GU812158	
				J-03-37		BN6				GU812159	
				J-03-38	B9	BN5			ACC	GU812158	
	King Talal Dam	32.2071	35.8517	ZFMK63514		BN6				GU812159	MHG2
	Mulaik Thoba	31.5533	35.7400	J-04-30	B10	BN5			ACC	GU812158	MHG2
				J-04-32	B12	BN8			ACC	ACC	
				J-04-33	B12	BN8			ACC	ACC	
				J-04-41	B10	BN5			ACC	GU812158	
				J-04-51	B12	BN8			ACC	ACC	
				J-04-52	B12	BN8			ACC	ACC	
				J-04-53	B12	BN8			ACC	ACC	
	Wadi Mujib	31.4455	35.8175	ZFMK64390	B4	BN5			GU812075	GU812158	MHG2
Kazakhstan	Almaty (Alma-Ata)	43.2827	76.8720	ZMB46963	C4		S1	SP1	GU812130	GU812229	MHG8
	Aktobe	50.2997	57.2179	Sp.250		AN27		ANT2		GQ902107	MHG6c
				Sp.251		AN27		ANT2		GQ902107	
	Atyrau	47.5442	52.3861	Sp.252	A29	AN27	AT79	ANT2	GU812116	GQ902107	MHG6c
				Sp.253	A29	AN27	AT79	ANT2	GU812116	GQ902107	
				Sp.254	A28	AN27	AT80	ANT2	GU812115	GQ902107	
				Sp.255	A29	AN27	AT79	ANT2	GU812116	GQ902107	
				Sp.256		AN27		ANT2		GQ902107	
	Chaganskoy	51.0354	51.7525	Sp.257		AN27		ANT2		GQ902107	MHG6c
Kyrgyzstan	Bishkek	42.8379	74.6360	L1	C5		S2	SP1	GU812131	GU812229	MHG8
				L3	C5		S2	SP1	GU812131	GU812229	
Libya	Shahhat (Cyrene)	32.7916	21.4297	AMPH\EGY\001		RE11				AJ310329	MHG1
				AMPH\LIB\002		RE11				AJ310329	

Table 3.2. (continued).

Libya	Shahhat (Cyrene)	32.7916	21.4297	AMPH\LIB\003		RE11				AJ310329	MHG1
				AMPH\LIB\004		RE11				AJ310329	
				AMPH\LIB\005		RE11				AJ310329	
				AMPH\LIB\006		RE11				AJ310329	
				AMPH\LIB\007		RE11				AJ310329	
				AMPH\LIB\008		RE11				AJ310329	
				AMPH\LIB\009		RE11				AJ310329	
				AMPH\LIB\010		RE11				AJ310329	
				AMPH\LIB\011		RE11				AJ310329	
				AMPH\LIB\012		RE11				AJ310329	
Macedonia	Lake Dojran	41.2166	22.7333	ZMB46692	R4	RE6			AM900652	AM900653	MHG1
	Skopje	42.0121	21.4715	ZMB46744		RE6				AM900653	MHG1
Poland	Poznan	52.3805	16.6674	Hotz18192	R1	RE1			AM900661	AJ310338	MHG1
Romania	Sfîntu-Gheorghe-stream, mile 52	44.6424	26.8504	ZMB47433	R1	RE1			AM900661	AJ310338	MHG1
				ZMB47434	R4	RE11			AM900652	AJ310329	
Russia	Armavir	44.9887	41.1563	ZISP.6130-Sp.137		AN44		ANT19		GU812201	MHG6c
	Baltiysk	54.6467	19.8820	ZISP.-Sp.273		RE3				GU812152	MHG1
	Chorgay Reservoir	45.5212	44.5678	ZISP.4255-Sp.65		RE10				GU812156	MHG1
	Dakhovskaya	44.2251	40.1997	ZMB57380	A31	AN43	AT76	ANT18	GU812117	GU812200	MHG6c
				ZMB57388	A32	AN43	AT77	ANT18	GU812118	GU812200	
	Yekaterinburg	56.8363	60.6379	ZISP.-Sp.244		RE6				AM900653	MHG1
	Ersi	42.0037	47.9904	ZISP.6760-Sp.136		AN27		ANT2		GQ902107	MHG6c
	Gaverdovsky	44.6281	40.0204	ZISP.6644-Sp.131		AN43		ANT18		GU812200	MHG6c
	Kaspiy Sanatorium	42.3504	48.0603	ZISP.-Sp.260		AN40		ANT15		GU812197	MHG6c
	Mochokh	42.6510	46.6347	ZISP.6761-Sp.134		AN27		ANT2		GQ902107	MHG6c

Table 3.2. (continued).

Russia	Moscow	55.7144	37.5857	ZMB46428	R1	RE1			AM900661	AJ310338	MHG1
				ZMB45920-25/1		RE1				AJ310338	
	Orsk	51.2177	58.6347	ZISP.6319-Sp.85-87		AN27		ANT2		GQ902107	MHG6c
				ZISP.6319-Sp.85-87		AN27		ANT2		GQ902107	
				ZISP.6319-Sp.85-87		AN27		ANT2		GQ902107	
	Psebai	44.1185	40.7853	ZISP.6549-Sp.74		AN27		ANT2		GQ902107	MHG6c
	Rossosh	50.2153	39.6006	ZISP.6553-Sp.108		RE9				GU812155	MHG1
				ZISP.6553-Sp.109		RE9				GU812155	
				ZISP.6553-Sp.110		RE9				GU812155	
	Sochi	43.5707	39.7625	ZISP.6751-Sp.77		AN42		ANT17		GU812199	MHG6c
	Saint Peterhof Station	59.8853	29.9098	ZISP.-Sp.247		AN31		ANT6		GU812188	MHG6c
				ZISP.-Sp.248		AN31		ANT6		GU812188	
				ZISP.-Sp.249		AN43		ANT18		GU812200	
	Step	44.5687	44.8150	ZISP.3280-Sp.68		RE9				GU812155	MHG1
	Volgograd	48.7106	44.4934	ZISP.6659-Sp.126		AN27		ANT2		GQ902107	MHG6c
Serbia	Belgrade	44.8332	20.5019	ZMB46740	R1	RE1			AM900661	AJ310338	MHG1
Slovakia	Bratislava-Devin	48.1579	16.9918	SLOV88	R1	RE1			AM900661	AJ310338	MHG1
	Brodské	48.6941	17.0092	SLOV171	R1	RE1			AM900661	AJ310338	MHG1
Switzerland	Embrach	47.5060	8.6123	Hotz16637		RE6				AM900653	MHG1
Syria	Abu Kamal	34.4496	40.9386	ZFMK61785	A40	AN55	EU11	EUP1	GU812126	AJ310313	MHG6d
				ZFMK61787	A36	AN63	EU36	EUP9	GU812122	AJ310311	
				ZFMK61788	A38	AN59	EU25	EUP5	GU812124	AJ310312	
	Ansari Mountains	34.8166	36.1166	ZFMK60903	B2	BN2			GU812073	AJ310320	MHG2
	As Suwayda	32.6855	36.5525	ZFMK64945	B6	BN4			GU812077	AJ310319	MHG2
	Qalat al-Hisn	34.7788	36.2655	ZFMK57959	B3	BN1			GU812074	AJ310322	MHG2
	(Crac des Chevaliers)			ZFMK57960		BN1				AJ310322	

Table 3.2. (continued).

Turkey	Adana-Ceyhan Cinderesi	37.0353	35.7470	CA1418				CIW3		GU812163	MHG4
				CA1419				CIW1		AJ313135	
				CA1420			CLE13	CIE2	ACC	GU812169	MHG5
				CA1421			CLW13	CIW3	ACC	GU812163	MHG4
				CA1422			CLW10	CIW1	ACC	AJ313135	
	Adana-Pozantı Şekerpınarı	37.4080	34.8842	CA1922			CLW15	CIW3	GU812083	GU812163	MHG4
				CA1923			CA8	CAR25	GU812089	ACC	MHG6a
				CA1924				CIW3		GU812163	MHG4
				CA1925				ANT1		AJ310337	MHG6c
				CA1926				ANT1		AJ310337	
	Adana-Pozantı Çakıt river	37.4299	34.8764	CA1927				CIE2		GU812169	MHG5
				CA1928			CLW15	CIW3	GU812083	GU812163	MHG4
				CA1929				CIW3		GU812163	
				CA1930				CIW3		GU812163	
				CA1931				CIW3		GU812163	
	Adapazarı-Poyrazlar lake	40.8336	30.4682	CA1540			AT27	ANT1	ACC	AJ310337	MHG6c
				CA1541			AT69	ANT2	ACC	GQ902107	
				CA1542				ANT1		AJ310337	
				CA1543				ANT1		AJ310337	
				CA1544				ANT2		GQ902107	
	Adapazarı-Saklıgöl	40.8549	30.3018	CA1545			AT40	ANT53	ACC	ACC	MHG6c
				CA1546				ANT2		GQ902107	
				CA1547			AT69	ANT2	ACC	GQ902107	
				CA1548			AT5	ANT1	ACC	AJ310337	
	Adıyaman-Abuzergaffar river	37.7415	38.3354	CA1270			CLW15	CIW3	GU812083	GU812163	MHG4
				CA1271			EU14	EUP1	ACC	AJ310313	MHG6d

Table 3.2. (continued).

Turkey	Adıyaman-Abuzergaffar river	37.7415	38.3354	CA1272			EU24	EUP5	ACC	AJ310312	MHG6d
				CA1273				EUP1		AJ310313	
				CA1274				EUP5		AJ310312	
				CA1275				EUP5		AJ310312	
				CA1276				EUP1		AJ310313	
	Adıyaman-Börgenek Çakal stream	37.7128	38.1663	CA1287				EUP5		AJ310312	MHG6d
				CA1288				EUP5		AJ310312	
				CA1289			EU14	EUP1	ACC	AJ310313	
				CA1290			EU14	EUP23	ACC	ACC	
				CA1291			EU36	EUP5	GU812122	AJ310312	
				CA1292			CLE12	CIE2	ACC	GU812169	MHG5
				CA1293				EUP1		AJ310313	MHG6d
	Adıyaman-Göksu river	37.6983	38.0799	CA1282			AT72	ANT1	ACC	AJ310337	MHG6c
				CA1283			EU36	EUP5	GU812122	AJ310312	MHG6d
				CA1284			EU12	EUP1	ACC	AJ310313	
				CA1285				ANT4		GU812186	MHG6C
				CA1286				ANT4		GU812186	
	Adıyaman-Kahta Bircik river	37.7447	38.5060	CA1277				EUP5		AJ310312	MHG6d
				CA1278				EUP1		AJ310313	
				CA1279			EU14	EUP1	ACC	AJ310313	
				CA1280			EU36	EUP5	GU812122	AJ310312	
				CA1281				EUP1		AJ310313	
	Afyonkarahisar-26 Agust Natural Park	38.7925	30.3816	CA1726			CA9	CAR17	ACC	AJ313132	MHG6a
				CA1727			AT110	ANT21	GU812104	GQ902114	MHG6c
				CA1728				ANT21		GQ902114	
				CA1729				CAR14		AJ313133	MHG6a

Table 3.2. (continued).

Turkey	Afyonkarahisar-26 Agust Natural Park	38.7925	30.3816	CA1730				CAR14		AJ313133	MHG6a
	Afyonkarahisar-Cumhuriyet village Çay	38.5923	30.9618	CA1720				ANT21		GQ902114	MHG6c
				CA1721			AT110	ANT21	GU812104	GQ902114	
				CA1722				CAR14		AJ313133	MHG6a
				CA1723			AT41	ANT2	ACC	GQ902107	MHG6c
				CA1724			CA8	CAR17	GU812089	AJ313132	MHG6a
	Afyonkarahisar-Karamık lake	38.4215	30.8869	CA1709			CA8	CAR17	GU812089	AJ313132	MHG6a
				CA1710				CAR14		AJ313133	
				CA1711				CAR17		AJ313132	
				CA1712				ANT21		GQ902114	MHG6c
				CA1713				CAR17		AJ313132	MHG6a
	Ağrı-Aşağı Yoldüzü Cuma River	39.8181	43.0892	CA679				EUP5		AJ310312	MHG6d
				CA680			EU8	EUP12	ACC	AJ310313	
				CA681				EUP12		AJ310313	
				CA683				EUP12		AJ310313	
	Ağrı-Çukuralan Village	39.7130	42.9920	CA684				EUP12		AJ310313	MHG6d
				CA685				EUP12		AJ310313	
				CA686			EU24	EUP5	ACC	AJ310312	
				CA687			EU8	EUP12	ACC	AJ310313	
				CA688				EUP12		AJ310313	
	Ağrı-Dambat village	39.6769	43.0228	CA672			EU10	EUP12	ACC	AJ310313	MHG6d
				CA673			AT70	ANT12	ACC	GU812194	MHG6c
				CA674				EUP12		AJ310313	MHG6d
				CA675				EUP12		AJ310313	
				CA676				EUP12		AJ310313	

Table 3.2. (continued).

Turkey	Ağrı-Dambat village	39.6769	43.0228	CA678			EU24	EUP5	ACC	AJ310312	MHG6d
	Ağrı-Doğu Beyazıt Bardaklı village	39.681	44.0655	CA658				ANT2		GQ902107	MHG6c
				CA659			EU24	EUP5	ACC	AJ310312	MHG6d
				CA660				EUP12		AJ310313	
				CA661			EU24	EUP18	ACC	ACC	
				CA662				ANT2		GQ902107	MHG6c
	Akçapınar	37.1133	28.4656	Hotz16808	A20	AN50	AT83	ANT25	GU812107	AJ313131	MHG6c
				Ploetner160.03	A20	AN50	AT83	ANT25	GU812107	AJ313131	
				Ploetner161.03	A21	AN50	AT85	ANT25	GU812108	AJ313131	
				Ploetner165.03	A20	AN50	AT83	ANT25	GU812107	AJ313131	
	Aksaray-Akın village stream	38.4313	34.0291	CA1225				CAR12		GQ902088	MHG6a
				CA1226				ANT1		AJ310337	MHG6c
				CA1227				ANT1		AJ310337	
				CA1228				ANT1		AJ310337	
	Aksaray-Helvadere	38.1999	34.2103	CA1212				ANT1		AJ310337	MHG6c
				CA1213				ANT1		AJ310337	
				CA1214				ANT1		AJ310337	
				CA1215				ANT1		AJ310337	
				CA1216				ANT1		AJ310337	
				CA1217				ANT1		AJ310337	
				CA1218				ANT1		AJ310337	
	Aksaray-Melendez river	38.2988	34.2662	CA1219				CAR12		GQ902088	MHG6a
				CA1220				ANT1		AJ310337	MHG6c
				CA1221				ANT1		AJ310337	
				CA1222				ANT1		AJ310337	
				CA1223				ANT1		AJ310337	

Table 3.2. (continued).

Turkey	Aksaray-Melendez river	38.2988	34.2662	CA1224				ANT1		AJ310337	MHG6c
	Aksaray-Sultanhanı	38.2414	33.5448	CA1205				ANT1		AJ310337	MHG6c
				CA1206			AT5	ANT1	ACC	AJ310337	
				CA1207				ANT1		AJ310337	
				CA1208				ANT1		AJ310337	
	Aksaray-Sultanhanı	38.2414	33.5448	CA1209				ANT1		AJ310337	MHG6c
				CA1210				ANT1		AJ310337	
				CA1211				ANT1		AJ310337	
	Akşehir-Eber Lakes	38.4544	31.4546	CBCAST4240		AN17		CAR17		AJ313132	MHG6a
				CBCA03184		AN27		ANT2		GQ902107	MHG6c
				CBCA03185		AN46		ANT21		GQ902114	
				CBCA03186		AN27		ANT2		GQ902107	
				CBCA03187		AN17		CAR17		AJ313132	MHG6a
				CBCA03188		AN36		ANT11		GU812193	MHG6c
				CBCA03189		AN46		ANT21		GQ902114	
				CBCA03190		AN17		CAR17		AJ313132	MHG6a
				CA1715			CA8	CAR17	GU812089	AJ313132	
				CA1716				ANT2		GQ902107	MHG6c
				CA1717				CAR14		AJ313133	MHG6a
				CA1718				ANT2		GQ902107	MHG6c
				CA1719				ANT2		GQ902107	
	Alanya	36.6031	32.0694	MTHTCA07177		AN1		CAR1		AJ310314	MHG6a
				MTHTCA07178		AN1		CAR1		AJ310314	
				ZFMK40193		AN1		CAR1		AJ310314	
				ZFMK40195	A4	AN1	CA20	CAR1	GU812091	AJ310314	
				ZFMK40198	A4	AN1	CA20	CAR1	GU812091	AJ310314	

Table 3.2. (continued).

Turkey	Amasya-Boğazköy Tersakan	40.7268	35.7702	CA909				ANT1		AJ310337	MHG6c
				CA910			AT33	ANT1	ACC	AJ310337	
				CA911				ANT1		AJ310337	
				CA912				ANT1		AJ310337	
				CA913				ANT1		AJ310337	
	Amasya-Doğantepe pond	40.6104	35.5869	CA902				ANT35		ACC	MHG6c
				CA903			AT1	ANT1	GU812111	AJ310337	
				CA904				ANT1		AJ310337	
				CA905				ANT1		AJ310337	
	Amasya-Suluoava Yedikır dam	40.7786	35.5751	CA914			AT1	ANT1	GU812111	AJ310337	MHG6c
				CA915				ANT1		AJ310337	
				CA916				ANT1		AJ310337	
				CA917				ANT1		AJ310337	
	Amasya-Yeşilırmak	40.6735	35.8528	CA907				ANT1		AJ310337	MHG6c
				CA908				ANT1		AJ310337	
	Ankara	39.5793	33.0453	KKOBCA06229		AN26		ANT1		AJ310337	MHG6c
				KKOBCA06230		AN26		ANT1		AJ310337	
				KKOBCA06231		AN26		ANT1		AJ310337	
				-	A24	AN26	AT1	ANT1	GU812111	AJ310337	
	Antakya Samandağı	36.0742	35.9982	BCA31291		CI1		CIW1		AJ313135	MHG4
				BCA31292		CI1		CIW1		AJ313135	
				BCA31293		CI1		CIW1		AJ313135	
				BCA31294		CI8		CIE1		GU812168	MHG5
	Antalya	37.2119	30.9415	CBCASTO702		AN1		CAR1		AJ310314	MHG6a
				CBCASTO704		AN1		CAR1		AJ310314	
				CBCASTO705		AN15		CAR15		GQ902085	
				CBCASTO706		AN1		CAR1		AJ310314	

Table 3.2. (continued).

Turkey	Antalya	37.2119	30.9415	CBCA0743		AN1		CAR1		AJ310314	MHG6a
				HKHSBKCA07111		AN10		CAR10		GQ902084	
				HKHSBKCA07112		AN1		CAR1		AJ310314	
				HKHSBKCA07113		AN1		CAR1		AJ310314	
				HKHSBKCA07114		AN1		CAR1		AJ310314	
				HKHSBKCA07115		AN1		CAR1		AJ310314	
				HKHSBKCA07116		AN1		CAR1		AJ310314	
				HKHSBKCA07117		AN1		CAR1		AJ310314	
				HKHSBKCA07118		AN5		CAR5		GQ902083	
				HKHSBKCA07119		AN1		CAR1		AJ310314	
				HKHSBKCA07120		AN9		CAR9		GU812178	
				HKHSBKCA07121		AN6		CAR6		GU812176	
				HKHSBKCA07122		AN1		CAR1		AJ310314	
				HKHSBKCA07123		AN10		CAR10		GQ902084	
				HKHSBKCA07124		AN1		CAR1		AJ310314	
				ZFMK45348		AN1		CAR1		AJ310314	
				ZFMK45349		AN1		CAR1		AJ310314	
	Antalya-Anamur	36.0429	32.8078	CA1433				CAR1		AJ310314	MHG6a
				CA1434			CA20	CAR1	GU812091	AJ310314	
				CA1435				CAR1		AJ310314	
				CA1436				CAR1		AJ310314	
				CA1437				CAR1		AJ310314	
	Antalya-Kemer Kesmeboğaz river	36.5954	30.5045	CA1862			CA17	CAR1	ACC	AJ310314	MHG6a
				CA1863				CAR1		AJ310314	
				CA1864				CAR1		AJ310314	
				CA1865				CAR1		AJ310314	

Table 3.2. (continued).

Turkey	Antalya-Kemer Kesmeboğaz river	36.5954	30.5045	CA1866				CAR1		AJ310314	MHG6a
	Antalya-Gazipaşa	36.1687	32.4467	CA1441			CA18	CAR1	ACC	AJ310314	MHG6a
	Antalya-Kumluca	36.3168	30.2512	CA1870			CA20	CAR24	GU812091	ACC	MHG6a
				CA1871				ANT46		ACC	MHG6c
	Ardahan-Göle Serme Bridge	40.9087	42.5928	CA732				ANT12		GU812194	MHG6c
				CA733				ANT12		GU812194	
				CA734			AT70	ANT12	ACC	GU812194	
				CA735				ANT12		GU812194	
				CA736				ANT12		GU812194	
				CA737				ANT12		GU812194	
	Ardahan-Kura River	41.1569	42.8728	CA743				EUP12		AJ310313	MHG6c
				CA744			AT70	ANT12	ACC	GU812194	
				CA745				ANT12		GU812194	
	Ardahan-Uzunova Village	41.0800	42.4991	CA739				EUP12		AJ310313	MHG6d
				CA740				ANT12		GU812194	MHG6c
				CA741				ANT14		GU812196	
	Ardahan-Uzunova Village	41.0800	42.4991	CA742				ANT14		GU812196	MHG6c
	Artvin-Ardanuç River	41.1247	42.0668	CA746				ANT12		GU812194	MHG6c
				CA747				ANT12		GU812194	
				CA748				ANT12		GU812194	
				CA749				ANT12		GU812194	
	Artvin Borçka	41.3649	41.6920	DC08241		AN28		ANT3		GU812185	MHG6c
				DC08242		AN39		ANT14		GU812196	
				DC08243		AN26		ANT1		AJ310337	
				CA757			AT70	ANT50	ACC	ACC	
				CA759				ANT1		AJ310337	

Table 3.2. (continued).

Turkey	Artvin Borçka	41.3649	41.6920	CA760				ANT50		ACC	MHG6c
				CA761			AT70	ANT50	ACC	ACC	
	Artvin-Hopa Kemalpaşa	41.4870	41.5269	CA764			AT1	ANT1	GU812111	AJ310337	MHG6c
				CA767			AT78	ANT14	ACC	GU812196	
				CA768				ANT1		AJ310337	
	Artvin Şavşat	41.3098	42.4837	ATDC08191		AN37		ANT12		GU812194	MHG6c
				ATDC08192		AN37		ANT12		GU812194	
				ATDC08193		AN37		ANT12		GU812194	
				ATDC08194		AN37		ANT12		GU812194	
	Artvin-Yolüstü Village	41.1613	42.0639	CA753				ANT12		GU812194	MHG6c
				CA754			AT70	ANT12	ACC	GU812194	MHG6c
				CA755				EUP12		AJ310313	MHG6d
	Lake Avlan	36.5825	29.9482	HS07165		AN23		CER3		GQ902087	MHG6b
				HS07166		AN23		CER3		GQ902087	
				HS07167		AN20		CAR20		GQ902086	MHG6a
				HS07168		AN20		CAR20		GQ902086	
				HS07169		AN20		CAR20		GQ902086	
	Aydın-Azap lake	37.5844	27.447	CA1800				ANT21		GQ902114	MHG6c
				CA1801				ANT21		GQ902114	
	Aydın-Azap lake	37.5844	27.447	CA1802			AT110	ANT21	GU812104	GQ902114	MHG6c
				CA1803			AT87	ANT25	ACC	AJ313131	
	Aydın-Bıyıkali pond	37.7716	27.5741	CA1785				ANT21		GQ902114	MHG6c
				CA1786				ANT21		GQ902114	
				CA1787			AT107	ANT21	ACC	GQ902114	
				CA1788				ANT21		GQ902114	
				CA1789				ANT21		GQ902114	

Table 3.2. (continued).

Turkey	Aydın-Menderes river	37.5476	27.2371	CA1796			AT87	ANT25	ACC	AJ313131	MHG6c
				CA1797				ANT21		GQ902114	
				CA1798			AT107	ANT21	ACC	GQ902114	
	Aydın-Söke water channel	37.6607	27.3087	CA1790				ANT21		GQ902114	MHG6c
				CA1791			AT87	ANT25	ACC	AJ313131	
				CA1792				ANT25		AJ313131	
				CA1793			AT110	ANT21	GU812104	GQ902114	
				CA1794				ANT21		GQ902114	
				CA1795				ANT21		GQ902114	
	Balıkesir-Erdek	40.2968	27.6273	CA1617				ANT21		GQ902114	MHG6c
				CA1618			AT110	ANT21	GU812104	GQ902114	
				CA1619			AT59	ANT2	GU812109	GQ902107	
				CA1620				ANT2		GQ902107	
				CA1621				ANT10		GU812192	
	Balıkesir-İkizcetepeler dam	39.4807	27.9274	CA1601				ANT21		GQ902114	MHG6c
				CA1602			AT86	ANT28	ACC	GU812208	
				CA1603			AT108	ANT21	ACC	GQ902114	
				CA1605				ANT10		GU812192	
	Balıkesir-Manyas Kuş Lake	40.2296	28.0461	CA1611				ANT21		GQ902114	MHG6c
				CA1612			AT96	ANT29	ACC	GU812209	
				CA1613			AT59	ANT2	GU812109	GQ902107	
				CA1615			AT60	ANT2	ACC	GQ902107	
	Balıkesir-Manyas Kuş Lake	40.2296	28.0461	CA1616				ANT10		GU812192	MHG6c
	Balıkesir-Pamukçu stream	39.5295	27.9091	CA1607			AT109	ANT21	ACC	GQ902114	MHG6c
				CA1608			AT91	ANT29	GU812101	GU812209	
				CA1609				ANT29		GU812209	

Table 3.2. (continued).

Turkey	Balıkesir-Pamukçu stream	39.5295	27.9091	CA1610				ANT29		GU812209	MHG6c
	Bartın-Potbaşı river	41.6087	32.3727	CA981				ANT1		AJ310337	MHG6c
				CA982				ANT1		AJ310337	
				CA984			AT12	ANT1	ACC	AJ310337	
				CA985				ANT1		AJ310337	
	Bartın-Bartın stream	41.5721	32.3267	CA989				ANT1		AJ310337	MHG6c
				CA990				ANT1		AJ310337	
				CA991			AT1	ANT1	GU812111	AJ310337	
				CA992				ANT1		AJ310337	
				CA993				ANT1		AJ310337	
	Batman-Dicle river	37.9177	41.0856	CA1355				EUP5		AJ310312	MHG6d
				CA1356				EUP5		AJ310312	
				CA1357				EUP5		AJ310312	
				CA1358				EUP5		AJ310312	
				CA1359			EU36	EUP5	GU812122	AJ310312	
				CA1360				EUP5		AJ310312	
	Batman-Hasankeyf	37.7356	41.3022	CA1370				EUP5		AJ310312	MHG6d
				CA1371				EUP5		AJ310312	
	Batman-Silvan road Çarıklı village	38.0463	41.1834	CA1361			EU33	EUP5	ACC	AJ310312	MHG6d
				CA1362				EUP5		AJ310312	
				CA1363				EUP5		AJ310312	
				CA1364				EUP5		AJ310312	
				CA1365				EUP5		AJ310312	
				CA1366				EUP5		AJ310312	
	Bayburt-Çamlık District	40.3009	40.2013	CA809				ANT37		ACC	MHG6c
				CA810				ANT37		ACC	

Table 3.2. (continued).

Turkey	Bayburt-Çamlık District	40.3009	40.2013	CA811				ANT1		AJ310337	MHG6c
				CA812				ANT37		ACC	
				CA813				ANT37		ACC	
				CA814				ANT1		AJ310337	
	Bayburt-Gökçedere pond	40.1156	39.7526	CA802				ANT1		AJ310337	MHG6c
				CA803				ANT1		AJ310337	
				CA804				ANT1		AJ310337	
				CA805				ANT1		AJ310337	
	Bayburt-Oruçbeyli pond	40.2316	40.0626	CA797				ANT1		AJ310337	MHG6c
				CA798				ANT1		AJ310337	
				CA799				ANT1		AJ310337	
				CA800				ANT37		ACC	
				CA801				ANT1		AJ310337	
	Bayburt-Toki	40.2729	40.1343	CA808				ANT1		AJ310337	MHG6c
	Bayramdere	40.2025	28.5003	Hotz17410		AN27		ANT2		GQ902107	MHG6c
				Hotz17421		AN27		ANT2		GQ902107	
	Lake Beyşehir	37.6802	31.7180	MEFUCA42195		AN13		CAR13		GU812179	MHG6a
				MEFUCA42196		AN12		CAR12		GQ902088	
				MEFUCA42197		AN12		CAR12		GQ902088	
				MEFUCA42198		AN12		CAR12		GQ902088	
				Hotz17310	A2	AN17	CA8	CAR17	GU812089	AJ313132	
				Hotz17313	A2	AN14	CA8	CAR14	GU812089	AJ313133	
				ZFMK40195		AN11		CAR11		AJ310316	
				CA1450				CAR13		GU812179	
				CA1451			CA1	CAR12	GU812088	GQ902088	
				CA1452				CAR21		ACC	

Table 3.2. (continued).

Turkey	Lake Beyşehir	37.6802	31.7180	CA1453			CA5	CAR21	ACC	ACC	MHG6a
				CA1454			CA2	CAR22	ACC	ACC	
				CA1455				CAR12		GQ902088	
				CA1456			CA6	CAR23	ACC	ACC	
				CA1457			CA8	CAR17	GU812089	AJ313132	
	Bilecik-Çiğdemlik	40.0646	30.3142	CA1656				ANT13		GU812195	MHG6c
				CA1657			AT1	ANT1	GU812111	AJ310337	
				CA1658			AT69	ANT2	ACC	GQ902107	
	Bilecik-İnhisar Sakarya river	40.0469	30.4124	CA1659			AT1	ANT43	GU812111	ACC	MHG6c
				CA1660				ANT2		GQ902107	
				CA1661			AT67	ANT13	GU812110	GU812195	
				CA1662				ANT1		AJ310337	
				CA1663				ANT2		GQ902107	
				CA1664				ANT1		AJ310337	
	Bilecik Söğüt	39.7118	30.0070	MAYGCA11303		AN27		ANT2		GQ902107	MHG6c
				MAYGCA11304		AN26		ANT1		AJ310337	
				MAYGCA11305		AN26		ANT1		AJ310337	
				MAYGCA11306		AN26		ANT1		AJ310337	
				CA1648				ANT1		AJ310337	
				CA1649			AT1	ANT43	GU812111	ACC	
				CA1651			AT68	ANT13	ACC	GU812195	
	Bingöl-Çeltiksuyu stream	38.8411	40.5654	CA570				EUP5		AJ310312	MHG6d
				CA571			EU35	EUP5	ACC	AJ310312	
				CA572				EUP5		AJ310312	
				CA573				EUP5		AJ310312	
				CA574			EU16	EUP16	ACC	ACC	

Table 3.2. (continued).

Turkey	Bingöl-Çobantaşı	39.0585	40.7976	CA582				EUP5		AJ310312	MHG6d
				CA583				EUP5		AJ310312	
				CA584				EUP5		AJ310312	
				CA585			EU33	EUP5	ACC	AJ310312	
	Bingöl-Sarıçiçek Lake	38.8844	40.5890	CA575				EUP5		AJ310312	MHG6d
				CA576				EUP5		AJ310312	
				CA577			EU36	EUP5	GU812122	AJ310312	
				CA578				EUP5		AJ310312	
				CA579				EUP5		AJ310312	
	Bingöl-Solhan Seref stream	38.9184	40.7859	CA586			EU36	EUP5	GU812122	AJ310312	MHG6d
				CA587				EUP5		AJ310312	
				CA588				EUP5		AJ310312	
				CA589				EUP5		AJ310312	
				CA590				EUP5		AJ310312	
	Bitlis-Ağaçköprü District	38.3328	42.0098	CA630			EU33	EUP5	ACC	AJ310312	MHG6d
	Bitlis-Güroymak Water Channel	38.5962	42.0243	CA618			EU33	EUP5	ACC	AJ310312	MHG6d
				CA619			EU17	EUP19	ACC	ACC	
				CA620				EUP5		AJ310312	
				CA621				EUP12		AJ310313	
	Bitlis-Kemah Stream	38.4407	42.1447	CA623			EU33	EUP5	ACC	AJ310312	MHG6d
				CA624				EUP5		AJ310312	
				CA625				EUP5		AJ310312	
	Bitlis-Tatvan Çağlayan	38.4748	42.3084	CA631			EU19	EUP5	ACC	AJ310312	MHG6d
				CA632			EU18	EUP15	ACC	ACC	
				CA633				EUP5		AJ310312	
				CA634				EUP5		AJ310312	

Table 3.2. (continued).

Turkey	Bitlis-Tatvan Çağlayan	38.4748	42.3084	CA635				EUP5		AJ310312	MHG6d
	Bolu-Gölköy	40.7116	31.5314	CA1520				ANT1		AJ310337	MHG6c
				CA1521			AT1	ANT1	GU812111	AJ310337	
				CA1522				ANT1		AJ310337	
	Bolu-Karamanlar lake	40.7619	31.5162	CA1525				ANT1		AJ310337	MHG6c
				CA1526				ANT1		AJ310337	
				CA1527			AT1	ANT1	GU812111	AJ310337	
	Bolu-Karamanlar lake	40.7619	31.5162	CA1528				ANT1		AJ310337	MHG6c
	Bucak	37.3500	30.5393	MTAECA1568		AN1		CAR1		AJ310314	MHG6a
				MTAECA1569		AN1		CAR1		AJ310314	
				MTAECA1570		AN1		CAR1		AJ310314	
				MTAECA1571		AN1		CAR1		AJ310314	
				MTAECA1572		AN14		CAR14		AJ313133	
				MTAECA1573		AN1		CAR1		AJ310314	
				MTAECA1574		AN17		CAR17		AJ313132	
				MTAECA1575		AN14		CAR14		AJ313133	
				MTAECA1576		AN1		CAR1		AJ310314	
				MTAECA1577		AN1		CAR1		AJ310314	
	Lake Burdur	37.8371	30.3854	CBCAST1517		AN1		CAR1		AJ310314	MHG6a
				CBCAST1519		AN1		CAR1		AJ310314	
				CBCAST1520		AN1		CAR1		AJ310314	
	Burdur-Çerçin dam	37.7603	30.4149	CA1882				CAR1		AJ310314	MHG6a
				CA1883				CAR1		AJ310314	
				CA1884				CAR1		AJ310314	
	Burdur-Karataş lake	37.3616	29.9869	CA1877			CA8	CAR17	GU812089	AJ313132	MHG6a
				CA1878				CAR17		AJ313132	

Table 3.2. (continued).

Turkey	Burdur-Karataş lake	37.3616	29.9869	CA1879				CAR17		AJ313132	MHG6a
				CA1880			AT103	ANT21	ACC	GQ902114	MHG6c
				CA1881			CA14	CAR1	ACC	AJ310314	MHG6c
	Burdur-Yarışlı lake	37.5907	29.9562	CA1872				ANT21		GQ902114	MHG6c
				CA1873				ANT21		GQ902114	
				CA1874				ANT21		GQ902114	
				CA1876				ANT1		AJ310337	
	Bursa-Akçalar village	40.1771	28.7453	CA1641			AT98	ANT29	ACC	GU812209	MHG6c
				CA1642			AT63	ANT52	ACC	ACC	
				CA1643			AT67	ANT2	GU812110	GQ902107	
	Bursa-Akçalar village	40.1771	28.7453	CA1644				ANT10		GU812192	MHG6c
				CA1646				ANT2		GQ902107	
	Bursa-Boğaz	40.2821	28.4483	CA1622				ANT2		GQ902107	MHG6c
				CA1623				ANT2		GQ902107	
				CA1624			AT59	ANT2	GU812109	GQ902107	
				CA1626				ANT29		GU812209	
	Bursa-Gölyazı	40.1653	28.6795	CA1635			AT67	ANT52	GU812110	ACC	MHG6c
				CA1636			AT96	ANT29	ACC	GU812209	
				CA1637				ANT29		GU812209	
				CA1638				ANT29		GU812209	
				CA1640			AT59	ANT58	GU812109	ACC	
	Bursa-Kemalpaşa	40.0346	28.4104	CA1628				ANT10		GU812192	MHG6c
				CA1629			AT110	ANT21	GU812104	GQ902114	
				CA1631				ANT52		ACC	
				CA1632				ANT2		GQ902107	
				CA1634			AT110	ANT61	GU812104	ACC	

Table 3.2. (continued).

Turkey	Büyükçekmece	41.0020	28.6009	Hotz16627		AN27		ANT2		GQ902107	MHG6c
				Hotz16628		AN27		ANT2		GQ902107	
	Ceyhan	37.0889	35.8302	Hotz17303	CL4	CI1	CLW15	CIW1	GU812083	AJ313135	MHG4
				Hotz17305	CL2	CI1	CLW9	CIW1	GU812081	AJ313135	
	Çanakkale-Karacaören	40.1884	26.4330	CA1575				ANT2		GQ902107	MHG6c
				CA1577				ANT2		GQ902107	
				CA1578				ANT2		GQ902107	
				CA1580			AT61	ANT2	ACC	GQ902107	
	Çanakkale-Kepez	40.0895	26.3852	CA1589				ANT2		GQ902107	MHG6c
				CA1590			AT59	ANT2	GU812109	GQ902107	
				CA1591				ANT2		GQ902107	
				CA1592				ANT2		GQ902107	
				CA1593				ANT10		GU812192	
	Çanakkale-Batakova Menderes river	39.9930	26.2078	CA1596				ANT2		GQ902107	MHG6c
				CA1597				ANT2		GQ902107	
				CA1598				ANT2		GQ902107	
				CA1599			AT59	ANT2	GU812109	GQ902107	
				CA1600				ANT2		GQ902107	
	Çanakkale-Sarıçay	40.1393	26.4855	CA1582			AT63	ANT52	ACC	ACC	MHG6c
				CA1584			AT64	ANT1	ACC	AJ310337	
				CA1585			AT67	ANT2	GU812110	GQ902107	
				CA1586				ANT2		GQ902107	
	Çankırı-Apsarı stream	40.7018	33.5393	CA1023				ANT1		AJ310337	MHG6c
				CA1024			AT1	ANT1	GU812111	AJ310337	
				CA1025				ANT1		AJ310337	
				CA1027				ANT1		AJ310337	

Table 3.2. (continued).

Turkey	Çankırı-Aşağıyanlar district	40.5540	33.5817	CA1028				ANT1		AJ310337	MHG6c
				CA1029			AT21	ANT1	ACC	AJ310337	
				CA1030				ANT1		AJ310337	
				CA1031				ANT1		AJ310337	
	Çankırı-Terme river	40.4377	33.7431	CA1032				ANT1		AJ310337	MHG6c
				CA1033				ANT1		AJ310337	
				CA1034			AT29	ANT1	ACC	AJ310337	
				CA1035				ANT1		AJ310337	
	Çankırı-Yapraklı pond	40.7675	33.7641	CA1018				ANT1		AJ310337	MHG6c
				CA1019			AT19	ANT1	ACC	AJ310337	
				CA1020				ANT1		AJ310337	
				CA1021				ANT1		AJ310337	
	Çevlik District, Antakya	36.1239	35.9281	AMPH\SUR\202	CL3	CI1	CLW8	CIW1	GU812082	AJ313135	MHG4
				AMPH\SUR\203	CL1	CI1	CLW7	CIW1	GU812080	AJ313135	
	Çorum-Alaca stream	40.3371	35.0628	CA1041			AT1	ANT1	GU812111	AJ310337	MHG6c
				CA1042				ANT1		AJ310337	
				CA1043				ANT1		AJ310337	
	Çorum-Çomar dam	40.5856	34.9998	CA1050				ANT1		AJ310337	MHG6c
				CA1051				ANT1		AJ310337	
				CA1052			AT1	ANT1	GU812111	AJ310337	
				CA1054				ANT1		AJ310337	
	Çorum-Yakacık stream	40.6000	34.9117	CA1046			AT1	ANT1	GU812111	AJ310337	MHG6c
				CA1047				ANT1		AJ310337	
				CA1049				ANT1		AJ310337	
	Çorum-Yılgınözü stream	40.4502	34.3789	CA1037				ANT1		AJ310337	MHG6c
				CA1038				ANT1		AJ310337	

Table 3.2. (continued).

Turkey	Çorum-Yılgınözü stream	40.4502	34.3789	CA1039			AT1	ANT1	GU812111	AJ310337	MHG6c
				CA1040				ANT1		AJ310337	
	Dalaman	36.7138	28.7856	IS48307		AN50		ANT25		AJ313131	MHG6c
				IS48308		AN50		ANT25		AJ313131	
				IS48309		AN17		CAR17		AJ313132	MHG6a
				IS48310		AN50		ANT25		AJ313131	MHG6c
				IS48311		AN17		CAR17		AJ313132	MHG6a
				IS48312		AN23		CER3		GQ902087	MHG6b
	Denizli-Derbent dam	38.1532	28.8443	CA1814				ANT21		GQ902114	MHG6c
				CA1815			AT110	ANT21	GU812104	GQ902114	
				CA1816				ANT21		GQ902114	
				CA1817				ANT21		GQ902114	
	Denizli-Emmiler district	37.6264	29.2087	CA1804				ANT21		GQ902114	MHG6c
				CA1805			AT110	ANT21	GU812104	GQ902114	
				CA1806				ANT21		GQ902114	
				CA1807				ANT21		GQ902114	
	Denizli-İncirlipınar park	37.7623	29.0972	CA1809				ANT21		GQ902114	MHG6c
				CA1810				ANT21		GQ902114	
				CA1811				ANT21		GQ902114	
				CA1812				ANT21		GQ902114	
	Denizli-İncirlipınar park	37.7623	29.0972	CA1813			AT105	ANT21	ACC	GQ902114	MHG6c
	Denizli-Süleymanlı lake	38.0513	28.7708	CA1820				ANT21		GQ902114	MHG6c
				CA1821				ANT21		GQ902114	
				CA1822			AT110	ANT21	GU812104	GQ902114	
				CA1823				ANT21		GQ902114	
				CA1824				ANT21		GQ902114	

Table 3.2. (continued).

Turkey	Diyarbakır-Batman road	37.8081	40.4055	CA1345			EU36	EUP22	GU812122	ACC	MHG6d
				CA1346			EU20	EUP5	ACC	AJ310312	
	Diyarbakır-Devegeçidi	38.0576	40.0697	CA1339				EUP5		AJ310312	MHG6d
				CA1340				EUP5		AJ310312	
				CA1341				EUP5		AJ310312	
				CA1342				EUP5		AJ310312	
				CA1343			EU36	EUP24	GU812122	ACC	
				CA1344			EU33	EUP5	ACC	AJ310312	
	Diyarbakır-Dicle river	37.8797	41.0217	CA1347				EUP5		AJ310312	MHG6d
				CA1348			EU36	EUP5	GU812122	AJ310312	
				CA1349				EUP5		AJ310312	
				CA1350				EUP5		AJ310312	
				CA1352				EUP5		AJ310312	
				CA1353				EUP5		AJ310312	
				CA1354				EUP5		AJ310312	
	Diyarbakır-Göksu Çınar	37.6916	40.4473	CA1331			EU36	EUP5	GU812122	AJ310312	MHG6d
				CA1332				EUP5		AJ310312	
				CA1333				EUP5		AJ310312	
				CA1334				EUP5		AJ310312	
				CA1335				EUP5		AJ310312	
				CA1336				EUP5		AJ310312	
				CA1337				EUP5		AJ310312	
				CA1338				EUP5		AJ310312	
	Düzce-Asarsu	40.8259	31.1840	CA1530			AT1	ANT1	GU812111	AJ310337	MHG6c
				CA1531			AT66	ANT2	ACC	GQ902107	
				CA1532			AT17	ANT48	ACC	ACC	

Table 3.2. (continued).

Turkey	Düzce-Asarsu	40.8259	31.1840	CA1533				ANT1		AJ310337	MHG6c
				CA1534				ANT1		AJ310337	
	Düzce-Efteni lake	40.7573	31.0404	CA1536			AT17	ANT48	ACC	ACC	MHG6c
				CA1537			AT57	ANT1	ACC	AJ310337	
				CA1538			AT57	ANT41	ACC	ACC	
				CA1539				ANT1		AJ310337	
	Edirne	41.6857	26.4932	MACA22179		RE1		RE1		AJ310338	MHG1
				MACA22180		RE1		RE1		AJ310338	
				MACA22181		RE1		RE1		AJ310338	
				MACA22182		RE1		RE1		AJ310338	
				MACA22183		AN35				GU812192	MHG6c
	Edremit	39.6119	27.0151	Ploetner179.03	A22	AN27	AT59	ANT2	GU812109	GQ902107	MHG6c
				Ploetner180.03	A23	AN27	AT67	ANT2	GU812110	GQ902107	
	Lake Eğirdir	38.1393	30.7588	CBCAST3233		AN27		ANT2		GQ902107	MHG6c
				CBCAST3234		AN1		CAR1		AJ310314	MHG6a
				CBCAST3238		AN14		CAR14		AJ313133	
				CBCAST3239		AN14		CAR14		AJ313133	
				CA1890				CAR14		AJ313133	
				CA1891			CA8	CAR17	GU812089	AJ313132	
				CA1892			CA20	CAR1	GU812091	AJ310314	
				CA1893				CAR14		AJ313133	
	Elazığ - Birvan stream	38.7260	38.8375	CA543				EUP5		AJ310312	MHG6d
	Elazığ - Cip	38.6819	39.0706	CA535				EUP5		AJ310312	MHG6d
				CA536			EU33	EUP5	ACC	AJ310312	
				CA537				EUP5		AJ310312	
				CA538				EUP5		AJ310312	

Table 3.2. (continued).

Turkey	Elazığ - Cip	38.6819	39.0706	CA539				EUP5		AJ310312	MHG6d
	Elazığ - Sivrice	38.4665	39.2753	CA545				EUP5		AJ310312	MHG6d
				CA546				EUP5		AJ310312	
	Erzincan - Türkmenoğlu village	39.6559	39.4996	CA520				ANT1		AJ310337	MHG6c
				CA521				ANT1		AJ310337	
				CA522				ANT1		AJ310337	
				CA523			AT1	ANT1	GU812111	AJ310337	
				CA524				CIE2		GU812169	MHG5
	Erzincan - Ekşisu	39.7328	39.6179	CA525				ANT1		AJ310337	MHG6c
				CA526			AT1	ANT1	GU812111	AJ310337	
				CA527			CLW15	CIW8	GU812083	ACC	MHG4
				CA528				ANT1		AJ310337	MHG6c
				CA529				ANT1		AJ310337	
	Erzincan-Sakaltutan	39.8832	39.1954	CA530			AT10	ANT1	ACC	AJ310337	MHG6c
				CA531			AT31	ANT1	ACC	AJ310337	
				CA532				ANT1		AJ310337	
				CA533				ANT1		AJ310337	
	Erzurum-Ilıca	39.8196	41.1521	CA695				ANT12		GU812194	MHG6c
				CA696			AT70	ANT12	ACC	GU812194	
				CA697			AT7	ANT1	ACC	AJ310337	
				CA699				ANT12		GU812194	
				CA700				ANT12		GU812194	
				CA701			EU7	EUP12	ACC	AJ310313	MHG6d
				CA702				ANT12		GU812194	MHG6c
	Erzurum-Pasinler	39.9611	41.4090	CA704			EU36	EUP5	GU812122	AJ310312	MHG6d
				CA705				ANT12		GU812194	MHG6c

Table 3.2. (continued).

Turkey	Erzurum-Pasinler	39.9611	41.4090	CA706			AT70	ANT12	ACC	GU812194	MHG6c
				CA707				ANT12		GU812194	
				CA708			EU7	EUP12	ACC	AJ310313	MHG6d
	Erzurum-Soğuk Çermik	39.9899	41.3052	CA709				ANT12		GU812194	MHG6c
				CA710				ANT12		GU812194	
				CA711			AT70	ANT12	ACC	GU812194	
				CA712				EUP12		AJ310313	MHG6d
				CA713			EU7	EUP12	ACC	AJ310313	
	Erzurum-Teke stream	39.8196	41.1521	CA689				ANT12		GU812194	MHG6c
				CA690			AT70	ANT12	ACC	GU812194	
				CA691				ANT12		GU812194	
				CA692				ANT12		GU812194	
				CA693				ANT12		GU812194	
	Erzurum-Yerlisu Village	40.0425	41.1833	CA714			EU9	EUP12	ACC	AJ310313	MHG6d
				CA715			EU36	EUP5	GU812122	AJ310312	
				CA716			AT8	ANT1	ACC	AJ310337	MHG6c
	Eskişehir-Alpu road	39.7825	30.6877	CA1672			AT41	ANT53	ACC	ACC	MHG6c
				CA1673			CA8	CAR17	GU812089	AJ313132	MHG6a
				CA1674			AT67	ANT2	GU812110	GQ902107	MHG6c
				CA1675				ANT43		ACC	
				CA1676				ANT2		GQ902107	
	Eskişehir-Porsuk river 1	39.7744	30.4511	CA1677				ANT1		AJ310337	MHG6c
				CA1678			AT1	ANT1	GU812111	AJ310337	
				CA1679				ANT10		GU812192	
				CA1680				ANT2		GQ902107	

Table 3.2. (continued).

Turkey	Eskişehir-Porsuk river 2	39.7139	30.4275	CA1683			AT110	ANT29	GU812104	GU812209	MHG6c
				CA1684				ANT10		GU812192	
	Eskişehir-Sarısungur	39.7082	30.5804	CA1666			AT110	ANT21	GU812104	GQ902114	MHG6c
				CA1667			AT67	ANT2	GU812110	GQ902107	
				CA1668				CAR17		AJ313132	
				CA1669			AT1	ANT43	GU812111	ACC	
				CA1670			AT67	ANT2	GU812110	GQ902107	
	Eşmekaya	38.2296	33.4876	TBOECA68170		AN26		ANT1		AJ310337	MHG6c
				TBOECA68171		AN26		ANT1		AJ310337	
				TBOECA68172		AN26		ANT1		AJ310337	
				TBOECA68173		AN26		ANT1		AJ310337	
				TBOECA68174		AN27		ANT2		GQ902107	
				TBOECA68175		AN17		CAR17		AJ313132	MHG6a
				TBOECA68176		AN17		CAR17		AJ313132	
	Fethiye	36.6288	29.1196	RCA48213		AN50		ANT25		AJ313131	MHG6c
				RCA48214	A10	AN23	CE8	CER3	GU812097	GQ902087	MHG6b
				RCA48215	A11	AN25	CE9	CER5	GU812098	GU812184	
				RCA48216		AN22		CER2		GU812182	
	Foça	38.6666	26.7645	Ploetner197.03	A26	AN35	AT56	ANT10	GU812113	GU812192	MHG6c
				Ploetner198.03	A17	AN46	AT110	ANT21	GU812104	GQ902114	
				Ploetner199.03	A27	AN35	AT52	ANT10	GU812114	GU812192	
				Ploetner205.03	A16	AN46	AT106	ANT21	GU812103	GQ902114	
	Gaziantep	37.0892	37.1735	OBMB27295		AN55		EUP12		AJ310313	MHG6d
				OBMB27296		CI9		CIE2		GU812169	MHG5
				OBMB27297		AN59		EUP5		AJ310312	MHG6d
				OBMB27298		AN59		EUP5		AJ310312	

Table 3.2. (continued).

Turkey	Gaziantep-Balıkalan village	37.2923	36.8877	CA1968				CIW3		GU812163	MHG5
				CA1969				CIE3		GU812170	
				CA1970				CIE2		GU812169	
				CA1971				CIE2		GU812169	
				CA1972			CLW15	CIW3	GU812083	GU812163	MHG4
	Gaziantep-Kakurt	37.1360	36.9400	CA1973				CIE6		ACC	MHG5
				CA1974				CIE10		ACC	
	Gaziantep-Sakçagözü	37.1803	36.9285	CA1965				CIE2		GU812169	MHG5
				CA1966				CIE2		GU812169	
				CA1967				CIE3		GU812170	
	Gemiş	37.7902	29.8708	CBCAST2021		AN46		ANT21		GQ902114	MHG6c
				CBCAST2022		AN46		ANT21		GQ902114	
				CBCAST2023		AN46		ANT21		GQ902114	
				CBCAST2024		AN46		ANT21		GQ902114	
				CBCAST2025		AN1		CAR1		AJ310314	MHG6a
				CBCAST2026		AN46		ANT21		GQ902114	MHG6c
				CBCAST2027		AN46		ANT21		GQ902114	
				CBCAST2028		AN46		ANT21		GQ902114	
				CBCAST2029		AN46		ANT21		GQ902114	
				CBCAST2031		AN46		ANT21		GQ902114	
	Giresun-Batlama stream	40.9067	38.3547	CA835				ANT36		ACC	MHG6c
				CA836				ANT1		AJ310337	
				CA837				ANT1		AJ310337	
				CA838				ANT1		AJ310337	
				CA839				ANT1		AJ310337	

Table 3.2. (continued).

Turkey	Giresun-Bulancak Domuz stream	40.9454	38.1673	CA854				ANT1		AJ310337	MHG6c
				CA855				ANT1		AJ310337	
				CA856				ANT1		AJ310337	
	Giresun-Espiye Gelivera Stream	40.9459	38.7224	CA849				ANT1		AJ310337	MHG6c
				CA850				ANT1		AJ310337	
				CA852				ANT1		AJ310337	
				CA853				ANT1		AJ310337	
	Giresun-Kesap Karabulduk stream	40.8988	38.5270	CA844				ANT1		AJ310337	MHG6c
				CA847				ANT1		AJ310337	
				CA848				ANT1		AJ310337	
	Giresun-Yavşan stream	40.8291	38.4584	CA842				ANT1		AJ310337	MHG6c
	Gödet Dam	37.1076	33.2918	OYCA70204		AN1		CAR1		AJ310314	MHG6a
				OYCA70206		AN1		CAR1		AJ310314	
				OYCA70207		AN1		CAR1		AJ310314	
	Gödet Dam	37.1076	33.2918	OYCA70208		AN8		CAR8		GU812177	MH6a
				CA1900				CAR1		AJ310314	
				CA1901				CAR1		AJ310314	
				CA1902			CA15	CAR1	ACC	AJ310314	
				CA1903			CA15	CAR8	ACC	GU812177	
	Gökpınar Dam	37.7851	29.1306	CCYZCA20153		AN46		ANT21		GQ902114	MHG6c
				CCYZCA20154		AN46		ANT21		GQ902114	
				CCYZCA20155		AN46		ANT21		GQ902114	
				CCYZCA20156		AN46		ANT21		GQ902114	
				CCYZCA20157		AN46		ANT21		GQ902114	
	Gümüşhane-Akbaba pond	40.1783	39.6521	CA817				ANT1		AJ310337	MHG6c
				CA818				ANT1		AJ310337	

Table 3.2. (continued).

Turkey	Gümüşhane-Akbaba pond	40.1783	39.6521	CA819				ANT1		AJ310337	MHG6c
				CA820				ANT1		AJ310337	
				CA821				ANT1		AJ310337	
	Gümüşhane-Kelkit river	40.1226	39.3737	CA822				ANT1		AJ310337	MHG6c
				CA823				ANT1		AJ310337	
				CA824				ANT1		AJ310337	
				CA825				ANT1		AJ310337	
				CA826				ANT1		AJ310337	
	Lake Işıklı	38.2350	29.9605	CBCA2047		AN17		CAR17		AJ313132	MHG6a
				CBCA2048		AN14		CAR14		AJ313133	
				CBCA2049		AN18		CAR18		GQ902097	
				CBCA2050		AN17		CAR17		AJ313132	
				CBCA2051		AN14		CAR14		AJ313133	
				CBCA2052		AN17		CAR17		AJ313132	
	Iğdır- Tuzluca Aras River	40.0356	43.6790	CA663			AT82	ANT2	HM356084	GQ902107	MHG6c
				CA664			AT82	ANT2	HM356084	GQ902107	
				CA665				ANT2		GQ902107	
				CA666				ANT2		GQ902107	
	Iğdır- Water Channel	39.9513	44.0419	CA667			AT82	ANT2	HM356084	GQ902107	MHG6c
				CA668				ANT2		GQ902107	
				CA669				ANT2		GQ902107	
				CA670				ANT2		GQ902107	
				CA671				ANT2		GQ902107	
	İstanbul	41.1340	28.7533	-	A39	AN26	EU27	ANT1	GU812125	AJ310337	MHG6d
	Istanbul Halkali	41.0432	28.7823	ZISP.6537-Sp.46		RE15				GU812157	MHG1
	Hatay-Deniz	36.0727	35.9508	CA1949			CLW15	CIW11	GU812083	ACC	MHG4

Table 3.2. (continued).

Turkey	Hatay-Deniz	36.0727	35.9508	CA1950				CIW1		AJ313135	MHG4
				CA1951			CLE16	CIE1	ACC	GU812168	MHG5
				CA1952				CIW1		AJ313135	MHG4
				CA1953			CLW5	CIW1	ACC	AJ313135	
				CA1954			CLE12	CIE2	ACC	GU812169	MHG5
	Hatay-Gölbaşı	36.4645	36.4778	CA1955			CLW15	CIW8	GU812083	ACC	MHG4
				CA1956				CIW3		GU812163	
	Hatay-Hassa	36.8449	36.6504	CA1403				CIW1		AJ313135	MHG4
				CA1404			CLE17	CIE9	ACC	ACC	MHG5
				CA1405				CIW1		AJ313135	MHG4
				CA1406			CLW15	CIW11	GU812083	ACC	
				CA1407				CIW1		AJ313135	
	Hatay-İskenderun Erzin	36.8887	36.1370	CA1416			CLW2	CIW2	ACC	GU812162	MHG4
				CA1417			CLW15	CIW10	GU812083	ACC	
	Hatay-İskenderun Sarıseki	36.6653	36.2157	CA1409				CIW1		AJ313135	MHG4
				CA1410			CLE11	CIE2	ACC	GU812169	MHG5
				CA1411			CLW11	CIW3	ACC	GU812163	MHG4
				CA1413				CIW1		AJ313135	
				CA1414				CIE2		GU812169	MHG5
				CA1415			CLW1	CIW2	ACC	GU812162	MHG4
	Hatay Kırıkhan	36.4973	36.4523	OBMB31341		CI9		CIE2		GU812169	MHG5
				OBMB31342		CI9		CIE2		GU812169	
				OBMB31343	CL6	CI10	CLE4	CIE3	GU812085	GU812170	
				OBMB31344		CI8		CIE1		GU812168	
				OBMB31345		CI10		CIE3		GU812170	
				OBMB31346		CI1		CIW1		AJ313135	MHG4

Table 3.2. (continued).

Turkey	Hatay Kırıkhan	36.4973	36.4523	OBMB31347		CI3		CIW3		GU812163	MHG4
	Hatay Reyhanlı	36.2379	36.5689	OBMB31336		CI3		CIW3		GU812163	MHG4
				OBMB31338		CI1		CIW1		AJ313135	
				OBMB31339		CI3		CIW3		GU812163	
				OBMB31340		CI10		CIE3		GU812170	MHG5
	Hatay Tahtalı Dam	36.8515	36.6861	OBMB31348		CI10		CIE3		GU812170	MHG5
				OBMB31349		CI9		CIE2		GU812169	
				OBMB31350		CI1		CIW1		AJ313135	MHG4
	Isparta-Bağıllı	38.1586	31.0825	CA1446			AT45	ANT2	ACC	GQ902107	MHG6c
				CA1447			CA20	CAR14	GU812091	AJ313133	MHG6a
				CA1448				ANT2		GQ902107	MHG6c
				CA1449				CAR1		AJ310314	MHG6a
	Isparta-Sevinçbey district	37.8748	30.7760	CA1885			CA13	CAR7	ACC	GQ902112	MHG6a
				CA1886				CAR7		GQ902112	
				CA1887				CAR7		GQ902112	
				CA1888				CAR7		GQ902112	
				CA1889				CAR1		AJ310314	
	İvriz	37.4408	34.1705	OK42203		AN12		CAR12		GQ902088	MHG6a
				OK42220		AN12		CAR12		GQ902088	
				OK42221		AN12		CAR12		GQ902088	
				OK42222		AN12		CAR12		GQ902088	
	İzmir-Çandarlı Bakırçay	38.9556	27.0100	CA1748				ANT21		GQ902114	MHG6c
				CA1749			AT110	ANT59	GU812104	ACC	
				CA1750			AT97	ANT29	ACC	GU812209	
				CA1751			AT63	ANT52	ACC	ACC	
				CA1752			AT110	ANT21	GU812104	GQ902114	

Table 3.2. (continued).

Turkey	İzmir-Gediz river	38.6599	27.0274	CA1759				ANT21		GQ902114	MHG6c
				CA1761			AT59	ANT2	GU812109	GQ902107	
				CA1762			AT104	ANT21	ACC	GQ902114	
				CA1763				ANT21		GQ902114	
	İzmir-Menemen	38.6955	26.9989	CA1754				ANT21		GQ902114	MHG6c
				CA1755			AT97	ANT29	ACC	GU812209	
				CA1756			AT106	ANT21	GU812103	GQ902114	
	İzmit-Çayırköy lake	40.8134	29.9910	CA1557			AT1	ANT42	GU812111	ACC	MHG6c
				CA1558			AT41	ANT53	ACC	ACC	
				CA1559				ANT1		AJ310337	
				CA1560			AT94	ANT29	ACC	GU812209	
				CA1561			AT4	ANT1	ACC	AJ310337	
	İzmit-Sapanca lake	40.7180	30.1542	CA1552				ANT1		AJ310337	MHG6c
				CA1553			AT5	ANT1	ACC	AJ310337	
				CA1554			AT65	ANT2	ACC	GQ902107	
				CA1555				ANT2		GQ902107	
	Kahramanmaraş-Göksun	37.9970	36.5211	CA1250			CLW15	CIW3	GU812083	GU812163	MHG4
				CA1251				CIW3		GU812163	
				CA1252				CIE3		GU812170	MHG5
				CA1253			CLE2	CIE3	ACC	GU812170	
	Kahramanmaraş-Elbistan Gölpınar	38.1959	37.0636	CA1256			CLE7	CIE3	ACC	GU812170	MHG5
				CA1257			AT2	ANT1	ACC	AJ310337	MHG6c
				CA1258				CIE3		GU812170	MHG5
				CA1259				ANT1		AJ310337	MHG6c
				CA1260				CIE3		GU812170	MHG5
				CA1261				CIE3		GU812170	

Table 3.2. (continued).

Turkey	Kahramanmaraş-Elbistan Gölpınar	38.1959	37.0636	CA1262				ANT1		AJ310337	MHG6c
				CA1263				ANT1		AJ310337	
	Kahramanmaraş-Kumaşır lake	37.5102	36.8983	CA1264				CIE2		GU812169	MHG5
				CA1265			CLE15	CIE2	ACC	GU812169	
				CA1266				CIE3		GU812170	
				CA1268			CLW12	CIW2	ACC	GU812162	MHG4
				CA1269				CIE2		GU812169	MHG5
	Karabük-Cemaller Soğanlı river	41.1313	32.6816	CA965			AT16	ANT44	ACC	ACC	MHG6c
				CA966				ANT33		ACC	
				CA967			AT15	ANT1	ACC	AJ310337	
				CA968				ANT1		AJ310337	
				CA969				ANT1		AJ310337	
	Karabük-Safranbolu Araç river	41.2165	32.7331	CA974				ANT1		AJ310337	MHG6c
				CA975				ANT1		AJ310337	
				CA976				ANT1		AJ310337	
				CA977			AT14	ANT1	ACC	AJ310337	
				CA978			AT1	ANT31	GU812111	ACC	
	Karacaören Dams I-II	37.4031	30.8703	CBCAST327		AN1		CAR1		AJ310314	MHG6a
				CBCAST328		AN1		CAR1		AJ310314	
				CBCAST329		AN1		CAR1		AJ310314	
				CBCAST3210		AN1		CAR1		AJ310314	
				CBCAST3211		AN1		CAR1		AJ310314	
				CBCAST3212		AN1		CAR1		AJ310314	
				CBCAST3213		AN1		CAR1		AJ310314	
				CBCA3241		AN1		CAR1		AJ310314	
				CBCA3242		AN2		CAR2		GU812173	

Table 3.2. (continued).

Turkey	Karacaören Dams I-II	37.4031	30.8703	OBBKCA32103		AN17		CAR17		AJ313132	MHG6a
				OBBKCA32104		AN1		CAR1		AJ310314	
				OBBKCA32105		AN1		CAR1		AJ310314	
				OBBKCA32106		AN1		CAR1		AJ310314	
				OBBKCA32107		AN1		CAR1		AJ310314	
				OBBKCA32108		AN1		CAR1		AJ310314	
	Karaman-Belpınarı	36.8333	32.5803	CA1909			CA19	CAR1	ACC	AJ310314	MHG6a
				CA1910				CAR1		AJ310314	
				CA1911				CAR1		AJ310314	
				CA1912				CAR1		AJ310314	
				CA1913				CAR1		AJ310314	
	Karaman-Yeşildere	37.2047	33.4035	CA1905				CAR8		GU812177	MHG6a
				CA1906			CA15	CAR8	ACC	GU812177	
				CA1907			CA15	CAR1	ACC	AJ310314	
				CA1908				CAR1		AJ310314	
	Kars-Arpaçay Akçalar	40.7735	43.2952	CA725				EUP12		AJ310313	MHG6d
				CA726				EUP12		AJ310313	
				CA727				EUP12		AJ310313	
				CA728				EUP12		AJ310313	
				CA729				EUP13		ACC	
				CA730				EUP17		ACC	
	Kars-Digor Pazarcık	40.5189	43.2690	CA717				ANT2		GQ902107	MHG6c
				CA718				ANT2		GQ902107	
				CA719				ANT2		GQ902107	
				CA720				ANT2		GQ902107	
	Kars-Selim	40.4702	42.7904	CA721				EUP17		ACC	MHG6d

Table 3.2. (continued).

Turkey	Kars-Selim	40.4702	42.7904	CA722				EUP12		AJ310313	MHG6d
				CA723				EUP12		AJ310313	
				CA724				EUP12		AJ310313	
	Kastamonu-Araç River	41.2389	33.3224	CA959				ANT1		AJ310337	MHG6c
				CA960			AT1	ANT1	GU812111	AJ310337	
				CA961				ANT1		AJ310337	
				CA963				ANT1		AJ310337	
	Kastamonu-Beyler dam	41.6903	33.8119	CA952				ANT1		AJ310337	MHG6c
				CA953				ANT1		AJ310337	
	Kastamonu-Beyler dam	41.6903	33.8119	CA954			AT44	ANT2	ACC	GQ902107	MHG6c
				CA955			AT57	ANT1	ACC	AJ310337	
	Kastamonu-Karaçomak dam	41.2852	33.7372	CA939				ANT1		AJ310337	MHG6c
				CA940			AT20	ANT1	ACC	AJ310337	
				CA941			AT39	ANT44	ACC	ACC	
				CA942			AT1	ANT49	GU812111	ACC	
				CA943				ANT1		AJ310337	
	Kastamonu-Taşlık Dam	41.4018	33.6963	CA945			AT43	ANT2	ACC	GQ902107	MHG6c
				CA946			AT21	ANT1	ACC	AJ310337	
				CA947				ANT1		AJ310337	
				CA948				ANT1		AJ310337	
				CA949				ANT1		AJ310337	
	Kaş	36.2769	29.6839	CA07217	A9	AN21	CE5	CER1	GU812096	GU812181	MHG6b
				CA07218		AN23		CER3		GQ902087	
				CA07219		AN23		CER3		GQ902087	
				ZFMK21047	A7	AN23	CE6	CER3	GU812094	GQ902087	
				ZFMK29521		AN23		CER3		GQ902087	

Table 3.2. (continued).

Turkey	Kayseri	38.7565	35.4229	DCA38313		AN26		ANT1		AJ310337	MHG6c
				DCA38314		AN29		ANT4		GU812186	
				DCA38315		AN26		ANT1		AJ310337	
				DCA38316		AN26		ANT1		AJ310337	
				DCA38317		AN30		ANT5		GU812187	
	Kayseri-Engir lake	38.8111	35.5915	CA1151			AT13	ANT1	ACC	AJ310337	MHG6c
				CA1152				ANT4		GU812186	
				CA1154				ANT1		AJ310337	
				CA1155				ANT1		AJ310337	
				CA1156				ANT1		AJ310337	
	Kayseri-Pınarbaşı	38.6618	36.104	CA1468			AT1	ANT1	GU812111	AJ310337	MHG6c
				CA1469				ANT1		AJ310337	
				CA1471				ANT1		AJ310337	
	Kayseri-Pınarbaşı	38.6618	36.104	CA1472				ANT1		AJ310337	MHG6c
				CA1473				ANT1		AJ310337	
	Kayseri-Sultansazlığı	38.3897	35.3657	CA1157				CAR12		GQ902088	MHG6a
				CA1158				ANT1		AJ310337	MHG6c
				CA1159				ANT1		AJ310337	
				CA1160				ANT1		AJ310337	
				CA1161				ANT1		AJ310337	
				CA1162				ANT1		AJ310337	
				CA1163				ANT1		AJ310337	
				CA1164				ANT1		AJ310337	
	Kayseri-Yahyalı	38.1348	35.3641	CA1165				CAR12		GQ902088	MHG6a
				CA1166				ANT2		GQ902107	MHG6c
				CA1167				ANT2		GQ902107	

Table 3.2. (continued).

Turkey	Kayseri-Yahyalı	38.1348	35.3641	CA1168				ANT40		ACC	MHG6c
				CA1169				ANT1		AJ310337	
				CA1170				ANT40		ACC	
	Kayseri-Zamantı Water	38.0345	35.5407	CA1171			AT2	ANT1	ACC	AJ310337	
				CA1172			AT26	ANT4	ACC	GU812186	
				CA1173				ANT2		GQ902107	
				CA1174				ANT2		GQ902107	
				CA1175			CLW3	CIW3	ACC	GU812163	MHG4
				CA1176				ANT1		AJ310337	MHG6c
				CA1177				ANT1		AJ310337	
				CA1178				ANT2		GQ902107	
				CA1179				ANT1		AJ310337	
	Kemer	37.4627	30.1118	MHSACA15137		AN46		ANT21		GQ902114	MHG6c
				MHSACA15138		AN1		CAR1		AJ310314	MHG6a
				MHSACA15139		AN7		CAR7		GQ902112	
				MHSACA15140		AN1		CAR1		AJ310314	
				MHSACA15141		AN1		CAR1		AJ310314	
	Kemer	37.4627	30.1118	MHSACA15142		AN1		CAR1		AJ310314	MHG6a
				MHSACA15143		AN1		CAR1		AJ310314	
	Kırıkkale-Hasandede Kızılırmak	38.7406	33.4879	CA1238				ANT1		AJ310337	MHG6c
				CA1239				ANT1		AJ310337	
				CA1242				ANT1		AJ310337	
				CA1243				ANT1		AJ310337	
	Kırıkkale-Yahşiyan Kızılırmak	39.8861	33.4146	CA1244				ANT1		AJ310337	MHG6c
				CA1245				ANT1		AJ310337	
				CA1246				ANT1		AJ310337	

Table 3.2. (continued).

Turkey	Kırıkkale-Yahşiyan Kızılırmak	39.8861	33.4146	CA1248				ANT1		AJ310337	MHG6c
	Kırklareli-Eriklice stream	41.7576	27.1814	CA1488		RE1				AJ310338	MHG1
				CA1489		RE1				AJ310338	
				CA1490		RE16				ACC	
				CA1491		RE1				AJ310338	
				CA1492		RE1				AJ310338	
				CA1493		RE1				AJ310338	
	Kırklareli-İnece stream	41.6836	27.0731	CA1494		RE1					MHG1
				CA1495		RE1					
				CA1496		RE1					
				CA1497			AT56	ANT10	GU812113	GU812192	MHG6c
				CA1498		RE1					MHG1
	Kırklareli-Karakoç pond	41.7817	27.2171	CA1499		RE1				AJ310338	MHG1
				CA1500		RE1				AJ310338	
				CA1501		RE1				AJ310338	
	Kırklareli-Şeytandere	41.7104	27.2627	CA1484				ANT10		GU812192	MHG6c
				CA1485		RE1				AJ310338	MHG1
				CA1486		RE1				AJ310338	
				CA1487			AT53	ANT10	ACC	GU812192	MHG6c
	Kırşehir-Çuvın	39.3168	34.1238	CA1141				ANT4		GU812186	MHG6c
				CA1142			AT1	ANT1	GU812111	AJ310337	
	Kırşehir-Çuvın	39.3168	34.1238	CA1144				ANT1		AJ310337	MHG6c
				CA1145			AT26	ANT4	ACC	GU812186	
	Kırşehir-Güneykent	39.0988	34.1600	CA1128				ANT1		AJ310337	MHG6c
				CA1129			AT1	ANT1	GU812111	AJ310337	
				CA1130			AT26	ANT4	ACC	GU812186	

Table 3.2. (continued).

Turkey	Kırşehir-Güneykent	39.0988	34.1600	CA1131				ANT1		AJ310337	MHG6c
	Kırşehir-Kışlapınar	39.2262	34.1338	CA1146			AT1	ANT1	GU812111	AJ310337	MHG6c
				CA1147				ANT1		AJ310337	
				CA1149				ANT1		AJ310337	
	Kırşehir-Sıddıklı	39.1007	33.9073	CA1135			AT1	ANT1	GU812111	AJ310337	MHG6c
				CA1136				ANT1		AJ310337	
				CA1137				ANT1		AJ310337	
				CA1138				ANT1		AJ310337	
	Kıyıköy	41.7038	28.0514	Hotz18003		AN38		ANT13		GU812195	MHG6c
				Hotz18004		AN38		ANT13		GU812195	
				Hotz18005		AN38		ANT13		GU812195	
				Hotz18006		AN35		ANT10		GU812192	
	Kilis	36.7641	37.2540	OB79321		CI9		CIE2		GU812169	MHG5
				OB79322		CI10		CIE3		GU812170	
				OB79323		AN59		EUP5		AJ310312	MHG6d
				OB79324		CI1		CIW1		AJ313135	MHG4
				OB79325		AN55		EUP1		AJ310313	MHG6d
				OB79326		AN55		EUP1		AJ310313	
	Kilis-Gaziantep road	36.8106	37.3095	OBMB79327		CI10		CIE3		GU812170	MHG5
				OBMB79328		AN59		EUP5		AJ310312	MHG6d
				OBMB79329		CI10		CIE3		GU812170	MHG5
				OBMB79330		CI10		CIE3		GU812170	
				OBMB79331		CI11		CIE4		GU812171	
				OBMB79335	CL5	CI10	CLE3	CIE3	GU812084	GU812170	
	Kilis-Polateli	36.7853	37.0588	CA1395			CLE2	CIE7	ACC	ACC	MHG5
				CA1396			CLE12	CIE2	ACC	GU812169	

Table 3.2. (continued).

Turkey	Kilis-Polateli	36.7853	37.0588	CA1397			CLE6	CIE3	ACC	GU812170	MHG5
				CA1398				CIE2		GU812169	
				CA1399				CIE3		GU812170	
				CA1400			CLW15	CIW2	GU812083	GU812162	MHG4
				CA1401				CIE3		GU812170	MHG5
	Kilis-Töreli Çapalı road	36.8549	37.3414	CA1390			CLW6	CIW1	ACC	AJ313135	MHG4
				CA1391				CIW1		AJ313135	
				CA1393			EU13	EUP1	ACC	AJ310313	MHG6d
				CA1394			CLE2	CIE3	ACC	GU812170	MHG5
	Kilis-Üçgöz	36.8045	37.0868	CA1957				CIE2		GU812169	MHG5
				CA1959				EUP1		AJ310313	MHG6d
	Kilis-Üçpınar	36.8669	36.9328	CA1960				CIE3		GU812170	MHG6d
				CA1961			CLE5	CIE6	ACC	ACC	
				CA1962				CIE2		GU812169	
				CA1963				CIE2		GU812169	
				CA1964				CIW1		AJ313135	MHG4
	Konya-Mehmetali dam	37.2124	32.6354	CA1463				CAR1		AJ310314	MHG6a
				CA1464				CAR1		AJ310314	
				CA1465			CA19	CAR1	ACC	AJ310314	
				CA1466			CA3	CAR12	ACC	GQ902088	
				CA1467			AT42	ANT2	ACC	GQ902107	MHG6c
	Korkuteli	36.9918	29.5279	VDBKCA07125		AN1		CAR1		AJ310314	MHG6a
				VDBKCA07126		AN46		ANT21		GQ902114	MHG6c
				VDBKCA07127		AN1		CAR1		AJ310314	MHG6a
				VDBKCA07128		AN7		CAR7		GQ902112	
				VDBKCA07129		AN17		CAR17		AJ313132	

Table 3.2. (continued).

Turkey	Korkuteli	36.9918	29.5279	VDBKCA07130		AN17		CAR17		AJ313132	MHG6a
				VDBKCA07131		AN1		CAR1		AJ310314	
	Kovada	37.6325	30.8641	CBCAST3214		AN1		CAR1		AJ310314	MHG6a
				CBCAST3215		AN27		ANT2		GQ902107	MHG6c
				CBCAST3216		AN14		CAR14		AJ313133	MHG6a
				OAOBBKCA1593		AN1		CAR1		AJ310314	
				OAOBBKCA1594		AN1		CAR1		AJ310314	
				OAOBBKCA1596		AN1		CAR1		AJ310314	
				OAOBBKCA1597		AN1		CAR1		AJ310314	MHG6a
				OAOBBKCA1598		AN3		CAR3		GU812174	
				OAOBBKCA1599		AN1		CAR1		AJ310314	
				OAOBBKCA1593101		AN1		CAR1		AJ310314	
				OAOBBKCA1593102		AN1		CAR1		AJ310314	
	Kütahya-Enne dam	39.4688	29.8657	CA1685			AT110	ANT61	GU812104	ACC	MHG6c
				CA1686			AT49	ANT10	ACC	GU812192	
				CA1687			AT110	ANT21	GU812104	GQ902114	
				CA1688				ANT61		ACC	
	Kütahya-Koçak stream	39.3090	29.9753	CA1697			AT110	ANT21	GU812104	GQ902114	MHG6c
				CA1698			AT45	ANT2	ACC	GQ902107	
				CA1699			AT110	ANT61	GU812104	ACC	
				CA1700				ANT21		GQ902114	
				CA1701				ANT21		GQ902114	
	Kütahya-Porsuk dam	39.5740	30.0918	CA1705			AT54	ANT55	ACC	ACC	MHG6c
				CA1706			AT41	ANT2	ACC	GQ902107	
				CA1707			AT56	ANT10	GU812113	GU812192	
				CA1708			AT110	ANT21	GU812104	GQ902114	

Table 3.2. (continued).

Turkey	Kütahya-Söğütözü stream	39.3374	29.9342	CA1690			AT50	ANT10	ACC	GU812192	MHG6c
				CA1691			AT111	ANT21	ACC	GQ902114	
				CA1692				ANT21		GQ902114	
				CA1693				ANT61		ACC	
				CA1694			AT41	ANT2	ACC	GQ902107	
	Malatya	38.4276	38.3505	SO44285		AN59		EUP5		AJ310312	MHG6d
				SO44286		AN59		EUP5		AJ310312	
	Malatya-Elemendik lake	38.3229	38.1551	CA552			EU33	EUP5	ACC	AJ310312	MHG6d
				CA553				EUP5		AJ310312	
				CA554				ANT4		GU812186	MHG6c
				CA555				EUP5		AJ310312	MHG6d
				CA556				EUP5		AJ310312	
				CA557			AT25	ANT4	ACC	GU812186	MHG6c
	Malatya-Karakaya dam	38.4882	38.3499	CA547				EUP5		AJ310312	MHG6d
				CA548			AT1		GU812111		MHG6c
				CA549				ANT4		GU812186	
				CA550				EUP5		AJ310312	MHG6d
				CA551			EU33	EUP5	ACC	AJ310312	
	Malatya-near Sultansuyu dam	38.3121	38.0434	CA558			AT1	ANT1	GU812111	AJ310337	MHG6c
				CA559			AT26	ANT4	ACC	GU812186	
				CA560				ANT4		GU812186	
				CA561			EU36	EUP5	GU812122	AJ310312	MHG6d
	Malatya-Oluklu district	38.2406	37.9964	CA562				ANT4		GU812186	MHG6c
				CA563				EUP5		AJ310312	MHG6d
				CA564				ANT4		GU812186	MHG6c
				CA565				ANT4		GU812186	

Table 3.2. (continued).

Turkey	Malatya-Oluklu district	38.2406	37.9964	CA566				EUP5		AJ310312	MHG6d
	Manisa	38.6110	27.4483	OA45274		AN49		ANT24		GU812205	MHG6c
				OA45275		AN46		ANT21		GQ902114	
				OA45276		AN46		ANT21		GQ902114	
				OA45277		AN53		ANT28		GU812208	
				OA45278		AN46		ANT21		GQ902114	
				OA45279		AN46		ANT21		GQ902114	
				OA45280		AN46		ANT21		GQ902114	
				OA45281		AN46		ANT21		GQ902114	
	Manisa	38.6110	27.4483	OA45282		AN46		ANT21		GQ902114	MHG6c
	Manisa City Forest	38.6021	27.3867	CA1764			AT91	ANT29	GU812101	GU812209	MHG6c
				CA1765			AT109	ANT21	ACC	GQ902114	
				CA1766				ANT21		GQ902114	
				CA1767				ANT21		GQ902114	
				CA1768				ANT21		GQ902114	
	Manisa-Köseler pond	38.8460	27.2006	CA1780				ANT21		GQ902114	MHG6c
				CA1781				ANT21		GQ902114	
				CA1782				ANT21		GQ902114	
				CA1783				ANT21		GQ902114	
				CA1784			AT110	ANT60	GU812104	ACC	
	Manisa-Örselli pond	38.8698	27.2620	CA1774				ANT21		GQ902114	MHG6c
				CA1775				ANT21		GQ902114	
				CA1776			AT100	ANT21	ACC	GQ902114	
				CA1777			AT51	ANT57	ACC	ACC	
				CA1778			AT52	ANT10	GU812114	GU812192	
	Manisa-Siyekli pond	38.7886	27.2559	CA1769			AT110	ANT21	GU812104	GQ902114	MHG6c

Table 3.2. (continued).

Turkey	Manisa-Siyekli pond	38.7886	27.2559	CA1770			AT91	ANT29	GU812101	GU812209	MHG6c
				CA1771				ANT29		GU812209	
				CA1772				ANT21		GQ902114	
				CA1773				ANT21		GQ902114	
	Mardin-Bülbül village	37.3219	40.8364	CA1319			EU33	EUP5	ACC	AJ310312	MHG6d
	Mardin-Kızıltepe	37.1970	40.2767	CA1313			EU36	EUP5	GU812122	AJ310312	MHG6d
				CA1314				EUP5		AJ310312	
				CA1315				EUP5		AJ310312	
	Mardin-Mazıdağ	37.4622	40.6169	CA1326				EUP5		AJ310312	MHG6d
				CA1327			EU36	EUP22	GU812122	ACC	
				CA1328				EUP5		AJ310312	
				CA1329			EU36	EUP5	GU812122	AJ310312	
	Mardin-Mazıdağ	37.4622	40.6169	CA1330				EUP5		AJ310312	MHG6d
	Mardin-Savur road	37.4406	40.8553	CA1320			EU28	EUP5	ACC	AJ310312	MHG6d
				CA1321				EUP5		AJ310312	
				CA1322				EUP5		AJ310312	
				CA1323				EUP5		AJ310312	
				CA1324				EUP5		AJ310312	
				CA1325				EUP5		AJ310312	
	Marmaris	36.8467	28.2879	AKCA48209		AN50		ANT25		AJ313131	MHG6c
				AKCA48210		AN51		ANT26		GU812206	
				AKCA48211		AN51		ANT26		GU812206	
				AKCA48212		AN52		ANT27		GU812207	
				Hotz16812		AN51		ANT26		GU812206	
	Mersin	36.7969	34.6019	SOCA33224		CI3		CIW3		GU812163	MHG4
				SOCA33225		CI3		CIW3		GU812163	

Table 3.2. (continued).

Turkey	Mersin	36.7969	34.6019	SOCA33226		CI3		CIW3		GU812163	MHG4
				SOCA33227		CI3		CIW3		GU812163	
				SOCA33228		CI1		CIW1		AJ313135	
	Mersin-Erdemli	36.5930	34.2873	CA1429				CIW8		ACC	MHG4
				CA1430			CLW4	CIW3	ACC	GU812163	
				CA1431			CLW4	CIW3	ACC	GU812163	
	Mersin-Mut Bice stream	36.5896	33.2850	CA1915				CAR1		AJ310314	MHG6a
	Mersin-Mut Bucakışla stream	36.6313	33.3675	CA1916			CA16	CAR1	GU812092	AJ310314	MHG6a
				CA1917				CAR1		AJ310314	
				CA1918				CAR1		AJ310314	
				CA1919				CAR1		AJ310314	
				CA1921				CAR1		AJ310314	
	Mersin-Yenice	36.9673	35.0305	CA1424				CIW3		GU812163	MHG4
				CA1425				CIW3		GU812163	
				CA1426				CIW1		AJ313135	
	Mersin-Yenice	36.9673	35.0305	CA1427			CLW15	CIW3	GU812083	GU812163	MHG4
				CA1428			CLW15	CIW1	GU812083	AJ313135	
	Muğla-Dalaman Tersakan	36.7794	28.8252	CA1845			CA11	CAR17	ACC	AJ313132	MHG6a
				CA1846			CE7	CER3	ACC	GQ902087	MHG6b
				CA1847				CAR17		AJ313132	MHG6a
				CA1848				CAR17		AJ313132	
				CA1849				ANT25		AJ313131	MHG6c
				CA1850			AT83	ANT25	GU812107	AJ313131	
	Muğla-Girdev plateau	36.7007	29.6509	CA1851			CA7	CAR20	ACC	GQ902086	MHG6a
				CA1852				CAR17		AJ313132	
				CA1853			CE4	CER3	ACC	GQ902087	MHG6b

Table 3.2. (continued).

Turkey	Muğla-Girdev plateau	36.7007	29.6509	CA1854			CA13	CAR1	ACC	AJ310314	MHG6a
				CA1855				CAR20		GQ902086	
				CA1856			CA12	CAR17	ACC	AJ313132	
				CA1857				CAR20		GQ902086	
				CA1858				CAR17		AJ313132	
				CA1859				CAR20		GQ902086	
	Muğla-Köyceğiz Zaferler village	36.9718	28.6299	CA1840			CA11	CAR17	ACC	AJ313132	MHG6a
				CA1841			CE3	CER1	ACC	GU812181	MHG6b
				CA1842				ANT25		AJ313131	MHG6c
				CA1843			AT84	ANT62	ACC	ACC	
				CA1844				ANT25		AJ313131	
	Muğla-Ula Nannan stream	37.0129	28.5105	CA1836			AT83	ANT25	GU812107	AJ313131	MHG6c
				CA1837			AT88	ANT26	ACC	GU812206	
				CA1838				ANT26		GU812206	
				CA1839				ANT26		GU812206	
	Muğla-Yatağan Dipsiz stream	37.3750	28.0916	CA1826				ANT21		GQ902114	MHG6c
				CA1827				ANT21		GQ902114	
				CA1828			AT101	ANT21	ACC	GQ902114	
				CA1829			AT87	ANT25	ACC	AJ313131	
	Muğla-Yemişendere	37.2516	28.5810	CA1830			AT87	ANT63	ACC	ACC	MHG6c
				CA1831			AT102	ANT21	ACC	GQ902114	
				CA1832				ANT21		GQ902114	
				CA1833				ANT21		GQ902114	
				CA1834				ANT63		ACC	
	Muş-Çizmeburnu	38.7159	41.6205	CA604			EU24	EUP5	ACC	AJ310312	MHG6d
				CA605				EUP14		ACC	

Table 3.2. (continued).

Turkey	Muş-Çizmeburnu	38.7159	41.6205	CA606			EU32	EUP5	ACC	AJ310312	MHG6d
				CA607				EUP5		AJ310312	
				CA608				EUP5		AJ310312	
				CA609				EUP5		AJ310312	
				CA610				EUP5		AJ310312	
	Muş-Murat River	38.9613	41.5115	CA600			AT81	ANT2	ACC	GQ902107	MHG6c
				CA601				EUP5		AJ310312	MHG6d
				CA602				EUP15		ACC	
				CA603				EUP15		ACC	
	Muş-Tigem Drenaj Channel	38.8017	41.4987	CA596				EUP5		AJ310312	MHG6d
				CA597			AT81	ANT2	ACC	GQ902107	MHG6c
				CA598				EUP5		AJ310312	MHG6d
				CA599			EU31	EUP5	ACC	AJ310312	
	Muş-Tigem Water Channel	38.7862	41.5969	CA611			EU32	EUP5	ACC	AJ310312	MHG6c
				CA612				EUP5		AJ310312	
				CA613				EUP5		AJ310312	
				CA615				EUP5		AJ310312	
				CA616				EUP5		AJ310312	
	Narlı	37.3322	37.0425	OBMBCA46364	CL8	CI9	CLE10	CIE2	GU812087	GU812169	MHG5
				OBMBCA46366		CI10		CIE3		GU812170	
				OBMBCA46367		CI3		CIW3		GU812163	MHG4
				OBMBCA46369		CI10		CIE3		GU812170	MHG5
				OBMBCA46370		CI10		CIE3		GU812170	
				OBMBCA46371		CI6		CIW6		GU812166	MHG4
				OBMBCA46372		CI12		CIE5		GU812172	MHG5
	National Observatory	36.8293	30.3407	VD07132		AN1		CAR1		AJ310314	MHG6a

Table 3.2. (continued).

Turkey	National Observatory	36.8293	30.3407	VD07134		AN1		CAR1		AJ310314	MHG6a
				VD07135		AN1		CAR1		AJ310314	
				VD07136		AN1		CAR1		AJ310314	
	Nevşehir-Avanos Kızılırmak	38.7174	34.8575	CA1234			AT26	ANT4	ACC	GU812186	MHG6c
				CA1235			AT41	ANT2	ACC	GQ902107	
	Nevşehir-Nar Ilıca river	38.6383	34.7089	CA1229				ANT1		AJ310337	MHG6c
				CA1230			AT1	ANT1	GU812111	AJ310337	
	Nevşehir-Gülşehir Kızılırmak	38.7564	34.6513	CA1236			AT41	ANT2	ACC	GQ902107	MHG6c
				CA1237				ANT5		GU812187	
	Nevşehir-Ürgüp	38.5741	34.9157	CA1231			AT1	ANT1	GU812111	AJ310337	MHG6c
				CA1232				ANT4		GU812186	
				CA1233				ANT4		GU812186	
	Niğde-Çamardı	37.9608	34.3572	CA1181			AT1	ANT1	GU812111	AJ310337	MHG6c
				CA1182				ANT1		AJ310337	
				CA1183				ANT1		AJ310337	
				CA1185				ANT1		AJ310337	
				CA1186				ANT1		AJ310337	
				CA1187				ANT1		AJ310337	
	Niğde-Çiftlik	38.1779	34.4629	CA1195				CAR12		GQ902088	MHG6a
				CA1196				CAR12		GQ902088	
				CA1197			AT5	ANT1	ACC	AJ310337	MHG6c
				CA1198				CIE3		GU812170	MHG5
				CA1199				ANT1		AJ310337	MHG6c
				CA1200				ANT1		AJ310337	
				CA1201				ANT1		AJ310337	
				CA1202				ANT1		AJ310337	

Table 3.2. (continued).

Turkey	Niğde-Çiftlik	38.1779	34.4629	CA1203				ANT1		AJ310337	MHG6c
				CA1204				ANT1		AJ310337	
	Niğde-15km to Ulukışla	37.6195	34.5366	CA1193				ANT1		AJ310337	MHG6c
	Ordu-Civil Stream	40.9733	37.9030	CA858				ANT1		AJ310337	MHG6c
				CA859				ANT1		AJ310337	
				CA860				ANT1		AJ310337	
				CA861				ANT46		ACC	
				CA862			AT1	ANT1	GU812111	AJ310337	
	Ordu-Fatsa	41.0753	37.4413	CA871				ANT1		AJ310337	MHG6c
				CA872				ANT1		AJ310337	
				CA873				ANT1		AJ310337	
				CA874			AT1	ANT1	GU812111	AJ310337	
				CA875				ANT1		AJ310337	
	Ordu-Perşembe	41.0251	37.8032	CA867				ANT1		AJ310337	MHG6c
				CA868			AT1	ANT1	GU812111	AJ310337	
				CA869				ANT1		AJ310337	
				CA870			AT9	ANT1	ACC	AJ310337	
	Osmaniye-Aslantaş dam	37.2769	36.2744	CA1933			CLW14	CIW9	ACC	ACC	MHG4
				CA1934				CIW3		GU812163	
				CA1935			CLE14	CIE8	ACC	ACC	MHG5
				CA1936				CIW3		GU812163	MHG4
				CA1937			CLE1	CIE3	ACC	GU812170	MHG5
	Osmaniye-Boru river	37.1780	36.4856	CA1943			CLE8	CIE8	ACC	ACC	MHG5
				CA1944			CLE12	CIE2	ACC	GU812169	
				CA1945				CIE8		ACC	
	Özbaşı	37.6178	27.4327	Hotz17510	A17	AN46	AT110	ANT21	GU812104	GQ902114	MHG6c
				Hotz17511	A17	AN46	AT110	ANT21	GU812104	GQ902114	

Table 3.2. (continued).

Turkey	Özbaşı	37.6178	27.4327	Hotz17716	A17	AN46	AT110	ANT21	GU812104	GQ902114	MHG6c
	Omerli	41.1003	29.4009	Hotz16630		AN31		ANT6		GU812188	MHG6c
	Pazarcık	37.2819	37.1249	OBMBCA46354		CI9		CIE2		GU812169	MHG5
				OBMBCA46355		CI9		CIE2		GU812169	
				OBMBCA46356	CL7	CI9	CLE9	CIE2	GU812086	GU812169	
				OBMBCA46358		CI10		CIE3		GU812170	
	Rize	41.0110	40.5792	BAYDCA53253		AN26		ANT1		AJ310337	MHG6c
				AA53287		AN26		ANT1		AJ310337	
				AA53288		AN26		ANT1		AJ310337	
				CA771			AT1	ANT39	GU812111	ACC	
	Rize-Çiftekavak	41.0283	40.4858	CA779				ANT1		AJ310337	MHG6c
				CA780				ANT1		AJ310337	
	Rize-Hemşin Stream	41.1554	40.9012	CA769			AT71	ANT2	ACC	GQ902107	MHG6c
	Samsun	41.3621	36.2169	YCDC55244		AN26		ANT1		AJ310337	MHG6c
				YCDC55245		AN26		ANT1		AJ310337	
				YCDC55246		AN26		ANT1		AJ310337	
				YCDC55247		AN26		ANT1		AJ310337	
	Samsun-Bafra	41.5167	36.0158	CA890				ANT1		AJ310337	MHG6c
				CA891				ANT1		AJ310337	
				CA892			AT1	ANT1	GU812111	AJ310337	
				CA893				ANT1		AJ310337	
	Samsun-Kavak	41.1567	36.0927	CA897				ANT1		AJ310337	MHG6c
				CA898				ANT1		AJ310337	
				CA899			AT28	ANT1	ACC	AJ310337	
				CA900				ANT1		AJ310337	
	Samsun-19 Mayıs	41.4674	36.0993	CA884				ANT1		AJ310337	MHG6c

Table 3.2. (continued).

Turkey	Samsun-19 Mayıs	41.4674	36.0993	CA886			AT1	ANT1	GU812111	AJ310337	MHG6c
				CA887			AT1	ANT1	GU812111	AJ310337	
				CA888				ANT1		AJ310337	
	Samsun-Tekkeköy	41.2126	36.4790	CA878				ANT1		AJ310337	MHG6c
				CA879				ANT1		AJ310337	
				CA880				ANT1		AJ310337	
				CA881			AT11	ANT1		AJ310337	
	Seydişehir	37.4557	31.8156	CBCAST421		AN27		ANT2		GQ902107	MHG6c
				SGCA42199		AN27		ANT2		GQ902107	
				SGCA42201		AN12		CAR12		GQ902088	MHG6a
				SGCA42202		AN17		CAR17		AJ313132	
				CA1458			CA4	CAR12	ACC	GQ902088	
				CA1459			CA1	CAR12	GU812088	GQ902088	
				CA1460				ANT1		AJ310337	MHG6c
	Seydişehir	37.4557	31.8156	CA1461			CA6	CAR1	ACC	AJ310314	MHG6a
	Siirt-Başyurt river	37.9726	41.7806	CA1372			EU33	EUP5	ACC	AJ310312	MHG6d
				CA1373				EUP5		AJ310312	
				CA1374				EUP5		AJ310312	
				CA1375				EUP5		AJ310312	
	Siirt-Kezer river	37.9610	41.8573	CA1378				EUP5		AJ310312	MHG6d
				CA1379			EU29	EUP15	ACC	ACC	
				CA1380			EU30	EUP5	ACC	AJ310312	
				CA1383				EUP5		AJ310312	
				CA1384				EUP15		ACC	
	Silifke	36.3130	33.9595	OBMB33257		AN1		CAR1		AJ310314	MHG6a
				OBMB33258		AN4		CAR4		GU812175	

Table 3.2. (continued).

Turkey	Silifke	36.3130	33.9595	OBMB33259		AN1		CAR1		AJ310314	MHG6a
				OBMB33260		AN1		CAR1		AJ310314	
				OBMB33261		CI1		CIW1		AJ313135	MHG4
				OBMB33263		AN1		CAR1		AJ310314	MHG6a
				OBMB33264		AN1		CAR1		AJ310314	
				OBMB33265		CI3		CIW3		GU812163	MHG4
				OBMB33266		AN1		CAR1		AJ310314	MHG6a
				OBMB33267		AN1		CAR1		AJ310314	
				OBMB33268		AN1		CAR1		AJ310314	
				OBMB33269		AN1		CAR1		AJ310314	
				OBMB33270		AN1		CAR1		AJ310314	
				OBMB33271		AN1		CAR1		AJ310314	
				OBMB33272		AN1		CAR1		AJ310314	
				OBMB33273		AN1		CAR1		AJ310314	
				Hotz19394	A5	AN1	CA16	CAR1	GU812092	AJ310314	
				Hotz19400	A5	AN1	CA16	CAR1	GU812092	AJ310314	
	Sinop-Ayancık	41.9483	34.7749	CA925				ANT1		AJ310337	MHG6c
				CA926				ANT1		AJ310337	
	Sinop-Ayancık	41.9483	34.7749	CA927			AT18	ANT1	ACC	AJ310337	MHG6c
	Sinop-Gerze	41.8567	35.0999	CA930			AT32	ANT34	ACC	ACC	MHG6c
				CA931				ANT1		AJ310337	
				CA932			AT18	ANT1	ACC	AJ310337	
				CA933			AT3	ANT33	ACC	ACC	
				CA934				ANT34		ACC	
	Sinop-Erfelek Çobanlar	41.9543	35.0196	CA920			AT6	ANT1	ACC	AJ310337	MHG6c
				CA921				ANT1		AJ310337	

Table 3.2. (continued).

Turkey	Sinop-Erfelek Çobanlar	41.9543	35.0196	CA922				ANT1		AJ310337	MHG6c
				CA923				ANT1		AJ310337	
	Sinop-Kabalı village	41.8468	35.0503	CA936				ANT1		AJ310337	MHG6c
				CA937				ANT1		AJ310337	
				CA938				ANT1		AJ310337	
	Sivas-Hafik lake	39.8727	37.3825	CA1090				ANT4		GU812186	MHG6c
				CA1091				ANT4		GU812186	
				CA1092			AT1	ANT1	GU812111	AJ310337	
				CA1093				ANT1		AJ310337	
	Sivas-Kızılırmak	39.7154	37.0117	CA1100				ANT1		AJ310337	MHG6c
				CA1101				ANT4		GU812186	
				CA1102				ANT1		AJ310337	
				CA1103				ANT1		AJ310337	
	Sivas-Tecer river	39.6922	37.0034	CA1084				ANT4		GU812186	MHG6c
				CA1085				ANT4		GU812186	
				CA1086				ANT1		AJ310337	
				CA1087			AT1	ANT1	GU812111	AJ310337	
				CA1088			AT24	ANT4	ACC	GU812186	
	Sivas-Tödürge lake	39.8713	37.6068	CA1096				ANT4		GU812186	MHG6c
				CA1097			AT26	ANT4	ACC	GU812186	
				CA1098				ANT1		AJ310337	
				CA1099				ANT1		AJ310337	
	Sorgun Dam	38.6555	29.3386	CBCA6444		AN46		ANT21		GQ902114	MHG6c
				CBCA6445		AN46		ANT21		GQ902114	
				CBCA6446		AN46		ANT21		GQ902114	
	Şanlıurfa-Bozova	37.3588	38.5284	CA1300				EUP5		AJ310312	MHG6d

Table 3.2. (continued).

Turkey	Şanlıurfa-Bozova	37.3588	38.5284	CA1301				EUP6		GU812213	MHG6d
				CA1302			EU25	EUP7	GU812124	ACC	
				CA1303				EUP21		ACC	
				CA1304				EUP5		AJ310312	
				CA1305				EUP5		AJ310312	
	Şanlıurfa-Harran road	37.1488	38.9681	CA1294				EUP5		AJ310312	MHG6d
				CA1295				EUP20		ACC	
				CA1296			EU21	EUP5	ACC	AJ310312	
				CA1297				EUP5		AJ310312	
				CA1298				EUP5		AJ310312	
				CA1299				EUP5		AJ310312	
	Şanlıurfa-Mardin road 30. km	37.1467	38.1144	CA1306				EUP5		AJ310312	MHG6d
				CA1307				EUP5		AJ310312	
				CA1308				EUP5		AJ310312	
				CA1309				EUP5		AJ310312	
				CA1310				EUP5		AJ310312	
				CA1311				EUP5		AJ310312	
				CA1312			EU36	EUP5	GU812122	AJ310312	
	Tefenni	37.2333	29.7113	YECA15144		AN20		CAR20		GQ902086	MHG6a
				YECA15145		AN17		CAR17		AJ313132	
				YECA15146		AN46		ANT21		GQ902114	MHG6c
				KYECA15147		AN46		ANT21		GQ902114	
				KYECA15148		AN46		ANT21		GQ902114	
				KYECA15149		AN17		CAR17		AJ313132	MHG6a
				KYECA15150		AN16		CAR16		GQ902109	
				MAHACA15151		AN48		ANT23		GU812204	MHG6c

Table 3.2. (continued).

Turkey	Tefenni	37.2333	29.7113	MAHACA15152		AN46		ANT21		GQ902114	MHG6c
	Tekirdağ-Bıyıkali lake	41.0114	27.3930	CA1508				ANT10		GU812192	MHG6c
				CA1509				ANT51		ACC	
				CA1510				ANT10		GU812192	
				CA1511				RE1		AJ310338	MHG1
				CA1512				ANT13		GU812195	MHG6c
	Tekirdağ-Kepenekli dam	41.1121	27.5519	CA1513				ANT10		GU812192	MHG6c
				CA1514			AT56	ANT10	GU812113	GU812192	
				CA1515			AT62	ANT54	ACC	ACC	
				CA1516			AT69	ANT2	ACC	GQ902107	
				CA1517				ANT10		GU812192	
				CA1518				ANT2		GQ902107	
	Tekirdağ-Yazır lake	40.9330	27.398	CA1503				ANT10		GU812192	MHG6c
				CA1504				ANT10		GU812192	
				CA1505			AT56	ANT10	GU812113	GU812192	
	Tekirdağ-Yazır lake	40.9330	27.398	CA1506				RE1		AJ310338	MHG1
				CA1507			AT67	ANT13	GU812110	GU812195	MHG6c
	Tokat-Avlunlar stream	40.5114	36.7342	CA1070			AT1	ANT1	GU812111	AJ310337	MHG6c
				CA1071				ANT1		AJ310337	
				CA1072				ANT1		AJ310337	
				CA1073				ANT1		AJ310337	
	Tokat-Çördük plataeu	40.2207	36.5622	CA1079				ANT1		AJ310337	MHG6c
				CA1080			AT1	ANT1	GU812111	AJ310337	
				CA1081				ANT1		AJ310337	
				CA1082				ANT1		AJ310337	
	Tokat-Kömeç Yeşilırmak	40.3396	36.4605	CA1055				ANT1		AJ310337	MHG6c

Table 3.2. (continued).

Turkey	Tokat-Kömeç Yeşilırmak	40.3396	36.4605	CA1057				ANT1		AJ310337	MHG6c
				CA1058			AT23	ANT1	ACC	AJ310337	
				CA1059				ANT1		AJ310337	
	Tokat-Yalancı stream	40.4106	36.7153	CA1062				ANT1		AJ310337	MHG6c
				CA1063			AT1	ANT1	GU812111	AJ310337	
				CA1064				ANT1		AJ310337	
				CA1065				ANT1		AJ310337	
	Tokat Yusufoğlan	40.3421	36.9325	KO60318		AN26		ANT1		AJ310337	MHG6c
				KO60319		AN29		ANT4		GU812186	
				KO60320		AN32		ANT7		GU812189	
	Trabzon-Arsin	40.9515	39.9009	CA792				ANT1		AJ310337	MHG6c
				CA793				ANT1		AJ310337	
				CA794				ANT1		AJ310337	
				CA795				ANT1		AJ310337	
	Trabzon-Darıca	41.0718	39.5113	CA782				ANT1		AJ310337	
				CA783				ANT1		AJ310337	
				CA787				ANT1		AJ310337	
				CA788				ANT1		AJ310337	
	Trabzon Derecik	41.0558	39.3900	RYDCA61254		AN26		ANT1		AJ310337	MHG6c
				RYDCA61255		AN26		ANT1		AJ310337	
				RYDCA61256		AN26		ANT1		AJ310337	
	Trabzon-Maçka	40.7839	39.6126	CA796				ANT38		ACC	MHG6c
	Trabzon-Söğütlü	41.0064	39.6310	CA790				ANT1		AJ310337	MHG6c
				CA791				ANT1		AJ310337	
	Tuzluca	40.0334	43.6652	AMPH\IRA\128	A37	AN58	EU34	EUP4	GU812123	GU812212	MHG6d
				AMPH\IRA\129	A30	AN27	AT82	ANT2	HM356084	GQ902107	MHG6c

Table 3.2. (continued).

Turkey	Türkoğlu	37.3808	36.8764	OBMBCA46373		CI9		CIE2		GU812169	MHG5
				OBMBCA46374		CI9		CIE2		GU812169	
				OBMBCA46375		CI10		CIE3		GU812170	
	Yalova-Altınova stream	40.7084	29.4730	CA1562				ANT45		ACC	MHG6c
				CA1563			AT34	ANT45	ACC	ACC	
				CA1564				ANT2		GQ902107	
				CA1565			AT48	ANT10	ACC	GU812192	
	Yalova-Altınova stream	40.7084	29.4730	CA1566			AT69	ANT2	ACC	GQ902107	MHG6c
				CA1567				ANT1		AJ310337	
	Yalova-Taşköprü	40.6801	29.3907	CA1568			AT95	ANT29	ACC	GU812209	MHG6c
				CA1569			AT48	ANT56	ACC	ACC	
				CA1570			AT58	ANT2	ACC	GQ902107	
				CA1571				ANT2		GQ902107	
				CA1572			AT48	ANT10	ACC	GU812192	
	Yeşilova	37.5348	29.6473	ISCA1578		AN46		ANT21		GQ902114	MHG6c
				ISCA1579		AN17		CAR17		AJ313132	MHG6a
				ISCA1580		AN1		CAR1		AJ310314	
				ISCA1581		AN1		CAR1		AJ310314	
				ISCA1582		AN46		ANT21		GQ902114	MHG6c
				ISCA1583		AN46		ANT21		GQ902114	
				ISCA1584		AN46		ANT21		GQ902114	
				ISCA1585		AN46		ANT21		GQ902114	
				ISCA1586		AN46		ANT21		GQ902114	
				ISCA1587		AN46		ANT21		GQ902114	
				ISCA1588		AN46		ANT21		GQ902114	
				ISCA1589		AN7		CAR7		GQ902112	MHG6a

Table 3.2. (continued).

Turkey	Yozgat-Gedikhasanlı	39.5720	35.1373	CA1111			AT1	ANT1	GU812111	AJ310337	MHG6c
				CA1112				ANT1		AJ310337	
				CA1113				ANT1		AJ310337	
				CA1114				ANT1		AJ310337	
	Yozgat-Mükremin lake	39.8030	35.2215	CA1117				ANT1		AJ310337	MHG6c
				CA1118			AT1	ANT1	GU812111	AJ310337	
				CA1119			AT35	ANT47	ACC	ACC	
				CA1120				ANT1		AJ310337	
				CA1121				ANT1		AJ310337	
	Yozgat-Sorgun	39.8042	35.2035	CA1105			AT37	ANT1	ACC	AJ310337	MHG6c
				CA1106				ANT1		AJ310337	
	Yozgat-Sorgun	39.8042	35.2035	CA1107				ANT1		AJ310337	MHG6c
				CA1108				ANT1		AJ310337	
	Yozgat-Yerköy Delice river	39.6117	34.5031	CA1124				ANT1		AJ310337	MHG6c
				CA1125				ANT1		AJ310337	
				CA1126			AT1	ANT1	GU812111	AJ310337	
				CA1127				ANT1		AJ310337	
	Yumurtalık	36.6925	35.6288	TBCASE0154		CI1		CIW1		AJ313135	MHG4
				TBCASE0155		CI1		CIW1		AJ313135	
				TBCASE0156		CI3		CIW3		GU812163	
				TBCASE0157		CI4		CIW4		GU812164	
				TBCASE0158		CI4		CIW4		GU812164	
				TBCASE0159		CI1		CIW1		AJ313135	
				TBCASE0160		CI5		CIW5		GU812165	
				TBCASE0161		CI3		CIW3		GU812163	
				TBCASE0162		CI3		CIW3		GU812163	

Table 3.2. (continued).

Turkey	Yumurtalık	36.6925	35.6288	TBCASE0163		CI7		CIW7		GU812167	MHG4
				TBCASE0164		CI2		CIW2		GU812162	
				TBCASE0165		CI2		CIW2		GU812162	
				TBCASE0166		CI1		CIW1		AJ313135	
	Van-Edremit Çiçekli	38.3443	43.1881	CA638			EU15	EUP1	ACC	AJ310313	MHG6d
				CA639				EUP1		AJ310313	
				CA641			EU24	EUP5	ACC	AJ310312	
				CA643				EUP1		AJ310313	
				CA644				EUP5		AJ310312	
	Van-Gevaş	38.3079	43.1232	CA645				EUP5		AJ310312	MHG6d
				CA646			EU24	EUP5	ACC	AJ310312	
				CA647			EU15	EUP1	ACC	AJ310313	
				CA649				EUP5		AJ310312	
				CA650				EUP5		AJ310312	
				CA651				EUP5		AJ310312	
	Van-Muradiye Bendimahı River	38.9366	43.6611	CA652				EUP5		AJ310312	MHG6d
				CA653			EU24	EUP14	ACC	ACC	
				CA654				EUP5		AJ310312	
				CA656				EUP5		AJ310312	
	Uşak-Gediz river	38.7878	29.2243	CA1732				ANT21		GQ902114	MHG6c
				CA1733				ANT21		GQ902114	
				CA1734				ANT21		GQ902114	
				CA1735				ANT29		GU812209	
				CA1736				ANT29		GU812209	
				CA1742				ANT21		GQ902114	
				CA1743				ANT21		GQ902114	

Table 3.2. (continued).

Turkey	Uşak-Gediz river	38.7878	29.2243	CA1744			AT110	ANT21	GU812104	GQ902114	MHG6c
	Uşak-Göğen lake	38.7207	29.5563	CA1745				ANT21		GQ902114	MHG6c
				CA1746				ANT21		GQ902114	
	Uşak-Karakoç lake	38,6542	29,3336	CA1737			AT110	ANT21	GU812104	GQ902114	MHG6c
				CA1738				ANT29		GU812209	
				CA1739				ANT13		GU812195	
				CA1740			AT55	ANT10	ACC	GU812192	
				CA1741				ANT21		GQ902114	
	Zonguldak	41.4271	31.7268	FGCA67248		AN33		ANT8		GU812190	MHG6c
				FGCA67249		AN34		ANT9		GU812191	
				FGCA67250		AN34		ANT9		GU812191	
				FGCA67251		AN26		ANT1		AJ310337	
				FGCA67252		AN26		ANT1		AJ310337	
	Zonguldak-Alaplı	41.1515	31.3521	CA1013			AT47	ANT9	ACC	GU812191	MHG6c
				CA1014			AT38	ANT1	ACC	AJ310337	
				CA1015				ANT1		AJ310337	
				CA1016				ANT1		AJ310337	
	Zonguldak-Kilimli	41.4005	31.6837	CA1002			AT1	ANT1	GU812111	AJ310337	MHG6c
				CA1003			AT46	ANT9	ACC	GU812191	
				CA1004				ANT1		AJ310337	
				CA1005				ANT1		AJ310337	
				CA1006				ANT9		GU812191	
	Zonguldak-Şirinköy	41.5065	31.9726	CA996			AT1	ANT30	GU812111	ACC	MHG6c
				CA997			AT36	ANT1	ACC	AJ310337	
				CA998			AT1	ANT30	GU812111	ACC	
				CA1000				ANT1		AJ310337	

Table 3.2. (continued).

Turkmenistan	Ashkhabad	38.3214	57.9498	ZMB45638	C1		T1	TE5	GU812127	AJ310317	MHG7
				ZMB45494				TE5		AJ310317	
Ukraine	Alushta	44.7528	34.4058	ZISP.6050-Sp.88		AN31		ANT6		GU812188	MHG6c
				ZISP.-Sp.245		AN31		ANT6		GU812188	
Ukraine	Chervlyonaya Gusirovka	49.4704	36.8705	ZISP.-Sp.305		RE9		RE9		GU812155	MHG1
	Belogorsk	45.0737	34.5973	Czech-U3-1		AN42		ANT17		GU812199	MHG6c
				Czech-U3-2		AN42		ANT17		GU812199	
	Belokamennoe	44.6847	33.8930	Czech-U19-1		AN45		ANT20		GU812202	MHG6c
				Czech-U19-2		AN45		ANT20		GU812202	
	Chernobyl	51.2696	30.2335	ZISP.5611-Sp.92		RE6		RE6		AM900653	MHG1
				ZISP.5611-Sp.93		RE6		RE6		AM900653	
				ZISP.5611-Sp.94		RE6		RE6		AM900653	
	Dolinnoe	44.7538	33.7673	Czech-U18		AN45		ANT20		GU812202	MHG6c
	Golaya Pristan	46.5344	32.5230	ZISP.6641-Sp.96		RE6		RE6		AM900653	MHG1
				ZISP.6641-Sp.97		RE6		RE6		AM900653	
				ZISP.6641-Sp.98		RE6		RE6		AM900653	
Ukraine	Irpen	50.5465	30.2773	Czech-U54		RE6		RE6		AM900653	MHG1
	Kerch	45.3607	36.4761	ZISP.6642-Sp.143		AN43		ANT18		GU812200	MHG6c
	Kiev	50.4170	30.5106	ZMB25779	R4	RE6	R4	RE6	AM900652	AM900653	MHG1
	Korostyshiv	50.3211	29.0726	Czech-U53		RE6		RE6		AM900653	MHG1
	Lavanda	44.7532	34.3696	ZISP.-Sp.245		AN31		ANT6		GU812188	MHG6c
	Luchistoe	44.7513	34.4045	ZISP.6050-Sp.88		AN31		ANT6		GU812188	MHG6c
Uzbekistan	Central Nuratau	40.0812	66.4177	-	C2		T2	TE13	GU812128	AJ310318	MHG7
				-	C3		T3	TE13	GU812129	AJ310318	

Table 3.2. (continued).

Outgroups											
Italy	Metaponto	40.3737	16.8028	No.6311	BER1	Ber1			GU812133	GU812231	*P. bergeri*
	Tarsia	39.6166	16.2666	Hotz19586	BER2	Ber2			GU812134	GU812232	
Corsica	Solenzara	41.8500	9.3999	-	BER3	Ber3			GU812135	GU812233	
Greece	Skinias/Crete	35.0632	25.3083	Hotz19852/ZMB56959	CRE1	Cre1			GU812136	GU812234	*P. cretensis*
				Hotz19854/ZMB56942	CRE2	Cre2			GU812137	AJ310336	
	Demati/Crete	35.0333	25.2833	Hotz19856/ZMB56960	CRE3	Cre2			GU812138	AJ313136	
Greece	Igoumenitsa	39.5000	20.2666	Hotz19421	EPE1	Epe1			GU812139	GU812235	*P. epeiroticus*
				Ploetner181.03	EPE2	Epe2			GU812140	GU812236	
	Lechena/Peloponnese	37.9174	21.2667	Hotz19552	EPE3	Epe3			GU812141	GU812237	
Italy	Carbonare	45.9333	11.2166	-	LES1	Les1			AM887975	AM887975	*P. lessonae*
Poland	Rogaczewo	52.0666	16.8166	Hotz18472	LES2	Les2			AM887976	AM887976	
Romania	Caraorman	45.1000	29.3333	ZMB47456	LES3	Les1			AM887968	AM887975	
France	Ligagnaeu	43.5333	4.7500	Lib11	PER1	Per1			GU812142	GU812238	*P. perezi*
	Narbonne	43.1833	3.0166	-	PER2	Per2			GU812143	GU812239	
Spain	Bajamar/Tenerife	28.5333	16.3333	-	PER3	Per3			GU812144	GU812240	
Algeria	Ain Salah	27.0000	2.4666	Hotz16724	SAH1	Sah1			GU812145	GU812241	*P. saharicus*
Morocco	Ait Boukha	28.9833	10.0666	Hotz16647	SAH2	Sah2			GU812146	GU812242	
Tunis	Tunis	c. 36.8001	10.17020	-	SAH3	Sah3			GU812147	GU812243	
Montenegro	Lake Skutari/Virpazar	42.2333	19.1000	ZMB47496	SHQ1	Shq1			GU812148	GU812244	*P. shqipericus*
				Hotz17523	SHQ2	Shq2			GU812149	GU812245	
North Korea	unknown			-	NIG1	Nig1			GU812150	GU812246	*P. nigromaculatus*
Japan	unknown			-	NIG2	Nig2			AB043889	AB043889	

Table 3.3. Locality information of nuclear SAI-1 alleles. Locality, collection or laboratory ID, nuclear allele composition for SAI-1 marker of the investigated individuals. Dark grey coloured fields show samples used in the first time in this study, the rest was taken from former publications. Sequences beginning with FN and HE were obtained from EMBL database. They refer to the publications of Plötner et al. 2009 and 2012. SAI-1: intron of the serum albumin gene containing a 5' truncated chicken repeat 1 like long interspersed nuclear element called as *Rana*CR1 by Plötner et al. (2009).

Country	Locality	Latitude	Longitude	Collection/ Laboratory ID	SAI-1 allele-A	SAI-1 allele-B	Accession Number		Allele Group/ Species
							Allele-A	Allele-B	
Armenia	Ararat Yeraskh	39.7357	44.8326	Ilona1	ant11-7	ant11-8	ACC	ACC	ANT
	Armavir Vanand village	40.1144	43.8235	Ilona2	ant6-2	ant6-2	ACC	ACC	ANT
	Gegharkunik Martuni town	40.1091	45.3000	Ilona3	ant6-1	ant6-2	ACC	ACC	ANT
	Kotaik Hrazdan	40.4961	44.7662	Ilona4	ant11-7	ant11-7	ACC	ACC	ANT
	Kotaik-Bjni town	40.3002	44.5047	Ilona5	ant6-1	ant11-8	ACC	ACC	ANT
	Vayots' Dzor -Yeghegnadzor	39.7539	45.3270	Ilona6	ant11-8	ant11-8	ACC	ACC	ANT
Karabakh Region	Nagorno-Sharifan	39.2649	46.9714	Ilona7	ant7-3	ter-2	ACC	ACC	ANT/TER
	Nagorno-Kubatlı	39.5559	46.9836	Ilona8	ant11-8	ant11-8	ACC	ACC	ANT
Cyprus	between Ayia Napa and Cape Greco	34.9774	34.0327	P36	cyp-2	cyp-2	HE858241	HE858241	CYP
	Northern Cyprus	35.1855	33.5674	Hotz19410	cyp-2	ant5-6	HE858241	HE858230	CYP/ANT
				Hotz19411	cyp-2	cyp-3	HE858241	ACC	CYP
				Hotz19412	cyp-2	cyp-2	HE858241	HE858241	
				Hotz19413	cyp-2	cyp-2	HE858241	HE858241	
				Hotz19416	cyp-2	ant5-5	HE858241	ACC	CYP/ANT
	Cape Greco (water reservoir in the west)	34.9794	34.0548	P24	cyp-1	cyp-2	HE858244	HE858241	CYP
	Stream close to Gialia	35.0769	32.5690	P32	cyp-1	cyp-1	HE858244	HE858244	CYP
				P33	cyp-1	cyp-2	HE858244	HE858241	
	Gönyeli dam	35.2332	33.2937	P3	cyp-2	cyp-2	HE858241	HE858241	CYP
	Maroullenas-1	35.0084	33.1477	P5	cyp-2	cyp-2	HE858242	HE858242	CYP

Table 3.3. (continued).

Cyprus	between Mathiatis and Kataliontas	34.9782	33.3321	P38	cyp-2	cyp-2	HE858241	HE858241	
	Nicosia-2	35.1951	33.3189	CA1985	cyp-3	cyp-3	ACC	ACC	CYP
	Panagia (forest station at stream Peristerona)	35.0156	33.0833	P4	cyp-2	cyp-2	HE858243	HE858243	CYP
	Lake Paralimni	35.0358	33.9753	P20	cyp-2	cyp-2	HE858241	HE858241	CYP
	Peristerona-1	34.9770	33.0912	P34	cyp-2	cyp-2	HE858241	HE858241	CYP
				P35	cyp-2	cyp-2	HE858241	HE858241	
	Pyrgos Dam	35.1495	32.6549	P9	cyp-1	cyp-1	HE858244	HE858244	CYP
				P11	cyp-1	cyp-1	HE858244	HE858244	
				P13	cyp-1	cyp-2	HE858244	HE858241	
	Troodos-2	34.9161	32.9003	ZISP10531	cyp-2	cyp-2	HE858245	HE858245	CYP
Czech Republic	Citov	50.3751	14.4415	PL01-2012	rid2-3	rid2-3	FN432365	FN432365	RID
				PL02-2012	kur-3	kur-3	ACC	ACC	KUR
				PL03-2012	rid2-3	rid2-3	FN432365	FN432365	RID
				PL06-2012	kur-3	kur-3	ACC	ACC	KUR
				PL07-2012	kur-3	kur-3	ACC	ACC	
				PL11-2013	ant7-3	ant7-3	ACC	ACC	ANT
Germany	Lebus near Frankfurt/O.	52.4141	14.5422		rid2-4	rid2-4	FN432364	FN432364	RID
	Oder River	52.4213	14.5333	PL82-2012	rid2-3	rid2-3	FN432365	FN432365	RID
				PL83-2012	rid2-3	rid2-3	FN432365	FN432365	
				PL84-2012	rid2-3	rid2-3	FN432365	FN432365	
				PL85-2012	rid2-3	ant7-3	FN432365	ACC	RID/ANT
				PL86-2013	rid2-3	rid2-3	FN432365	FN432365	RID
Greece	Aliartos	38.3688	23.0841	Hotz17357	rid2-2	rid2-2	HE857212	HE857212	RID
				Hotz17360	rid2-2	rid2-2	HE857213	HE857213	
	Archipolis/Rhodos	36.3117	28.1360	Hotz17220	cer-1	cer-1	HE850228	HE850228	CER

Table 3.3. (continued).

Greece	Archipolis/Rhodos	36.3117	28.1360	Hotz17221	cer-1	cer-1	HE850228	HE850228	CER
	Kavasilas	37.8762	21.2854	Hotz19510	kur-5	kur-5	HE858214	HE858214	KUR
				Hotz19528	kur-2	kur-2	FN432366	FN432366	
	Nea Manolada	38.0316	21.3611	Hotz19532	kur-1	kur-4	ACC	HE858215	KUR
				Hotz19538	kur-4	kur-4	FN432367	FN432367	
	Olympos/Karpathos	35.7427	27.1685	Hotz17207	cer-1	cer-1	HE858227	HE858227	CER
				Hotz17208	cer-1	cer-1	HE858227	HE858227	
	Skala	38.6675	23.0712	Hotz19483	kur-4	kur-4	HE858215	HE858215	KUR
				Hotz19485	kur-1	kur-1	ACC	ACC	
	Skala	38.6675	23.0712	Hotz19500	kur-1	kur-4	ACC	HE858215	KUR
				Hotz19501	kur-1	kur-1	ACC	ACC	
	Zakynthos	37.8052	20.8627	Ploetner30.03	kur-4	kur-4	HE858215	HE858215	KUR
				Ploetner31.03	kur-4	kur-4	HE858215	HE858215	
				Ploetner32.03	kur-4	kur-4	HE858215	HE858215	
Iran	Babol Sar	36.6803	52.6357	AMPH\IRA\509	ter-2	ter-2	ACC	ACC	TER
				AMPH\IRA\510	ter-2	ter-2	ACC	ACC	
				AMPH\IRA\511	ter-2	ter-2	ACC	ACC	
	Bavineh	33.6042	47.2026	AMPH\IRA\338	ter-5	ter-2	ACC	ACC	TER
	Bisotun	34.4038	47.4483	AMPH\IRA\308	ter-2	ter-2	ACC	ACC	TER
				AMPH\IRA\309	ter-5	ter-2	ACC	ACC	
				AMPH\IRA\310	ter-2	ter-2	ACC	ACC	
	Choplu	36.4739	47.0393	AMPH\IRA\302	ter-2	ter-2	ACC	ACC	TER
	Choqa Zanbil	32.0177	48.5451	AMPH\IRA\328	ter-3	ter-2	ACC	ACC	TER
				AMPH\IRA\331	ter-2	ter-2	ACC	ACC	
				AMPH\IRA\332	ter-2	ter-2	ACC	ACC	
				AMPH\IRA\333	ant11-7	ant3-5	ACC	HE858238	ANT

Table 3.3. (continued).

Iran	Choqa Zanbil	32.0177	48.5451	AMPH\IRA\336	ter-3	ter-6	ACC	ACC	TER
	Now Kandeh	36.7154	53.8836	AMPH\IRA\520	ter-2	ter-2	ACC	ACC	TER
Jordan	Al Kerak	31.1833	35.7000	J-06-54	bed1-3	cil3-3	HE858221	ACC	BED1/CIL
	Al shouna Al Shamaliya	32.6155	35.6388	J-02-50	bed1-3	bed1-3	HE858221	HE858221	BED1
	Bab Amman	32.2042	35.8867	J-01-31	bed1-3	bed1-4	HE858221	ACC	BED1
				J-01-44	bed2-3	bed2-3	ACC	ACC	BED2
				J-01-55	bed2-3	bed2-2	ACC	ACC	
				J-01-56	bed2-1	bed2-1	HE858239	HE858239	
				J-01-57	bed2-2	bed2-2	ACC	ACC	
	Canyon near Wadi Mujib	31.4492	35.7892	J-05-39	bed2-1	bed2-1	HE858240	HE858240	BED2
				J-05-45	bed2-1	bed2-1	HE858240	HE858240	
				J-05-46	bed2-1	bed2-1	HE858240	HE858240	
				J-05-47	bed2-4	bed2-1	ACC	HE858240	
				J-05-48	bed2-1	bed2-1	HE858240	HE858240	
	16 km southward from Jesus Baptisizing site	31.4939	35.5861	J-03-35	bed1-3	bed1-3	HE858221	HE858221	BED1
				J-03-36	bed1-3	cil3-2	HE858221	ACC	BED1/CIL
				J-03-37	bed1-3	bed1-3	HE858221	HE858221	BED1
				J-03-38	bed1-3	cil3-2	HE858221	ACC	BED1/CIL
	Mulaik Thoba	31.5533	35.7400	J-04-30	bed2-1	bed2-1	HE858218	HE858218	BED2
				J-04-31	bed1-3	bed1-3	HE858218	HE858218	
				J-04-32	bed2-1	bed2-1	HE858218	HE858218	
				J-04-33	bed2-1	bed2-1	HE858219	HE858219	
				J-04-41	bed2-1	bed2-1	HE858219	HE858219	
				J-04-51	bed2-1	bed2-1	HE858219	HE858219	
				J-04-52	bed2-1	bed2-1	HE858220	HE858220	
				J-04-53	bed2-1	bed2-1	HE858220	HE858220	

Table 3.3. (continued).

Kazakhstan	Atyrau	47.5442	52.3861	Sp.253	rid1-5	rid1-5	FN432363	FN432363	RID
				Sp.254	ant8-4	rid1-4	HE858222	HE858211	RID/ANT
				Sp.255	ant8-4	ant8-4	HE858222	HE858222	ANT
				41-1	ant7-3	rid1-5	ACC	FN432363	RID/ANT
				41-1L	ant7-3	rid1-5	ACC	FN432363	
				41-2	ant7-3	rid1-5	ACC	FN432363	
				41-2L	ant7-3	rid1-5	ACC	FN432363	
				41-3	ant8-2	ant8-2	ACC	ACC	ANT
				41-5	ant7-3	rid1-5	ACC	FN432363	RID/ANT
	Atyrau-Kulsary town	46.9611	54.0091	40-3	ant7-3	ant7-3	ACC	ACC	ANT
				40-5	ant7-3	ant6-2	ACC	ACC	
	Mangistau-The Saura spring	44.2319	50.803	39-03	rid1-6	rid1-6	ACC	ACC	RID
				39-19	rid1-5	rid1-5	ACC	ACC	
				39-24	rid1-5	rid1-5	ACC	ACC	
	Mangistau-The Tymshaly spring	44.6014	50.5966	38-03	rid1-5	rid1-5	ACC	ACC	RID
				38-06	rid1-5	rid1-5	ACC	ACC	
				38-07	rid1-5	rid1-5	ACC	ACC	
				38-08	rid1-5	rid1-5	ACC	ACC	
				38-09	ant8-2	ant8-2	ACC	ACC	ANT
	Dzhambul-Taraz city	42.8838	71.4122	36-20	sp nov-1	sp nov-1	ACC	ACC	SP NOV
Poland	Poznan	52.3805	16.6674	Hotz18192	rid2-3	rid2-3	FN432365	FN432365	RID
Syria	As Suwayda	32.6855	36.5525	ZFMK64945	bed1-1	bed1-1	FN432368	ACC	BED1
Turkey	Adana-Ceyhan Cinderesi	37.0353	35.7470	CA1418	cil1-4	cil1-4	HE858225	HE858225	CIL
				CA1421	cil1-6	cil1-5	ACC	ACC	
				CA1422	cil1-4	ant3-5	HE858225	HE858238	CIL/ANT
				CA1423	cil1-4	cil1-4	HE858225	HE858225	CIL

Table 3.3. (continued).

Turkey	Adana-Pozantı Şekerpınarı	37.4080	34.8842	CA1922	cil1-4	ant11-7	HE858225	ACC	CIL/ANT
				CA1924	cil1-4	cil1-4	HE858225	HE858225	CIL
				CA427	cil1-4	ant7-3	HE858225	ACC	CIL/ANT
	Adana-Pozantı Çakıt river	37.4299	34.8764	CA1927	cil1-4	cil1-4	HE858225	HE858225	CIL
				CA1928	cil1-4	cil1-4	HE858225	HE858225	
				CA1929	cil1-4	ant11-7	HE858225	ACC	CIL/ANT
				CA1930	cil1-4	ant3-5	HE858225	HE858238	
				CA1931	cil1-4	ant11-7	HE858225	ACC	
				CA1932	rid3-5	rid3-6	ACC	ACC	RID
	Adapazarı-Poyrazlar lake	40.8336	30.4682	CA1541	rid2-1	ant11-7	ACC	ACC	RID/ANT
				CA1542	ant7-2	ant7-3	ACC	ACC	ANT
	Adapazarı-Saklıgöl	40.8549	30.3018	CA1545	ant7-2	ant11-7	ACC	ACC	ANT
				CA1547	rid2-1	ant7-2	ACC	ACC	RID/ANT
				CA1548	ant11-7	ant11-7	ACC	ACC	ANT
	Adıyaman-Abuzergaffar river	37.7415	38.3354	CA1270	ant11-7	ant3-5	ACC	HE858238	ANT
				CA1271	ant11-7	cil1-4	ACC	HE858225	CIL/ANT
				CA1273	ant11-9	ant11-9	ACC	ACC	ANT
				CA1275	ant3-5	ant3-5	HE858238	HE858238	
				CA1276	ant11-7	ant11-9	ACC	ACC	
	Adıyaman-Börgenek Çakal stream	37.7128	38.1663	CA1287	rid3-8	rid3-8	ACC	ACC	RID
				CA1289	rid3-8	ant3-5	ACC	HE858238	RID/ANT
				CA1290	ant10-3	cil2-1	ACC	ACC	CIL/ANT
				CA1292	rid3-8	ant11-7	ACC	ACC	RID/ANT
				CA1293	rid3-7	ant3-5	ACC	HE858238	
	Adıyaman-Göksu river	37.6983	38.0799	CA1282	rid3-8	cil2-1	ACC	ACC	CIL/RID
				CA1283	rid3-8	ant11-7	ACC	ACC	RID/ANT

Table 3.3. (continued).

Turkey	Adıyaman-Göksu river	37.6983	38.0799	CA1284	ant11-7	cil2-1	ACC	ACC	CIL/ANT
				CA1286	rid3-8	cil1-4	ACC	HE858225	CIL/RID
	Adıyaman-Kahta Bircik river	37.7447	38.5060	CA1277	rid3-5	ant11-9	ACC	ACC	RID/ANT
				CA1278	rid3-8	rid3-8	ACC	ACC	RID
				CA1279	rid3-8	rid3-8	ACC	ACC	
				CA1280	ant11-9	cil1-4	ACC	HE858225	CIL/ANT
	Afyonkarahisar-26 Agust Natural Park	38.7925	30.3816	CA1725	ant10-1	ant10-1	ACC	ACC	ANT
				CA1726	ant3-2	ant7-3	ACC	ACC	
				CA1727	rid2-1	ant3-2	ACC	ACC	RID/ANT
				CA1728	ant1-4	ant10-4	ACC	ACC	ANT
				CA1729	ant10-1	ant10-4	ACC	ACC	
				CA1731	ant2-1	ant8-5	ACC	ACC	
	Afyonkarahisar-Cumhuriyet village Çay	38.5923	30.9618	CA1720	ant11-7	ant10-1	ACC	ACC	ANT
				CA1721	ant10-1	ant10-4	ACC	ACC	
				CA1722	rid2-1	ant10-4	ACC	ACC	RID/ANT
				CA1723	ant10-1	ant10-4	ACC	ACC	ANT
				CA1724	ant1-3	ant8-3	ACC	ACC	
	Afyonkarahisar-Karamık lake	38.4215	30.8869	CA1710	ant10-4	ant10-4	ACC	ACC	ANT
				CA1711	ant10-4	ant10-4	ACC	ACC	
				CA1712	ant10-1	ant10-4	ACC	ACC	
				CA1713	ant8-3	ant10-4	ACC	ACC	
				CA1714	ant8-3	ant10-4	ACC	ACC	
	Ağrı-Aşağı Yoldüzü Cuma River	39.8181	43.0892	CA679	ant11-8	ant11-8	ACC	ACC	ANT
				CA680	rid3-8	ant11-8	ACC	ACC	RID/ANT
				CA681	ant11-7	rid3-8	ACC	ACC	
				CA683	ant11-8	ant11-8	ACC	ACC	ANT

Table 3.3. (continued).

Turkey	Ağrı-Çukuralan Village	39.7130	42.9920	CA684	rid3-8	rid3-8	ACC	ACC	RID
				CA686	rid3-8	ant11-8	ACC	ACC	RID/ANT
				CA688	ant11-8	ant11-8	ACC	ACC	ANT
	Ağrı-Dambat village	39.6769	43.0228	CA672	ant11-8	ant11-8	ACC	ACC	ANT
				CA673	ant6-1	rid3-8	ACC	ACC	RID/ANT
				CA674	rid3-8	ant11-8	ACC	ACC	
				CA675	ant11-8	ant11-8	ACC	ACC	ANT
				CA676	rid3-8	ant11-8	ACC	ACC	RID/ANT
				CA678	ant11-8	ant11-8	ACC	ACC	ANT
	Ağrı-Doğu Beyazıt Bardaklı village	39.681	44.0655	CA658	ant11-8	ant11-8	ACC	ACC	ANT
				CA659	rid3-8	ant11-8	ACC	ACC	RID/ANT
				CA660	ant11-8	ant11-8	ACC	ACC	ANT
				CA661	rid3-8	ant11-8	ACC	ACC	RID/ANT
	Aksaray-Akın village stream	38.4313	34.0291	CA1225	rid3-5	rid3-5	ACC	ACC	RID
				CA1226	rid3-5	rid3-5	ACC	ACC	
				CA1227	ant11-7	rid2-1	ACC	ACC	RID/ANT
	Aksaray-Helvadere	38.1999	34.2103	CA1212	ant11-7	ant11-7	ACC	ACC	ANT
				CA1213	rid3-5	rid3-5	ACC	ACC	RID
				CA1214	rid3-5	ant3-5	ACC	HE858238	RID/ANT
				CA1215	ant11-6	ant3-5	ACC	HE858238	
				CA1216	rid3-5	rid3-5	ACC	ACC	RID
				CA1217	rid3-5	rid3-5	ACC	ACC	
				CA1218	rid3-5	rid3-5	ACC	ACC	
	Aksaray-Melendez river	38.2988	34.2662	CA1219	rid3-5	rid3-5	ACC	ACC	RID
				CA1220	ant1-4	rid3-5	ACC	ACC	RID/ANT
				CA1221	ant1-1	ant11-7	ACC	ACC	ANT

Table 3.3. (continued).

Turkey	Aksaray-Melendez river	38.2988	34.2662	CA1222	rid2-1	ant11-7	ACC	ACC	RID/ANT
				CA1223	rid3-5	rid3-5	ACC	ACC	RID
				CA1224	ant11-7	ant3-5	ACC	HE858238	ANT
	Aksaray-Sultanhanı	38.2414	33.5448	CA1205	rid3-5	rid3-5	ACC	ACC	RID
				CA1206	rid3-5	rid3-5	ACC	ACC	
				CA1207	rid3-5	rid3-5	ACC	ACC	
				CA1208	rid3-5	rid3-5	ACC	ACC	
				CA1209	rid3-5	rid3-5	ACC	ACC	
				CA1210	rid3-5	rid3-5	ACC	ACC	
				CA1211	rid3-5	ant11-7	ACC	ACC	RID/ANT
	Akşehir-Eber Lakes	38.4544	31.4546	CBCA03184	ant10-4	ant10-4	ACC	ACC	ANT
				CBCA03186	ant7-3	ant10-4	ACC	ACC	
				CBCA03187	ant1-4	ant10-4	ACC	ACC	
				CBCA03188	ant10-1	ant10-4	ACC	ACC	
				CBCA03189	ant10-1	ant10-1	ACC	ACC	
				CBCA03190	ant10-4	rid2-1	ACC	ACC	RID/ANT
				CA1715	ant10-4	rid2-1	ACC	ACC	
				CA1716	ant10-4	ant8-2	ACC	ACC	ANT
				CA1717	ant1-6	ant10-4	ACC	ACC	
				CA1718	ant10-4	ant10-4	ACC	ACC	
				CA1719	ant8-3	ant10-4	ACC	ACC	
	Alanya	36.6031	32.0694	MTHTCA07178	ant3-5	ant5-2	HE858238	ACC	ANT
				CA1442	ant5-6	ant5-6	ACC	ACC	
				CA1443	ant5-6	ant5-1	ACC	ACC	
				CA1444	ant5-6	ant3-5	ACC	HE858238	
	Amasya-Boğazköy Tersakan	40.7268	35.7702	CA909	ant11-7	ant11-7	ACC	ACC	ANT

Table 3.3. (continued).

Turkey	Amasya-Boğazköy Tersakan	40.7268	35.7702	CA910	ant11-7	ant11-6	ACC	ACC	ANT
				CA911	ant3-5	ant11-7	HE858238	ACC	
				CA912	ant3-2	ant11-7	ACC	ACC	
	Amasya-Doğantepe pond	40.6104	35.5869	CA902	ant11-7	ant11-7	ACC	ACC	ANT
				CA903	ant3-5	rid2-1	HE858238	ACC	RID/ANT
				CA904	ant11-7	ant11-7	ACC	ACC	ANT
				CA905	rid2-1	ant11-7	ACC	ACC	RID/ANT
	Amasya-Suluoava Yedikır dam	40.7786	35.5751	CA915	ant7-3	rid2-1	ACC	ACC	RID/ANT
				CA917	ant11-7	ant7-3	ACC	ACC	ANT
	Amasya-Yeşilırmak	40.6735	35.8528	CA907	ant11-7	ant11-7	ACC	ACC	ANT
	Ankara	39.5793	33.0453	KKOBCA06230	ant11-7	rid2-1	ACC	ACC	RID/ANT
				KKOBCA06231	ant11-7	rid2-1	ACC	ACC	
				KKOBCA06232	ant11-7	ant10-4	ACC	ACC	ANT
				KKOBCA06235	ant3-5	ant11-7	HE858238	ACC	
				KKOBCA06237	rid2-1	rid2-1	ACC	ACC	RID
	Antakya Samandağı	36.0742	35.9982	BCA31292	cil1-4	cil1-4	HE858225	HE858225	CIL
				BCA31293	cil1-4	cil1-7	HE858225	ACC	
	Antalya	37.2119	30.9415	CBCASTO704	ant5-3	ant5-6	ACC	HE858230	ANT
				CBCASTO705	ant1-2	ant3-4	ACC	ACC	
				CBCASTO706	ant4-3	ant8-3	ACC	ACC	
				CBCA0743	ant5-5	ant5-2	ACC	ACC	
				HKHSBKCA07111	ant5-5	ant5-2	ACC	ACC	
				HKHSBKCA07112	ant5-6	ant5-6	HE858230	HE858230	
				HKHSBKCA07113	ant5-6	ant5-6	HE858230	HE858230	
				HKHSBKCA07114	ant7-3	ant5-6	ACC	HE858230	
				HKHSBKCA07115	ant5-6	ant3-4	HE858230	ACC	

Table 3.3. (continued).

Turkey	Antalya	37.2119	30.9415	HKHSBKCA07116	ant5-6	ant5-6	HE858230	HE858230	ANT
				HKHSBKCA07117	ant5-5	ant5-2	ACC	ACC	
				HKHSBKCA07118	ant5-6	ant5-2	HE858230	ACC	
				HKHSBKCA07119	ant5-6	ant5-5	HE858230	ACC	
				HKHSBKCA07120	ant2-1	ant10-1	ACC	ACC	
				HKHSBKCA07121	ant5-6	ant5-6	HE858230	HE858230	
				HKHSBKCA07122	ant5-6	ant5-5	HE858230	ACC	
				HKHSBKCA07124	ant5-4	ant5-5	ACC	ACC	
	Antalya-Anamur	36.0429	32.8078	CA1433	ant5-6	ant5-1	HE858230	ACC	ANT
				CA1434	cil1-4	ant5-6	HE858225	HE858230	CIL/ANT
				CA1435	ant5-6	ant5-2	HE858230	ACC	ANT
				CA1437	ant5-6	ant5-1	HE858230	ACC	
	Antalya-Kemer Kesmeboğaz river	36.5954	30.5045	CA1863	ant8-3	ant8-3	ACC	ACC	ANT
				CA1865	ant8-3	ant5-6	ACC	HE858230	
				CA1866	ant8-3	ant8-3	ACC	ACC	
	Antalya-Gazipaşa	36.1687	32.4467	CA1441	ant5-2	ant3-5	ACC	HE858238	ANT
	Antalya-Kumluca	36.3168	30.2512	CA1871	ant8-3	ant8-3	ACC	ACC	ANT
	Ardahan-Göle Serme Bridge	40.9087	42.5928	CA732	ant11-7	rid2-5	ACC	ACC	RID/ANT
				CA733	ant6-1	rid3-7	ACC	ACC	
				CA734	ant6-1	rid2-5	ACC	ACC	
				CA735	ant6-1	ant6-1	ACC	ACC	ANT
				CA736	ant6-1	ant6-1	ACC	ACC	
	Ardahan-Kura River	41.1569	42.8728	CA743	ant6-1	ant11-8	ACC	ACC	ANT
				CA744	ant6-1	rid3-8	ACC	ACC	RID/ANT
				CA745	ant6-1	ant11-8	ACC	ACC	ANT
	Ardahan-Uzunova Village	41.0800	42.4991	CA739	rid3-8	rid3-8	ACC	ACC	RID

Table 3.3. (continued).

Turkey	Ardahan-Uzunova Village	41.0800	42.4991	CA740	rid3-8	rid3-8	ACC	ACC	RID
				CA741	ant6-1	ant6-1	ACC	ACC	ANT
	Artvin-Ardanuç River	41.1247	42.0668	CA746	ant6-1	ant6-1	ACC	ACC	ANT
				CA747	ant6-1	ant6-1	ACC	ACC	
				CA748	ant6-1	ant6-1	ACC	ACC	
				CA749	ant6-1	rid2-5	ACC	ACC	RID/ANT
	Artvin Borçka	41.3649	41.6920	DC08241	rid2-5	rid2-5	ACC	ACC	RID
				DC08242	ant11-7	ant11-7	ACC	ACC	ANT
				CA757	ant6-1	ant11-7	ACC	ACC	
				CA759	ant6-1	ant11-7	ACC	ACC	
				CA761	ant6-1	ant11-7	ACC	ACC	
	Artvin-Hopa Kemalpaşa	41.4870	41.5269	CA764	ant11-7	rid2-5	ACC	ACC	RID/ANT
				CA765	ant6-1	rid2-5	ACC	ACC	
				CA767	rid2-5	rid2-5	ACC	ACC	RID
	Artvin Şavşat	41.3098	42.4837	ATDC08191	rid2-5	rid2-5	ACC	ACC	RID
				ATDC08193	ant6-1	ant6-1	ACC	ACC	ANT
				ATDC08194	ant6-1	rid2-5	ACC	ACC	RID/ANT
	Artvin-Yolüstü Village	41.1613	42.0639	CA751	ant6-1	ant6-1	ACC	ACC	ANT
				CA752	ant6-1	rid3-8	ACC	ACC	RID/ANT
				CA753	ant6-1	rid2-5	ACC	ACC	
				CA754	ant6-1	ant6-1	ACC	ACC	ANT
				CA755	ant6-1	ant6-1	ACC	ACC	
	Lake Avlan	36.5825	29.9482	HS07165	ant3-5	ant3-5	HE858238	HE858238	ANT
				HS07166	ant4-2	ant3-5	ACC	HE858238	
				HS07167	ant3-5	ant9-2	HE858238	ACC	
				HS07168	ant4-3	ant3-5	ACC	HE858238	

Table 3.3. (continued).

Turkey	Lake Avlan	36.5825	29.9482	HS07169	ant3-5	ant2-1	HE858238	ACC	ANT
	Aydın-Azap lake	37.5844	27.447	CA1800	ant9-2	ant10-1	ACC	ACC	ANT
				CA1801	ant10-1	ant10-4	ACC	ACC	
				CA1803	ant11-7	ant10-1	ACC	ACC	
	Aydın-Bıyıkali pond	37.7716	27.5741	CA1787	ant7-3	ant10-1	ACC	ACC	ANT
				CA1789	ant7-3	ant7-3	ACC	ACC	
	Aydın-Menderes river	37.5476	27.2371	CA1796	ant8-1	ant4-3	ACC	ACC	ANT
				CA1797	ant9-2	ant9-2	ACC	ACC	
				CA1798	ant10-1	ant10-4	ACC	ACC	
	Aydın-Söke water channel	37.6607	27.3087	CA1790	ant7-3	ant11-7	ACC	ACC	ANT
				CA1792	ant7-3	ant11-7	ACC	ACC	
				CA1793	ant9-2	ant10-1	ACC	ACC	
				CA1794	ant10-1	ant10-1	ACC	ACC	
				CA1795	ant4-3	ant4-3	ACC	ACC	
	Balıkesir-Erdek	40.2968	27.6273	CA1618	ant11-7	ant11-7	ACC	ACC	ANT
				CA1619	ant7-3	ant11-7	ACC	ACC	
				CA1620	ant11-7	ant11-7	ACC	ACC	
				CA1621	ant11-7	ant11-7	ACC	ACC	
	Balıkesir-İkizcetepeler dam	39.4807	27.9274	CA1601	ant11-7	ant10-1	ACC	ACC	ANT
				CA1602	ant11-5	ant11-7	ACC	ACC	
				CA1603	ant11-7	ant11-7	ACC	ACC	
				CA1605	ant11-7	ant11-7	ACC	ACC	
	Balıkesir-Manyas Kuş Lake	40.2296	28.0461	CA1612	ant7-3	ant11-7	ACC	ACC	ANT
				CA1613	ant11-7	ant11-7	ACC	ACC	
				CA1615	ant7-2	ant11-7	ACC	ACC	
				CA1616	ant7-2	ant11-7	ACC	ACC	

Table 3.3. (continued).

Turkey	Balıkesir-Pamukçu stream	39.5295	27.9091	CA1608	ant11-7	ant11-7	ACC	ACC	ANT
				CA1609	ant11-7	ant11-7	ACC	ACC	
				CA1610	ant7-3	ant11-7	ACC	ACC	
	Bartın-Potbaşı river	41.6087	32.3727	CA982	ant12-1	ant11-3	ACC	ACC	ANT
				CA983	ant11-6	ant11-6	ACC	ACC	
				CA984	ant3-2	ant11-3	ACC	ACC	
				CA985	ant11-6	ant12-1	ACC	ACC	
				CA986	ant11-6	ant12-1	ACC	ACC	
				CA987	ant3-2	ant12-1	ACC	ACC	
				CA988	ant7-3	ant12-1	ACC	ACC	
	Bartın-Bartın stream	41.5721	32.3267	CA989	ant11-6	ant12-1	ACC	ACC	ANT
				CA992	ant3-2	ant11-6	ACC	ACC	
				CA993	ant11-7	ant11-6	ACC	ACC	
				CA995	ant10-1	ant7-3	ACC	ACC	
	Batman-Dicle river	37.9177	41.0856	CA1355	ant11-9	ant11-9	ACC	ACC	ANT
				CA1356	rid3-8	ant11-7	ACC	ACC	RID/ANT
				CA1357	rid3-8	rid3-8	ACC	ACC	RID
				CA1358	rid3-8	ant11-7	ACC	ACC	RID/ANT
				CA1359	rid3-7	ant11-7	ACC	ACC	
				CA1360	ant11-7	ant11-9	ACC	ACC	ANT
	Batman-Hasankeyf	37.7356	41.3022	CA1370	rid3-8	ant11-9	ACC	ACC	RID/ANT
				CA1371	rid3-7	ant11-7	ACC	ACC	
	Batman-Silvan road Çarıklı village	38.0463	41.1834	CA1361	ant11-7	ant11-9	ACC	ACC	ANT
				CA1362	ant11-7	ant3-5	ACC	HE858238	
				CA1363	rid3-8	rid3-7	ACC	ACC	RID
				CA1364	rid3-8	rid3-7	ACC	ACC	

Table 3.3. (continued).

Turkey	Batman-Silvan road Çarıklı village	38.0463	41.1834	CA1365	ant11-7	ant11-7	ACC	ACC	ANT
				CA1366	rid3-8	ant11-9	ACC	ACC	RID/ANT
	Bayburt-Çamlık District	40.3009	40.2013	CA809	rid3-8	rid3-8	ACC	ACC	RID
				CA812	rid3-8	rid2-5	ACC	ACC	
	Bayburt-Gökçedere pond	40.1156	39.7526	CA802	ant11-7	ant11-7	ACC	ACC	ANT
				CA804	ant3-5	ant11-7	HE858238	ACC	
				CA805	ant11-6	rid2-5	ACC	ACC	RID/ANT
	Bayburt-Oruçbeyli pond	40.2316	40.0626	CA797	rid3-8	ant3-5	ACC	HE858238	RID/ANT
				CA799	rid3-8	rid2-5	ACC	ACC	RID
				CA801	ant11-7	ant11-7	ACC	ACC	ANT
	Bayburt-Toki	40.2729	40.1343	CA808	rid3-8	ant11-7	ACC	ACC	RID/ANT
	Lake Beyşehir	37.6802	31.7180	MEFUCA42195	ant1-4	ant1-5	ACC	ACC	ANT
				MEFUCA42196	ant1-4	ant1-5	ACC	ACC	
				MEFUCA42197	ant3-5	ant1-5	HE858238	ACC	
				MEFUCA42198	ant1-5	ant10-4	ACC	ACC	
				CA1450	ant1-5	ant3-2	ACC	ACC	
				CA1451	ant1-4	ant1-5	ACC	ACC	
				CA1452	rid2-1	ant10-4	ACC	ACC	RID/ANT
				CA1453	ant1-5	ant3-2	ACC	ACC	ANT
				CA1454	ant1-4	ant10-4	ACC	ACC	
				CA1456	ant1-5	rid2-1	ACC	ACC	RID/ANT
				CA1457	ant1-5	ant10-4	ACC	ACC	ANT
	Bilecik-Çiğdemlik	40.0646	30.3142	CA1657	ant7-3	ant7-2	ACC	ACC	ANT
				CA1658	ant7-3	ant7-3	ACC	ACC	
	Bilecik-İnhisar Sakarya river	40.0469	30.4124	CA1660	ant7-3	ant11-7	ACC	ACC	ANT
				CA1662	ant7-3	ant7-3	ACC	ACC	

Table 3.3. (continued).

Turkey	Bilecik-İnhisar Sakarya river	40.0469	30.4124	CA1663	ant7-2	ant11-7	ACC	ACC	ANT
	Bilecik Söğüt	39.7118	30.0070	MAYGCA11303	ant11-7	ant10-4	ACC	ACC	ANT
				MAYGCA11304	ant7-3	ant11-7	ACC	ACC	
				MAYGCA11305	ant7-3	ant10-1	ACC	ACC	
				MAYGCA11306	ant11-7	rid2-1	ACC	ACC	RID/ANT
				CA1649	rid2-1	ant7-2	ACC	ACC	
				CA1652	ant7-2	ant7-3	ACC	ACC	ANT
	Bingöl-Çeltiksuyu stream	38.8411	40.5654	CA570	rid3-8	ant11-8	ACC	ACC	RID/ANT
				CA571	ant11-8	ant3-5	ACC	HE858238	ANT
				CA572	ant3-5	ant3-5	HE858238	HE858238	
	Bingöl-Çobantaşı	39.0585	40.7976	CA582	ant11-7	rid3-7	ACC	ACC	RID/ANT
				CA583	rid3-7	ant11-9	ACC	ACC	
				CA584	rid3-7	ant3-5	ACC	HE858238	
				CA585	rid3-8	rid3-8	ACC	ACC	RID
	Bingöl-Sarıçiçek Lake	38.8844	40.5890	CA575	ant11-7	ant3-5	ACC	HE858238	ANT
				CA576	rid3-8	ant3-5	ACC	HE858238	RID/ANT
				CA578	ant3-5	ant3-5	HE858238	HE858238	ANT
				CA579	ant3-5	ant3-5	HE858238	HE858238	
	Bingöl-Solhan Seref stream	38.9184	40.7859	CA586	rid3-8	ant11-9	ACC	ACC	RID/ANT
				CA587	ant11-7	rid3-8	ACC	ACC	
				CA588	rid3-8	ant3-5	ACC	HE858238	
				CA589	ant11-7	rid3-8	ACC	ACC	
				CA590	rid3-8	ant11-9	ACC	ACC	
	Bitlis-Ağaçköprü District	38.3328	42.0098	CA630	rid3-8	rid3-8	ACC	ACC	RID
	Bitlis-Güroymak Water Channel	38.5962	42.0243	CA618	rid3-8	ant11-8	ACC	ACC	RID/ANT

Table 3.3. (continued).

Turkey	Bitlis-Güroymak Water Channel	38.5962	42.0243	CA619	rid3-8	ant11-8	ACC	ACC	ANT
				CA620	ant3-5	ant3-5	HE858238	HE858238	
				CA621	rid3-8	rid3-8	ACC	ACC	RID
	Bitlis-Kemah Stream	38.4407	42.1447	CA623	rid3-7	ant11-9	ACC	ACC	RID/ANT
				CA624	ant11-9	ant11-9	ACC	ACC	ANT
				CA625	rid3-7	ant3-5	ACC	HE858238	RID/ANT
	Bitlis-Tatvan Çağlayan	38.4748	42.3084	CA631	ant11-8	ant3-5	ACC	HE858238	ANT
				CA632	rid3-8	ant3-5	ACC	HE858238	RID/ANT
				CA634	ant11-9	ant11-8	ACC	ACC	ANT
				CA635	ant11-9	ant11-8	ACC	ACC	
	Bolu-Gölköy	40.7116	31.5314	CA1520	ant11-7	ant10-4	ACC	ACC	ANT
				CA1521	ant7-2	ant7-2	ACC	ACC	
				CA1522	ant7-2	rid1-1	ACC	ACC	RID/ANT
				CA1524	ant11-7	rid1-7	ACC	ACC	
	Bolu-Karamanlar lake	40.7619	31.5162	CA1525	ant7-2	ant7-2	ACC	ACC	ANT
				CA1526	ant7-3	ant7-3	ACC	ACC	
				CA1527	ant11-7	ant3-2	ACC	ACC	
				CA1528	ant7-2	ant11-7	ACC	ACC	
	Bucak	37.3500	30.5393	MTAECA1568	ant5-6	ant10-1	HE858230	ACC	ANT
				MTAECA1569	ant3-5	ant10-1	HE858238	ACC	
				MTAECA1570	ant3-5	ant10-1	HE858238	ACC	
				MTAECA1571	ant5-7	ant3-5	ACC	HE858238	
				MTAECA1572	ant3-5	ant2-1	HE858238	HE858238	
				MTAECA1573	ant5-6	ant10-1	HE858230	ACC	
				MTAECA1574	ant3-5	ant4-3	HE858238	HE858238	
				MTAECA1575	ant3-5	ant3-5	HE858238	HE858238	

Table 3.3. (continued).

Turkey	Bucak	37.3500	30.5393	MTAECA1576	ant3-5	ant5-6	HE858238	HE858230	ANT
	Lake Burdur	37.8371	30.3854	CBCAST1518	ant4-3	ant10-5	ACC	ACC	ANT
	Burdur-Çerçin dam	37.7603	30.4149	CA1883	ant3-2	ant3-2	ACC	ACC	ANT
	Burdur-Karataş lake	37.3616	29.9869	CA1877	ant10-1	ant4-3	ACC	ACC	ANT
				CA1880	ant10-1	ant10-1	ACC	ACC	
	Burdur-Yarışlı lake	37.5907	29.9562	CA1872	ant3-5	ant3-5	HE858238	HE858238	ANT
				CA1873	ant10-1	ant10-1	ACC	ACC	
	Bursa-Akçalar village	40.1771	28.7453	CA1642	ant11-7	ant11-7	ACC	ACC	ANT
				CA1644	ant7-3	ant10-4	ACC	ACC	
				CA1646	ant7-2	ant10-1	ACC	ACC	
	Bursa-Boğaz	40.2821	28.4483	CA1622	ant11-7	ant10-1	ACC	ACC	ANT
				CA1623	ant7-3	ant11-7	ACC	ACC	
				CA1625	ant7-3	ant11-7	ACC	ACC	
	Bursa-Gölyazı	40.1653	28.6795	CA1636	ant7-2	ant11-7	ACC	ACC	ANT
				CA1637	ant7-2	ant11-7	ACC	ACC	
				CA1638	ant11-7	ant11-7	ACC	ACC	
				CA1640	ant7-3	ant11-7	ACC	ACC	
	Bursa-Kemalpaşa	40.0346	28.4104	CA1628	ant11-7	ant11-7	ACC	ACC	ANT
				CA1629	ant7-3	ant7-3	ACC	ACC	
				CA1630	ant7-3	ant11-7	ACC	ACC	
				CA1634	ant11-7	ant11-7	ACC	ACC	
	Çanakkale-Karacaören	40.1884	26.4330	CA1576	ant11-7	ant11-7	ACC	ACC	ANT
				CA1577	ant11-7	ant11-7	ACC	ACC	
				CA1578	ant11-7	ant11-7	ACC	ACC	
				CA1580	ant7-3	ant11-7	ACC	ACC	
				CA1581	ant11-7	ant11-7	ACC	ACC	

Table 3.3. (continued).

Turkey	Çanakkale-Kepez	40.0895	26.3852	CA1590	ant11-7	ant11-7	ACC	ACC	ANT
				CA1591	ant7-3	ant11-7	ACC	ACC	
				CA1592	ant11-7	ant11-7	ACC	ACC	
				CA1595	ant11-7	ant11-7	ACC	ACC	
	Çanakkale-Batakova Menderes river	39.9930	26.2078	CA1596	ant11-7	ant11-7	ACC	ACC	ANT
				CA1597	ant7-3	ant11-7	ACC	ACC	
				CA1598	ant7-3	ant11-7	ACC	ACC	
				CA1599	ant7-3	ant11-7	ACC	ACC	
				CA1600	ant11-7	ant11-7	ACC	ACC	
	Çanakkale-Sarıçay	40.1393	26.4855	CA1582	ant7-3	ant11-7	ACC	ACC	ANT
				CA1584	ant7-3	ant11-7	ACC	ACC	
				CA1585	ant11-7	ant11-7	ACC	ACC	
				CA1586	ant7-3	ant11-7	ACC	ACC	
	Çankırı-Apsarı stream	40.7018	33.5393	CA1023	rid2-1	ant7-3	ACC	ACC	RID/ANT
				CA1024	ant11-7	rid2-1	ACC	ACC	
				CA1025	ant11-7	rid2-1	ACC	ACC	
				CA1026	ant11-7	rid2-1	ACC	ACC	
	Çankırı-Aşağıyanlar district	40.5540	33.5817	CA1028	ant11-7	ant11-6	ACC	ACC	ANT
				CA1029	ant3-2	rid1-7	ACC	ACC	RID/ANT
				CA1030	ant11-6	ant3-2	ACC	ACC	ANT
	Çankırı-Terme river	40.4377	33.7431	CA1033	ant11-7	ant3-2	ACC	ACC	ANT
				CA1034	ant11-7	ant3-2	ACC	ACC	
				CA1035	ant10-4	ant10-4	ACC	ACC	
	Çankırı-Yapraklı pond	40.7675	33.7641	CA1019	ant11-7	rid2-1	ACC	ACC	RID/ANT
				CA1020	ant11-7	ant3-5	ACC	HE858238	ANT
	Çorum-Alaca stream	40.3371	35.0628	CA1041	ant11-7	ant11-7	ACC	ACC	ANT

Table 3.3. (continued).

Turkey	Çorum-Alaca stream	40.3371	35.0628	CA1042	ant11-7	ant11-6	ACC	ACC	ANT
				CA1043	ant11-7	ant3-5	ACC	HE858238	
				CA1044	ant11-7	ant3-2	ACC	ACC	
	Çorum-Çomar dam	40.5856	34.9998	CA1052	ant11-7	rid2-1	ACC	ACC	RID/ANT
				CA1053	ant11-7	ant10-4	ACC	ACC	ANT
				CA1054	ant11-6	ant3-2	ACC	ACC	
	Çorum-Yakacık stream	40.6000	34.9117	CA1046	ant11-7	ant11-7	ACC	ACC	ANT
				CA1047	rid2-1	ant3-2	ACC	ACC	RID/ANT
	Çorum-Yılgınözü stream	40.4502	34.3789	CA1037	ant3-2	ant3-2	ACC	ACC	ANT
				CA1038	ant11-7	ant11-6	ACC	ACC	
				CA1039	ant11-7	ant3-5	ACC	HE858238	
	Dalaman	36.7138	28.7856	IS48307	ant11-7	ant9-2	ACC	ACC	ANT
				IS48308	ant4-3	ant4-3	ACC	ACC	
				IS48309	ant9-3	ant10-3	ACC	ACC	
				IS48310	ant4-3	ant10-1	ACC	ACC	
				IS48312	ant4-3	ant10-3	ACC	ACC	
	Denizli-Derbent dam	38.1532	28.8443	CA1815	ant9-2	ant7-3	ACC	ACC	ANT
				CA1817	ant11-7	ant11-7	ACC	ACC	
				CA1819	ant10-4	ant4-3	ACC	ACC	
	Denizli-Emmiler district	37.6264	29.2087	CA1804	ant11-7	ant10-1	ACC	ACC	ANT
				CA1805	ant7-3	ant11-7	ACC	ACC	
				CA1806	ant7-3	ant11-7	ACC	ACC	
				CA1807	ant11-7	ant11-7	ACC	ACC	
	Denizli-İncirlipınar park	37.7623	29.0972	CA1810	ant11-7	ant11-7	ACC	ACC	ANT
				CA1812	ant7-3	ant7-3	ACC	ACC	
				CA1813	ant11-7	ant11-7	ACC	ACC	

Table 3.3. (continued).

Turkey	Denizli-Süleymanlı lake	38.0513	28.7708	CA1820	ant11-7	ant11-7	ACC	ACC	ANT
				CA1821	ant10-4	ant8-1	ACC	ACC	
				CA1822	ant10-1	ant10-1	ACC	ACC	
				CA1823	ant9-2	ant10-4	ACC	ACC	
				CA1824	ant11-7	ant4-3	ACC	ACC	
				CA1825	ant7-3	ant10-1	ACC	ACC	
	Diyarbakır-Batman road	37.8081	40.4055	CA1345	rid3-8	rid3-7	ACC	ACC	RID
				CA1346	ant11-7	ant3-5	ACC	HE858238	ANT
	Diyarbakır-Devegeçidi	38.0576	40.0697	CA1339	rid3-8	rid3-7	ACC	ACC	RID
				CA1340	ant11-7	ant11-7	ACC	ACC	ANT
				CA1341	rid3-8	ant11-7	ACC	ACC	RID/ANT
				CA1342	rid3-8	ant11-7	ACC	ACC	
				CA1343	rid3-7	ant3-5	ACC	HE858238	
				CA1344	rid3-8	rid3-7	ACC	ACC	RID
	Diyarbakır-Dicle river	37.8797	41.0217	CA1347	rid3-8	rid3-7	ACC	ACC	RID
				CA1348	rid3-8	ant11-7	ACC	ACC	RID/ANT
				CA1349	rid3-8	rid3-9	ACC	ACC	RID
				CA1350	ant11-7	ant11-7	ACC	ACC	ANT
				CA1352	rid3-8	rid3-7	ACC	ACC	RID
				CA1353	ant11-9	ant11-9	ACC	ACC	ANT
				CA1354	rid3-7	ant11-9	ACC	ACC	RID/ANT
	Diyarbakır-Göksu Çınar	37.6916	40.4473	CA1331	rid3-7	ant11-7	ACC	ACC	RID/ANT
				CA1332	rid3-8	ant11-7	ACC	ACC	
				CA1333	rid3-8	rid3-7	ACC	ACC	RID
				CA1334	rid3-8	rid3-7	ACC	ACC	
				CA1335	rid3-7	ant11-7	ACC	ACC	RID/ANT

Table 3.3. (continued).

Turkey	Diyarbakır-Göksu Çınar	37.6916	40.4473	CA1337	rid3-8	rid3-8	ACC	ACC	RID
				CA1338	ant11-7	ant11-9	ACC	ACC	ANT
	Düzce-Asarsu	40.8259	31.1840	CA1530	ant7-2	ant7-2	ACC	ACC	ANT
				CA1531	ant7-3	ant11-7	ACC	ACC	
				CA1532	ant3-5	ant11-7	HE858238	ACC	
				CA1533	ant7-2	rid1-7	ACC	ACC	RID/ANT
				CA1534	ant7-2	ant11-7	ACC	ACC	ANT
	Düzce-Efteni lake	40.7573	31.0404	CA1536	ant7-2	ant7-2	ACC	ACC	ANT
				CA1538	ant11-7	ant11-7	ACC	ACC	
				CA1539	ant11-7	ant11-7	ACC	ACC	
	Edirne	41.6857	26.4932	MACA22180	ant7-3	rid1-8	ACC	ACC	RID/ANT
				MACA22181	ant7-3	ant10-4	ACC	ACC	ANT
				MACA22182	ant7-3	ant3-2	ACC	ACC	
				MACA22183	ant7-3	rid2-1	ACC	ACC	ANT/RID
				MA497	ant11-7	ant7-3	ACC	ACC	ANT
				MA500	ant11-7	ant11-7	ACC	ACC	
				MA501	rid3-5	rid3-5	ACC	ACC	RID
				MA503	ant11-7	rid1-3	ACC	ACC	RID/ANT
	Lake Eğirdir	38.1393	30.7588	CBCAST3234	ant5-6	ant10-4	HE858230	ACC	ANT
				CBCAST3238	ant4-3	ant8-3	ACC	ACC	
				CBCAST3239	ant3-2	ant1-2	ACC	ACC	
	Elazığ - Cip	38.6819	39.0706	CA535	rid3-8	rid3-7	ACC	ACC	RID
				CA536	rid3-8	ant3-5	ACC	HE858238	RID/ANT
				CA537	ant11-7	ant3-5	ACC	HE858238	ANT
				CA539	ant11-7	rid3-7	ACC	ACC	RID/ANT
	Elazığ - Sivrice	38.4665	39.2753	CA545	ant11-7	rid3-8	ACC	ACC	RID/ANT

Table 3.3. (continued).

Turkey	Elazığ - Sivrice	38.4665	39.2753	CA546	rid3-8	rid3-8	ACC	ACC	RID
	Erzincan - Türkmenoğlu village	39.6559	39.4996	CA520	rid3-8	rid2-5	ACC	ACC	RID
				CA521	rid3-8	rid3-8	ACC	ACC	
				CA522	ant11-7	ant3-5	ACC	HE858238	ANT
				CA523	ant11-7	ant3-5	ACC	HE858238	
				CA524	rid3-8	cil1-5	ACC	ACC	CIL/RID
	Erzincan - Ekşisu	39.7328	39.6179	CA525	ant11-7	ant3-5	ACC	HE858238	ANT
				CA526	ant3-5	ant3-5	HE858238	HE858238	
				CA527	ant11-7	ant11-7	ACC	ACC	
				CA528	ant11-7	ant3-5	ACC	HE858238	
				CA529	ant11-7	ant11-7	ACC	ACC	
	Erzincan-Sakaltutan	39.8832	39.1954	CA530	ant11-7	ant11-7	ACC	ACC	ANT
				CA531	ant11-7	ant3-5	ACC	HE858238	
				CA532	ant11-7	ant3-5	ACC	HE858238	
				CA533	ant11-7	ant3-5	ACC	HE858238	
	Erzurum-Ilıca	39.8196	41.1521	CA696	ant11-7	rid3-8	ACC	ACC	RID/ANT
				CA697	rid3-8	ant3-5	ACC	HE858238	
				CA699	ant3-5	ant3-5	HE858238	HE858238	ANT
				CA701	rid3-8	rid3-7	ACC	ACC	RID
				CA702	ant11-8	ant3-5	ACC	HE858238	ANT
	Erzurum-Pasinler	39.9611	41.4090	CA704	ant3-5	ant3-5	HE858238	HE858238	ANT
				CA706	rid3-8	rid3-8	ACC	ACC	RID
				CA707	rid3-7	ant3-5	ACC	HE858238	RID/ANT
				CA708	rid3-8	ant3-5	ACC	HE858238	
	Erzurum-Soğuk Çermik	39.9899	41.3052	CA709	ant3-5	ant3-5	HE858238	HE858238	ANT
				CA710	rid3-8	rid3-8	ACC	ACC	RID

Table 3.3. (continued).

Turkey	Erzurum-Soğuk Çermik	39.9899	41.3052	CA711	rid3-8	ant3-5	ACC	HE858238	RID/ANT
				CA712	rid3-7	ant3-5	ACC	HE858238	
	Erzurum-Teke stream	39.8196	41.1521	CA689	rid3-8	rid3-8	ACC	ACC	RID
				CA690	rid3-8	rid3-8	ACC	ACC	
				CA691	rid3-8	ant3-5	ACC	HE858238	RID/ANT
				CA692	rid3-8	rid3-8	ACC	ACC	RID
				CA693	rid3-8	rid3-8	ACC	ACC	
	Erzurum-Yerlisu Village	40.0425	41.1833	CA714	rid3-8	rid3-8	ACC	ACC	RID
				CA715	rid3-8	ant3-5	ACC	HE858238	RID/ANT
	Eskişehir-Alpu road	39.7825	30.6877	CA1672	ant7-3	ant10-1	ACC	ACC	ANT
				CA1673	ant7-3	ant10-4	ACC	ACC	
				CA1674	ant7-2	ant11-7	ACC	ACC	
				CA1675	ant3-2	rid1-7	ACC	ACC	RID/ANT
				CA1676	ant11-7	ant3-2	ACC	ACC	ANT
	Eskişehir-Porsuk river 1	39.7744	30.4511	CA1677	ant11-7	ant11-7	ACC	ACC	ANT
				CA1678	ant11-7	ant10-4	ACC	ACC	
				CA1679	ant11-7	ant10-4	ACC	ACC	
				CA1680	ant11-7	ant10-4	ACC	ACC	
	Eskişehir-Porsuk river 2	39.7139	30.4275	CA1681	ant11-7	ant11-7	ACC	ACC	ANT
				CA1683	ant7-3	ant11-7	ACC	ACC	
				CA1684	ant10-4	ant10-4	ACC	ACC	
	Eskişehir-Sarısungur	39.7082	30.5804	CA1666	ant7-3	ant11-7	ACC	ACC	ANT
				CA1667	ant7-2	ant11-7	ACC	ACC	
				CA1668	ant11-7	ant11-7	ACC	ACC	
				CA1669	ant9-1	ant11-7	ACC	ACC	
				CA1670	ant7-3	ant10-1	ACC	ACC	

Table 3.3. (continued).

Turkey	Giresun-Batlama stream	40.9067	38.3547	CA840	ant3-2	ant7-3	ACC	ACC	ANT
	Giresun-Bulancak Domuz stream	40.9454	38.1673	CA854	ant3-2	ant7-3	ACC	ACC	ANT
				CA855	ant3-2	ant3-2	ACC	ACC	
				CA856	ant3-2	ant11-7	ACC	ACC	
	Giresun-Espiye Gelivera Stream	40.9459	38.7224	CA849	ant3-5	ant7-3	HE858238	ACC	ANT
				CA850	ant7-3	ant7-3	ACC	ACC	
				CA852	ant3-2	ant3-2	ACC	ACC	
				CA853	ant11-7	ant11-6	ACC	ACC	
	Gödet Dam	37.1076	33.2918	OYCA70204	ant5-6	ant5-6	HE858230	HE858230	ANT
				OYCA70205	ant5-6	ant5-6	HE858230	HE858230	
				OYCA70207	ant11-7	ant11-7	ACC	ACC	
				OYCA70208	ant5-6	ant11-7	HE858230	ACC	
				CA1900	ant5-6	ant5-6	HE858230	HE858230	
				CA1901	ant1-4	ant11-7	ACC	ACC	
				CA1902	ant5-6	ant11-7	HE858230	ACC	
				CA1903	ant1-4	ant5-6	ACC	HE858230	
	Gökpınar Dam	37.7851	29.1306	CCYZCA20153	ant5-6	ant5-6	HE858230	HE858230	ANT
				CCYZCA20154	ant9-2	ant11-7	ACC	ACC	
				CCYZCA20155	ant5-6	ant5-6	HE858230	HE858230	
				CCYZCA20157	ant4-3	ant11-7	ACC	ACC	
	Gümüşhane-Akbaba pond	40.1783	39.6521	CA818	ant3-5	ant11-7	HE858238	ACC	ANT
				CA821	ant11-7	ant11-7	ACC	ACC	
	Gümüşhane-Kelkit river	40.1226	39.3737	CA822	ant11-7	rid2-5	ACC	ACC	RID/ANT
				CA824	ant3-5	ant3-5	HE858238	HE858238	ANT
				CA826	ant3-5	ant3-5	HE858238	HE858238	
	Lake Işıklı	38.2350	29.9605	CBCA2047	ant11-10	ant11-7	ACC	ACC	ANT

Table 3.3. (continued).

Turkey	Lake Işıklı	38.2350	29.9605	CBCA2048	ant8-3	ant5-2	ACC	ACC	ANT
				CBCA2049	ant2-1	ant10-4	ACC	ACC	
				CBCA2050	ant1-4	ant1-5	ACC	ACC	
				CBCA2051	ant1-4	ant3-2	ACC	ACC	
				CBCA2052	ant11-10	ant11-10	ACC	ACC	
	Iğdır- Tuzluca Aras River	40.0356	43.6790	CA663	ant6-1	ant6-1	ACC	ACC	ANT
				CA664	ant6-2	rid3-7	ACC	ACC	RID/ANT
				CA665	ant6-2	ant6-2	ACC	ACC	ANT
	Iğdır- Water Channel	39.9513	44.0419	CA667	ant11-8	ant11-8	ACC	ACC	ANT
				CA668	ant6-1	ant11-8	ACC	ACC	
				CA669	ant6-2	ant11-8	ACC	ACC	
				CA670	ant11-8	ant11-8	ACC	ACC	
				CA671	ant11-8	ant11-8	ACC	ACC	
	Hatay-Deniz	36.0727	35.9508	CA1949	cil1-4	cil1-4	HE858225	HE858225	CIL
				CA1950	cil1-4	cil1-4	HE858225	HE858225	
				CA1951	cil1-4	cil1-4	HE858225	HE858225	
				CA1953	cil1-4	cil1-3	HE858225	ACC	
				CA1954	cil1-4	cil1-4	HE858225	HE858225	
	Hatay-Hassa	36.8449	36.6504	CA1403	cil1-4	cil1-1	HE858225	ACC	CIL
				CA1404	cil1-4	cil1-4	HE858225	HE858225	
				CA1405	cil1-4	ant3-5	HE858225	HE858238	CIL/ANT
				CA1406	cil1-4	cil2-1	HE858225	ACC	CIL
				CA1407	cil1-4	cil1-4	HE858225	HE858225	
				CA1408	cil1-4	ant3-5	HE858225	HE858238	CIL/ANT
	Hatay-İskenderun Erzin	36.8887	36.1370	CA1416	cil1-4	cil2-1	HE858225	ACC	CIL
				CA1417	cil1-6	cil1-4	ACC	HE858225	

Table 3.3. (continued).

Turkey	Hatay-İskenderun Sarıseki	36.6653	36.2157	CA1409	ant3-5	cil1-4	HE858238	HE858225	CIL/ANT
				CA1411	cil1-4	cil1-4	HE858225	HE858225	CIL
				CA1413	cil1-4	cil1-8	HE858225	ACC	
				CA1414	cil1-4	cil1-4	HE858225	HE858225	
				CA1415	ant11-7	cil1-4	ACC	HE858225	CIL/ANT
	Hatay Kırıkhan	36.4973	36.4523	OBMB31342	cil3-1	cil3-1	ACC	ACC	CIL
				OBMB31343	ant3-5	cil1-4	HE858238	HE858225	CIL/ANT
				OBMB31345	cil1-4	cil1-4	HE858225	HE858225	CIL
				OBMB31346	cil1-4	cil1-4	HE858225	HE858225	
	Hatay Reyhanlı	36.2379	36.5689	OBMB31336	ant3-5	cil1-4	HE858238	HE858225	CIL/ANT
				OBMB31338	ant3-5	cil1-4	HE858238	HE858225	
				OBMB31340	cil1-4	rid3-5	HE858225	ACC	CIL/RID
	Hatay Tahtalı Dam	36.8515	36.6861	OBMB31348	cil1-4	cil1-4	HE858225	HE858225	CIL
				OBMB31349	cil1-4	cil1-4	HE858225	HE858225	
	Isparta-Bağıllı	38.1586	31.0825	CA1446	ant3-5	ant10-4	HE858238	ACC	ANT
				CA1447	ant1-4	ant10-1	ACC	ACC	
				CA1449	ant10-4	ant10-4	ACC	ACC	
	Isparta-Sevinçbey district	37.8748	30.7760	CA1885	ant4-3	ant3-2	ACC	ACC	ANT
	İvriz	37.4408	34.1705	OK42203	cil1-4	ant1-4	HE858225	ACC	CIL/ANT
				OK42221	ant1-4	ant1-2	ACC	ACC	ANT
				OK42222	ant1-5	ant11-7	ACC	ACC	
	İzmir-Çandarlı Bakırçay	38.9556	27.0100	CA1748	ant11-7	ant10-1	ACC	ACC	ANT
				CA1749	ant11-7	ant11-7	ACC	ACC	
				CA1751	ant7-3	ant11-7	ACC	ACC	
				CA1752	ant11-7	ant2-1	ACC	ACC	
				CA1753	ant11-7	ant11-7	ACC	ACC	

Table 3.3. (continued).

Turkey	Kahramanmaraş-Elbistan Gölpınar	38.1959	37.0636	CA1263	rid3-8	cil2-1	ACC	ACC	CIL/RID
	Kahramanmaraş-Kumaşır lake	37.5102	36.8983	CA1264	cil2-1	ant3-5	ACC	HE858238	CIL/ANT
				CA1266	cil1-4	cil2-1	HE858225	ACC	CIL
				CA1267	cil1-4	cil1-4	HE858225	HE858225	
				CA1268	cil1-1	bed1-5	ACC	ACC	CIL/BED1
				CA1269	cil1-4	cil3-1	HE858225	ACC	CIL
				OB379	cil1-6	cil1-1	ACC	ACC	
				OB381	cil1-4	cil3-1	HE858225	ACC	
				OB383	cil1-4	cil3-1	HE858225	ACC	
				OB384	cil1-4	cil1-4	HE858225	HE858225	
	Karabük-Cemaller Soğanlı river	41.1313	32.6816	CA965	ant11-3	ant11-6	ACC	ACC	ANT
				CA966	ant10-4	ant11-6	ACC	ACC	
				CA967	ant11-7	ant7-2	ACC	ACC	
				CA968	ant3-2	rid2-1	ACC	ACC	RID/ANT
				CA969	ant10-4	ant12-1	ACC	ACC	ANT
				CA970	ant10-4	rid1-7	ACC	ACC	RID/ANT
				CA971	ant3-2	ant10-4	ACC	ACC	ANT
				CA972	ant10-4	rid1-7	ACC	ACC	RID/ANT
				CA973	rid2-1	ant12-1	ACC	ACC	
	Karabük-Safranbolu Araç river	41.2165	32.7331	CA974	ant11-6	ant3-1	ACC	ACC	ANT
				CA975	ant3-2	ant12-1	ACC	ACC	
				CA976	rid2-1	ant12-1	ACC	ACC	RID/ANT
				CA977	ant3-2	ant12-1	ACC	ACC	ANT
				CA978	ant11-6	ant12-1	ACC	ACC	
				CA979	ant10-4	rid1-7	ACC	ACC	RID/ANT

Table 3.3. (continued).

Turkey	Karacaören Dams I-II	37.4031	30.8703	CBCAST328	ant3-2	ant8-3	ACC	ACC	ANT
				CBCAST329	ant5-3	ant5-7	ACC	ACC	
				CBCAST3213	ant7-3	ant5-2	ACC	ACC	
				CBCA3241	ant5-6	ant5-6	ACC	HE858230	
				CBCA3242	ant5-4	ant7-3	ACC	ACC	
				OBBKCA32103	ant3-5	ant5-2	HE858238	ACC	
				OBBKCA32104	ant5-7	ant10-4	ACC	ACC	
				OBBKCA32106	ant7-3	ant5-6	ACC	HE858230	
				OBBKCA32107	ant10-1	ant5-7	ACC	ACC	
				OBBKCA32108	ant3-3	ant3-2	ACC	ACC	
	Karaman-Belpınarı	36.8333	32.5803	CA1909	ant5-6	ant5-6	HE858230	HE858230	ANT
				CA1912	ant5-6	ant5-6	HE858230	HE858230	
				CA1913	ant5-6	ant5-6	HE858230	HE858230	
	Karaman-Yeşildere	37.2047	33.4035	CA1906	ant5-6	ant11-7	HE858230	ACC	ANT
				CA1907	ant11-7	ant11-7	ACC	ACC	
				CA1908	ant5-6	ant11-7	HE858230	ACC	
	Kars-Arpaçay Akçalar	40.7735	43.2952	CA725	ant11-8	ant11-8	ACC	ACC	ANT
				CA726	ant6-1	ant11-8	ACC	ACC	
				CA727	ant11-8	ant11-8	ACC	ACC	
				CA729	ant11-8	ant11-8	ACC	ACC	
				CA730	ant6-1	ant11-8	ACC	ACC	
	Kars-Digor Pazarcık	40.5189	43.2690	CA717	ant11-8	ant11-8	ACC	ACC	ANT
				CA718	ant11-8	ant11-8	ACC	ACC	
				CA719	ant6-2	ant11-8	ACC	ACC	
				CA720	ant11-8	ant11-8	ACC	ACC	
	Kars-Selim	40.4702	42.7904	CA721	ant11-8	ant11-8	ACC	ACC	ANT

Table 3.3. (continued).

Turkey	Kars-Selim	40.4702	42.7904	CA722	ant11-8	ant11-8	ACC	ACC	ANT
				CA723	ant11-7	ant11-8	ACC	ACC	
				CA724	ant11-8	ant11-8	ACC	ACC	ANT
	Kastamonu-Araç River	41.2389	33.3224	CA959	ant11-3	ant11-6	ACC	ACC	ANT
				CA960	ant3-2	ant11-7	ACC	ACC	
				CA963	ant3-5	rid2-1	HE858238	ACC	RID/ANT
				CA964	ant11-6	ant12-1	ACC	ACC	ANT
	Kastamonu-Beyler dam	41.6903	33.8119	CA952	rid2-1	ant12-1	ACC	ACC	RID/ANT
				CA954	ant3-2	ant3-2	ACC	ACC	ANT
				CA955	ant11-7	ant11-7	ACC	ACC	
	Kastamonu-Karaçomak dam	41.2852	33.7372	CA939	ant7-2	rid2-1	ACC	ACC	RID/ANT
				CA941	ant3-2	ant12-1	ACC	ACC	ANT
				CA942	ant3-2	ant3-2	ACC	ACC	
				CA943	ant3-1	ant3-2	ACC	ACC	
	Kastamonu-Taşlık Dam	41.4018	33.6963	CA945	ant11-7	ant11-7	ACC	ACC	ANT
				CA946	ant3-2	ant3-2	ACC	ACC	
				CA947	ant7-3	rid2-1	ACC	ACC	RID/ANT
				CA948	ant3-2	ant11-6	ACC	ACC	ANT
				CA950	ant3-2	ant11-6	ACC	ACC	
	Kaş	36.2769	29.6839	CA07217	ant4-4	ant10-1	ACC	ACC	ANT
				CA07218	ant4-4	ant10-1	ACC	ACC	
	Kayseri	38.7565	35.4229	DCA38315	ant11-6	rid2-1	ACC	ACC	RID/ANT
				YC38445	rid3-5	ant11-7	ACC	ACC	
	Kayseri-Engir lake	38.8111	35.5915	CA1151	rid2-1	ant3-2	ACC	ACC	RID/ANT
				CA1153	rid3-8	rid3-8	ACC	ACC	RID
				CA1154	ant11-7	ant3-5	ACC	HE858238	ANT

Table 3.3. (continued).

Turkey	Kayseri-Engir lake	38.8111	35.5915	CA1155	ant11-7	ant3-5	ACC	HE858238	ANT
				CA1156	ant11-7	ant3-2	ACC	ACC	
	Kayseri-Pınarbaşı	38.6618	36.104	CA1468	ant3-5	ant11-7	HE858238	ACC	ANT
				CA1469	ant3-5	ant11-7	HE858238	ACC	
				CA1471	ant11-7	ant3-2	ACC	ACC	
				CA1472	ant11-7	ant11-7	ACC	ACC	
				CA1473	ant11-7	ant11-7	ACC	ACC	
	Kayseri-Sultansazlığı	38.3897	35.3657	CA1157	cil1-7	ant3-5	ACC	HE858238	CIL/ANT
				CA1158	ant3-5	rid3-8	HE858238	ACC	RID/ANT
				CA1159	cil1-4	ant3-5	HE858225	HE858238	CIL/ANT
				CA1160	cil1-7	rid3-6	ACC	ACC	CIL/RID
				CA1161	ant1-4	ant1-4	ACC	ACC	ANT
				CA1162	cil1-4	rid3-6	HE858225	ACC	CIL/RID
				CA1163	cil1-4	ant3-5	HE858225	HE858238	CIL/ANT
				CA1164	cil1-7	ant3-5	ACC	HE858238	
	Kayseri-Yahyalı	38.1348	35.3641	CA1165	cil1-4	cil1-4	HE858225	HE858225	CIL
				CA1166	cil1-4	ant11-7	HE858225	ACC	CIL/ANT
				CA1167	ant3-5	ant3-5	HE858238	HE858238	ANT
				CA1168	cil1-4	ant3-5	HE858225	HE858238	CIL/ANT
				CA1169	cil1-7	ant3-5	ACC	HE858238	
				CA1170	cil1-4	rid3-6	HE858225	ACC	CIL/RID
	Kayseri-Zamantı Water	38.0345	35.5407	CA1171	ant11-7	ant3-5	ACC	HE858238	ANT
				CA1172	ant11-7	ant3-5	ACC	HE858238	
				CA1173	ant11-7	ant11-7	ACC	ACC	
				CA1174	ant11-7	ant3-5	ACC	HE858238	
				CA1175	ant11-7	ant11-7	ACC	ACC	

Table 3.3. (continued).

Turkey	Kayseri-Zamantı Water	38.0345	35.5407	CA1176	ant11-7	ant11-7	ACC	ACC	ANT
				CA1177	ant11-7	ant11-7	ACC	ACC	
				CA1178	ant11-7	ant3-5	ACC	HE858238	
				CA1179	ant11-6	ant11-7	ACC	ACC	
				CA1180	ant11-7	ant11-7	ACC	ACC	
	Kemer	37.4627	30.1118	MHSACA15137	ant3-5	ant3-5	HE858238	HE858238	ANT
				MHSACA15138	ant3-5	ant9-2	HE858238	ACC	
				MHSACA15139	ant8-3	ant10-1	ACC	ACC	
				MHSACA15140	ant3-6	ant3-6	ACC	ACC	
				MHSACA15142	ant2-1	ant4-3	ACC	ACC	
	Kemer	37.4627	30.1118	MHSACA15143	ant4-3	ant10-5	ACC	ACC	ANT
	Kırıkkale-Hasandede Kızılırmak	38.7406	33.4879	CA1238	ant11-7	ant11-7	ACC	ACC	ANT
				CA1239	ant11-7	ant3-2	ACC	ACC	
				CA1242	rid2-1	ant3-2	ACC	ACC	RID/ANT
	Kırıkkale-Yahşiyan Kızılırmak	39.8861	33.4146	CA1244	ant11-7	ant3-5	ACC	HE858238	ANT
				CA1245	ant11-7	ant10-4	ACC	ACC	
				CA1247	ant11-7	ant7-3	ACC	ACC	
	Kırklareli-Eriklice stream	41.7576	27.1814	CA1488	ant11-7	rid1-8	ACC	ACC	RID/ANT
				CA1489	ant11-7	rid1-2	ACC	ACC	
				CA1490	ant7-3	ant11-7	ACC	ACC	ANT
				CA1491	ant11-7	rid1-7	ACC	ACC	RID/ANT
				CA1492	ant7-3	ant11-7	ACC	ACC	ANT
				CA1493	rid3-5	rid1-8	ACC	ACC	RID
	Kırklareli-İnece stream	41.6836	27.0731	CA1494	ant7-2	rid2-1	ACC	ACC	RID/ANT
				CA1495	ant7-3	rid2-6	ACC	ACC	
				CA1496	ant11-7	ant3-2	ACC	ACC	ANT

Table 3.3. (continued).

Turkey	Kırklareli-İnece stream	41.6836	27.0731	CA1497	ant11-7	ant11-7	ACC	ACC	ANT
				CA1498	ant7-2	ant10-4	ACC	ACC	
	Kırklareli-Karakoç pond	41.7817	27.2171	CA1499	rid3-5	ant11-7	ACC	ACC	RID/ANT
				CA1500	ant11-7	rid1-2	ACC	ACC	
				CA1501	ant7-3	ant11-7	ACC	ACC	ANT
				CA1502	ant11-7	ant11-7	ACC	ACC	ANT
	Kırklareli-Şeytandere	41.7104	27.2627	CA1484	ant11-7	rid1-8	ACC	ACC	RID/ANT
				CA1485	ant7-3	rid1-8	ACC	ACC	
				CA1486	ant11-7	ant11-7	ACC	ACC	ANT
				CA1487	ant3-2	rid2-7	ACC	ACC	RID/ANT
	Kırşehir-Çuvın	39.3168	34.1238	CA1141	rid2-1	ant11-7	ACC	ACC	RID/ANT
				CA1142	ant7-3	ant3-5	ACC	HE858238	ANT
				CA1145	ant11-6	rid2-1	ACC	ACC	RID/ANT
	Kırşehir-Güneykent	39.0988	34.1600	CA1128	rid2-1	rid2-1	ACC	ACC	RID
				CA1129	ant11-7	rid2-1	ACC	ACC	RID/ANT
				CA1130	ant11-6	rid2-1	ACC	ACC	
				CA1131	ant11-7	ant11-7	ACC	ACC	ANT
	Kırşehir-Kışlapınar	39.2262	34.1338	CA1146	rid2-1	ant7-3	ACC	ACC	RID/ANT
				CA1147	ant11-7	rid2-1	ACC	ACC	
				CA1148	rid2-1	ant3-5	ACC	HE858238	RID/ANT
				CA1149	ant11-7	ant10-4	ACC	ACC	ANT
	Kırşehir-Sıddıklı	39.1007	33.9073	CA1135	rid2-1	ant3-5	ACC	HE858238	RID/ANT
				CA1136	ant11-7	ant11-7	ACC	ACC	ANT
				CA1138	ant11-7	ant3-2	ACC	ACC	
	Kilis	36.7641	37.2540	OB79322	cil1-4	cil1-4	HE858225	HE858225	CIL
				OB79326	rid3-8	cil1-4	ACC	HE858225	CIL/RID

Table 3.3. (continued).

Turkey	Kilis-Gaziantep road	36.8106	37.3095	OBMB79327	cil1-4	cil1-4	HE858225	HE858225	CIL
				OBMB79328	cil1-4	rid3-5	HE858225	HE858238	CIL/RID
				OBMB79329	rid3-8	ant11-7	ACC	ACC	RID/ANT
				OBMB79330	cil1-4	rid3-5	HE858225	ACC	CIL/RID
	Kilis-Polateli	36.7853	37.0588	CA1395	ant3-5	cil1-4	HE858238	HE858225	CIL/ANT
				CA1396	ant3-5	ant3-5	HE858238	HE858238	ANT
				CA1397	cil1-4	cil1-4	HE858225	HE858225	CIL
				CA1398	ant3-5	ant3-5	HE858238	HE858238	ANT
				CA1400	ant11-7	cil1-4	ACC	HE858225	CIL/ANT
	Kilis-Töreli Çapalı road	36.8549	37.3414	CA1390	ant3-5	cil1-4	HE858238	HE858225	CIL/ANT
				CA1391	rid3-7	ant3-5	ACC	HE858238	RID/ANT
				CA1393	rid3-8	cil1-4	ACC	HE858225	CIL/RID
				CA1394	ant11-7	cil1-4	ACC	HE858225	CIL/ANT
	Kilis-Üçpınar	36.8669	36.9328	CA1961	cil1-4	cil1-4	HE858225	HE858225	CIL
				CA1964	cil1-1	cil1-1	ACC	ACC	
	Konya-Mehmetali dam	37.2124	32.6354	CA1463	ant11-7	ant10-4	ACC	ACC	ANT
				CA1465	ant5-6	ant3-5	HE858230	HE858238	
				CA1466	ant1-5	ant1-5	ACC	ACC	
	Korkuteli	36.9918	29.5279	VDBKCA07125	ant3-5	ant2-1	HE858238	ACC	ANT
				VDBKCA07130	ant3-5	ant3-5	HE858238	HE858238	
	Kovada	37.6325	30.8641	CBCAST3215	ant5-7	ant3-2	ACC	ACC	ANT
				OAOBBKCA1593	ant5-6	ant2-1	HE858230	ACC	
				OAOBBKCA1596	ant4-3	ant2-1	ACC	ACC	
				OAOBBKCA1597	ant8-3	ant5-2	ACC	ACC	
				OAOBBKCA1598	ant1-5	ant7-3	ACC	ACC	
				OAOBBKCA1599	ant5-4	ant5-7	ACC	ACC	

Table 3.3. (continued).

Turkey	Kovada	37.6325	30.8641	OAOBBKCA1593101	ant5-6	ant10-1	HE858230	ACC	ANT
				OAOBBKCA1593102	ant10-1	ant10-1	ACC	ACC	
	Kütahya-Enne dam	39.4688	29.8657	CA1685	ant10-4	ant8-3	ACC	ACC	ANT
				CA1686	ant1-6	ant10-4	ACC	ACC	
				CA1687	ant7-3	ant7-3	ACC	ACC	
	Kütahya-Koçak stream	39.3090	29.9753	CA1697	ant11-7	ant10-4	ACC	ACC	ANT
				CA1698	ant7-3	ant10-4	ACC	ACC	
				CA1699	ant11-7	ant10-4	ACC	ACC	
				CA1701	ant11-7	ant11-7	ACC	ACC	
	Kütahya-Porsuk dam	39.5740	30.0918	CA1705	ant7-3	ant10-1	ACC	ACC	ANT
				CA1707	ant7-3	ant10-4	ACC	ACC	
				CA1708	ant10-4	ant10-4	ACC	ACC	
	Kütahya-Söğütözü stream	39.3374	29.9342	CA1690	ant10-4	ant10-4	ACC	ACC	ANT
				CA1691	ant10-1	ant10-4	ACC	ACC	
				CA1692	ant10-4	ant10-4	ACC	ACC	
				CA1694	ant10-1	ant10-4	ACC	ACC	
	Malatya	38.4276	38.3505	SO44286	ant11-7	ant11-7	ACC	ACC	ANT
	Malatya-Elemendik lake	38.3229	38.1551	CA552	ant11-9	ant3-5	ACC	HE858238	ANT
				CA554	ant3-5	ant3-5	HE858238	HE858238	
				CA555	ant3-5	ant3-5	HE858238	HE858238	
	Malatya-Karakaya dam	38.4882	38.3499	CA547	ant11-7	rid3-8	ACC	ACC	RID/ANT
				CA548	ant3-5	ant3-5	HE858238	HE858238	ANT
				CA551	rid3-8	ant11-9	ACC	ACC	RID/ANT
	Malatya-near Sultansuyu dam	38.3121	38.0434	CA558	ant11-7	ant11-7	ACC	ACC	ANT
				CA559	rid3-8	rid3-8	ACC	ACC	RID
				CA560	rid3-8	ant3-5	ACC	HE858238	RID/ANT

Table 3.3. (continued).

Turkey	Malatya-near Sultansuyu dam	38.3121	38.0434	CA561	ant11-9	ant11-7	ACC	ACC	ANT
	Malatya-Oluklu district	38.2406	37.9964	CA563	ant3-5	ant3-5	HE858238	HE858238	ANT
				CA564	rid3-8	ant11-9	ACC	ACC	RID/ANT
				CA565	rid3-8	ant3-5	ACC	HE858238	
	Manisa	38.6110	27.4483	OA45274	ant7-3	ant10-4	ACC	ACC	ANT
				OA45275	ant11-7	ant11-7	ACC	ACC	
				OA45276	ant4-3	ant10-1	ACC	ACC	
				OA45278	ant7-3	ant10-1	ACC	ACC	
				OA45279	ant11-7	ant10-4	ACC	ACC	
				OA45280	ant7-3	ant4-3	ACC	ACC	
				OA45281	ant10-4	ant10-4	ACC	ACC	
				OA45282	ant10-4	ant10-4	ACC	ACC	
	Manisa City Forest	38.6021	27.3867	CA1764	ant7-3	ant11-7	ACC	ACC	ANT
				CA1766	ant10-1	ant10-4	ACC	ACC	
				CA1768	ant7-3	ant7-3	ACC	ACC	
	Manisa-Köseler pond	38.8460	27.2006	CA1780	ant7-3	ant10-1	ACC	ACC	ANT
				CA1781	ant11-7	ant11-7	ACC	ACC	
				CA1784	ant7-3	ant7-3	ACC	ACC	
	Manisa-Örselli pond	38.8698	27.2620	CA1774	ant11-7	ant11-7	ACC	ACC	ANT
				CA1776	ant11-7	ant11-7	ACC	ACC	
				CA1777	ant11-7	ant11-7	ACC	ACC	
				CA1778	ant7-3	ant11-7	ACC	ACC	
	Manisa-Siyekli pond	38.7886	27.2559	CA1769	ant7-3	ant4-3	ACC	ACC	ANT
				CA1770	ant7-3	ant11-7	ACC	ACC	
				CA1771	ant7-3	ant11-7	ACC	ACC	
				CA1772	ant11-7	ant10-1	ACC	ACC	

Table 3.3. (continued).

Turkey	Manisa-Siyekli pond	38.7886	27.2559	CA1773	ant7-3	ant11-7	ACC	ACC	ANT
	Mardin-Bülbül village	37.3219	40.8364	CA1319	rid3-8	rid3-8	ACC	ACC	RID
	Mardin-Kızıltepe	37.1970	40.2767	CA1313	rid3-8	rid3-8	ACC	ACC	RID
				CA1314	rid3-8	rid3-8	ACC	ACC	
				CA1315	ant11-9	ant11-9	ACC	ACC	ANT
	Mardin-Mazıdağ	37.4622	40.6169	CA1326	ant11-9	ant11-9	ACC	ACC	ANT
				CA1327	rid3-8	ant11-7	ACC	ACC	RID/ANT
				CA1328	rid3-7	ant3-5	ACC	HE858238	
				CA1329	rid3-8	ant11-7	ACC	ACC	
				CA1330	rid3-8	ant3-5	ACC	HE858238	
	Mardin-Savur road	37.4406	40.8553	CA1320	rid3-8	rid3-7	ACC	ACC	RID
				CA1321	ant3-5	ant3-5	HE858238	HE858238	ANT
				CA1322	ant11-7	ant3-5	ACC	HE858238	
				CA1323	rid3-8	ant11-7	ACC	ACC	RID/ANT
				CA1324	rid3-8	rid3-8	ACC	ACC	RID
	Marmaris	36.8467	28.2879	AKCA48209	ant9-2	ant4-1	ACC	ACC	ANT
				AKCA48210	ant10-2	ant9-2	ACC	ACC	
				AKCA48211	ant7-3	ant4-3	ACC	ACC	
				AKCA48212	ant9-2	ant4-3	ACC	ACC	
	Mersin	36.7969	34.6019	SOCA33226	cil1-4	cil2-1	HE858225	ACC	CIL
	Mersin-Erdemli	36.5930	34.2873	CA1429	cil1-5	cil1-5	ACC	ACC	CIL
				CA1430	cil1-4	cil1-4	HE858225	HE858225	
				CA1431	cil1-4	ant5-6	HE858225	HE858230	CIL/ANT
	Mersin-Mut Bice stream	36.5896	33.2850	CA1915	ant5-6	ant5-6	HE858230	HE858230	ANT
	Mersin-Mut Bucakışla stream	36.6313	33.3675	CA1916	ant5-6	ant5-6	HE858230	HE858230	ANT
				CA1917	ant5-6	ant5-6	HE858230	HE858230	

Table 3.3. (continued).

Turkey	Mersin-Mut Bucakışla stream	36.6313	33.3675	CA1919	ant5-6	ant5-6	HE858230	HE858230	ANT
				CA1921	ant5-6	ant5-6	HE858230	HE858230	
	Mersin-Yenice	36.9673	35.0305	CA1424	cil2-2	cil1-8	ACC	ACC	CIL
				CA1425	cil1-6	cil1-6	ACC	ACC	
				CA1426	cil1-6	cil1-2	ACC	ACC	
				CA1427	cil1-4	ant11-7	HE858225	ACC	CIL/ANT
				CA1428	cil1-1	cil1-8	ACC	ACC	CIL
	Muğla-Dalaman Tersakan	36.7794	28.8252	CA1845	ant10-1	ant4-3	ACC	ACC	ANT
				CA1846	ant11-7	ant4-3	ACC	ACC	
				CA1847	ant9-2	ant4-3	ACC	ACC	
				CA1849	ant11-7	ant4-3	ACC	ACC	
				CA1850	ant10-1	ant3-5	ACC	HE858238	
	Muğla-Girdev plateau	36.7007	29.6509	CA1851	ant10-1	ant2-1	ACC	ACC	ANT
				CA1852	ant2-1	ant2-1	ACC	ACC	
				CA1853	ant2-1	ant10-1	ACC	ACC	
				CA1857	ant3-5	ant3-5	HE858238	HE858238	
				CA1861	ant3-5	ant2-1	HE858238	ACC	
	Muğla-Köyceğiz Zaferler village	36.9718	28.6299	CA1840	ant10-1	ant3-5	ACC	HE858238	ANT
				CA1841	ant9-2	ant11-7	ACC	ACC	
				CA1842	ant9-2	ant10-1	ACC	ACC	
				CA1844	ant10-1	ant4-3	ACC	ACC	
	Muğla-Ula Nannan stream	37.0129	28.5105	CA1836	ant9-2	ant10-1	ACC	ACC	ANT
				CA1837	ant4-3	ant10-1	ACC	ACC	
				CA1838	ant11-7	ant11-7	ACC	ACC	
				CA1839	ant11-7	ant10-1	ACC	ACC	
	Muğla-Yatağan Dipsiz stream	37.3750	28.0916	CA1826	ant7-3	ant11-7	ACC	ACC	ANT

Table 3.3. (continued).

Turkey	Narlı	37.3322	37.0425	OBMBCA46365	cil1-4	cil1-4	HE858225	HE858225	CIL
				OBMBCA46366	cil1-4	ant3-5	HE858225	HE858238	CIL/ANT
				OBMBCA46367	cil1-4	ant11-7	HE858225	ACC	
				OBMBCA46369	cil1-4	cil1-4	HE858225	HE858225	CIL
				OBMBCA46370	cil1-4	cil1-4	HE858225	HE858225	
				OBMBCA46371	cil1-1	cil1-1	ACC	ACC	
				OBMBCA46372	cil1-4	cil1-6	HE858225	ACC	
	National Observatory	36.8293	30.3407	VD07132	ant5-6	ant5-5	HE858230	ACC	ANT
				VD07134	ant5-6	ant5-5	HE858230	ACC	
				VD07135	ant5-6	ant5-5	HE858230	ACC	
				VD07136	ant5-6	ant5-5	HE858230	ACC	
	Nevşehir-Avanos Kızılırmak	38.7174	34.8575	CA1234	rid2-1	rid2-1	ACC	ACC	RID
				CA1235	ant3-5	rid3-8	HE858238	ACC	RID/ANT
	Nevşehir-Nar Ilıca river	38.6383	34.7089	CA1229	ant11-7	rid2-1	ACC	ACC	RID/ANT
				CA1230	ant11-7	ant11-7	ACC	ACC	ANT
	Nevşehir-Gülşehir Kızılırmak	38.7564	34.6513	CA1236	rid2-1	ant3-5	ACC	HE858238	RID/ANT
				CA1237	ant11-7	rid2-1	ACC	ACC	
	Nevşehir-Ürgüp	38.5741	34.9157	CA1231	ant11-7	rid2-1	ACC	ACC	RID/ANT
				CA1232	ant11-7	rid2-1	ACC	ACC	
				CA1233	ant11-7	ant11-7	ACC	ACC	ANT
	Niğde-Çamardı	37.9608	34.3572	CA1181	ant3-5	rid3-6	HE858238	ACC	RID/ANT
				CA1182	ant11-7	rid3-6	ACC	ACC	
				CA1183	cil1-4	ant3-5	HE858225	HE858238	CIL/ANT
				CA1185	ant3-5	rid3-6	HE858238	ACC	RID/ANT
				CA1186	cil1-4	rid2-1	HE858225	ACC	CIL/ANT
				CA1187	ant11-7	rid3-6	ACC	ACC	RID/ANT

Table 3.3. (continued).

Turkey	Niğde-Çiftlik	38.1779	34.4629	CA1195	rid3-5	rid3-5	ACC	ACC	RID
				CA1196	ant11-7	ant11-7	ACC	ACC	ANT
				CA1197	rid3-5	rid3-5	ACC	ACC	RID
				CA1198	cil1-4	cil2-1	HE858225	ACC	CIL
				CA1199	rid3-5	rid3-5	ACC	ACC	RID
				CA1200	ant11-7	rid3-5	ACC	ACC	RID/ANT
				CA1201	ant1-4	rid3-5	ACC	ACC	
				CA1202	ant11-7	ant11-7	ACC	ACC	ANT
				CA1203	rid3-5	rid3-5	ACC	HE858238	RID
				CA1204	ant11-7	rid3-5	ACC	HE858238	RID/ANT
	Niğde-15km to Ulukışla	37.6195	34.5366	CA1193	cil1-4	cil1-4	HE858225	HE858225	CIL
	Ordu-Civil Stream	40.9733	37.9030	CA858	ant11-7	ant7-3	ACC	ACC	ANT
				CA860	ant3-2	ant11-7	ACC	ACC	
				CA861	ant11-7	ant7-3	ACC	ACC	
	Ordu-Civil Stream	40.9733	37.9030	CA862	ant11-7	ant7-3	ACC	ACC	ANT
	Ordu-Fatsa	41.0753	37.4413	CA871	ant3-2	ant11-7	ACC	ACC	ANT
				CA872	ant11-7	ant11-1	ACC	ACC	
				CA873	ant3-2	ant11-7	ACC	ACC	
				CA874	ant3-2	ant11-7	ACC	ACC	
	Ordu-Perşembe	41.0251	37.8032	CA867	ant11-7	ant11-7	ACC	ACC	ANT
				CA869	ant3-5	ant11-6	HE858238	ACC	
				CA870	ant3-5	ant11-6	HE858238	ACC	
	Osmaniye-Aslantaş dam	37.2769	36.2744	CA1933	cil1-4	cil2-1	HE858225	ACC	CIL
				CA1935	cil1-4	cil1-6	HE858225	ACC	
				CA1936	cil1-4	cil2-1	HE858225	ACC	
	Osmaniye-Boru river	37.1780	36.4856	CA1943	cil1-4	cil1-8	HE858225	ACC	CIL

Table 3.3. (continued).

Turkey	Osmaniye-Boru river	37.1780	36.4856	CA1944	cil1-4	cil1-4	HE858225	HE858225	CIL
				CA1945	cil1-4	cil1-5	HE858225	ACC	
	Pazarcık	37.2819	37.1249	OBMBCA46353	cil1-4	cil1-4	HE858225	HE858225	CIL
				OBMBCA46354	ant3-5	cil1-4	HE858238	HE858225	CIL/ANT
				OBMBCA46355	ant3-5	cil1-4	HE858238	HE858225	
				OBMBCA46356	rid3-8	cil2-1	ACC	ACC	CIL/RID
				OBMBCA46357	cil1-4	cil1-4	HE858225	HE858225	CIL
				OBMBCA46358	cil1-4	cil1-4	HE858225	HE858225	
				OBMBCA46359	cil1-4	cil1-4	HE858225	HE858225	
				OBMBCA46360	rid3-8	cil1-4	ACC	HE858225	CIL/RID
				OBMBCA46361	cil1-4	cil1-1	HE858225	ACC	CIL
				OBMBCA46362	cil1-4	cil1-4	HE858225	HE858225	
	Rize	41.0110	40.5792	CA771	ant11-7	ant11-7	ACC	ACC	ANT
				CA772	ant11-7	ant11-7	ACC	ACC	
	Rize-Çiftekavak	41.0283	40.4858	CA779	ant11-7	ant11-6	ACC	ACC	ANT
	Rize-Hemşin Stream	41.1554	40.9012	CA769	ant11-7	ant11-7	ACC	ACC	ANT
				CA770	ant3-5	ant11-7	HE858238	ACC	
	Samsun-Bafra	41.5167	36.0158	CA891	ant3-2	ant11-7	ACC	ACC	ANT
				CA892	ant3-2	ant7-3	ACC	ACC	
				CA893	ant3-2	ant7-3	ACC	ACC	
	Samsun-Kavak	41.1567	36.0927	CA897	ant3-2	ant3-2	ACC	ACC	ANT
				CA899	ant11-7	ant11-1	ACC	ACC	
				CA900	ant11-7	ant11-6	ACC	ACC	
	Samsun-19 Mayıs	41.4674	36.0993	CA886	ant11-6	ant7-3	ACC	ACC	ANT
				CA887	ant3-5	ant7-3	HE858238	ACC	
				CA888	ant3-2	ant11-7	ACC	ACC	

Table 3.3. (continued).

Turkey	Samsun-19 Mayıs	41.4674	36.0993	CA889	ant3-2	ant11-6	ACC	ACC	ANT
	Samsun-Tekkeköy	41.2126	36.4790	CA878	ant3-2	ant11-7	ACC	ACC	ANT
				CA879	ant3-2	ant11-7	ACC	ACC	
				CA881	ant11-7	ant11-7	ACC	ACC	
				CA882	ant3-2	ant7-3	ACC	ACC	
	Seydişehir	37.4557	31.8156	SGCA42202	ant1-4	ant1-5	ACC	ACC	ANT
				CA1458	ant11-7	ant10-4	ACC	ACC	
				CA1459	ant10-4	ant8-3	ACC	ACC	
				CA1460	ant1-4	ant8-3	ACC	ACC	
	Siirt-Başyurt river	37.9726	41.7806	CA1372	rid3-8	ant11-7	ACC	ACC	RID/ANT
				CA1373	rid3-8	ant11-7	ACC	ACC	
				CA1374	rid3-8	rid3-7	ACC	ACC	RID
				CA1375	ant11-9	ant11-9	ACC	ACC	ANT
				CA1376	ant11-7	ant11-7	ACC	ACC	
				CA1377	ant11-7	ant11-9	ACC	ACC	
	Siirt-Kezer river	37.9610	41.8573	CA1378	ant11-7	ant11-7	ACC	ACC	ANT
				CA1379	ant11-7	ant11-9	ACC	ACC	
				CA1380	rid3-8	ant11-7	ACC	ACC	RID/ANT
				CA1383	ant11-9	ant3-5	ACC	HE858238	ANT
				CA1384	ant11-9	ant11-9	ACC	ACC	
	Silifke	36.3130	33.9595	OBMB33257	cil2-1	ant10-1	ACC	ACC	CIL/ANT
				OBMB33258	ant5-6	cil1-4	HE858230	HE858225	
				OBMB33264	ant5-6	cil1-4	HE858230	HE858225	
				OBMB33265	ant5-6	cil1-4	HE858230	HE858225	
				OBMB33270	ant5-6	cil1-4	HE858230	HE858225	
				OBMB33271	ant5-6	ant5-6	HE858230	HE858230	ANT

Table 3.3. (continued).

Turkey	Silifke	36.3130	33.9595	OBMB33272	ant5-6	cil1-4	HE858230	HE858225	CIL/ANT
	Sinop-Ayancık	41.9483	34.7749	CA925	ant11-7	ant7-3	ACC	ACC	ANT
				CA926	ant11-7	ant11-7	ACC	ACC	
				CA927	ant11-7	ant11-7	ACC	ACC	
	Sinop-Gerze	41.8567	35.0999	CA930	ant11-7	ant11-6	ACC	ACC	ANT
				CA932	ant11-7	ant7-3	ACC	ACC	
				CA933	ant11-7	ant7-3	ACC	ACC	
				CA934	ant11-7	ant7-3	ACC	ACC	
	Sinop-Erfelek Çobanlar	41.9543	35.0196	CA920	ant11-7	ant7-3	ACC	ACC	ANT
				CA921	ant11-7	ant7-3	ACC	ACC	
				CA922	ant11-7	ant7-3	ACC	ACC	
				CA923	ant11-7	ant7-3	ACC	ACC	
	Sinop-Kabalı village	41.8468	35.0503	CA936	ant11-7	ant11-6	ACC	ACC	ANT
				CA938	ant11-7	ant11-7	ACC	ACC	
	Sivas-Hafik lake	39.8727	37.3825	CA1090	ant11-7	ant3-5	ACC	HE858238	ANT
				CA1091	ant11-7	ant3-5	ACC	HE858238	
				CA1092	ant11-7	ant11-7	ACC	ACC	
				CA1093	ant11-7	ant3-5	ACC	HE858238	
				CA1094	ant11-7	ant11-7	ACC	ACC	
				CA1095	ant11-7	ant11-7	ACC	ACC	
	Sivas-Kızılırmak	39.7154	37.0117	CA1100	ant11-7	ant11-7	ACC	ACC	ANT
				CA1101	ant11-7	ant11-7	ACC	ACC	
				CA1102	ant11-7	ant11-7	ACC	ACC	
	Sivas-Tecer river	39.6922	37.0034	CA1085	ant11-7	ant11-7	ACC	ACC	ANT
				CA1087	ant11-7	ant11-7	ACC	ACC	
				CA1088	ant3-5	ant3-5	HE858238	HE858238	

Table 3.3. (continued).

Turkey	Sivas-Tödürge lake	39.8713	37.6068	CA1097	ant11-7	ant11-7	ACC	ACC	ANT
				CA1098	ant11-7	ant3-5	ACC	HE858238	
				CA1099	ant11-7	ant11-7	ACC	ACC	
	Sorgun Dam	38.6555	29.3386	CBCA6444	ant11-7	ant11-7	ACC	ACC	ANT
				CBCA6445	ant7-3	ant10-1	ACC	ACC	
				CBCA6446	ant7-3	ant7-3	ACC	ACC	
	Şanlıurfa-Bozova	37.3588	38.5284	CA1300	rid3-8	rid3-7	ACC	ACC	RID
				CA1302	rid3-8	ant3-5	ACC	HE858238	RID/ANT
				CA1303	rid3-8	rid3-8	ACC	ACC	RID
				CA1304	cil1-4	cil1-4	HE858225	HE858225	CIL
	Şanlıurfa-Harran road	37.1488	38.9681	CA1294	rid3-8	ant11-7	ACC	ACC	RID/ANT
				CA1295	rid3-8	rid3-8	ACC	ACC	RID
				CA1296	rid3-8	ant3-5	ACC	HE858238	RID/ANT
				CA1298	rid3-8	rid3-7	ACC	ACC	RID
	Şanlıurfa-Mardin road 30. km	37.1467	38.1144	CA1306	rid3-8	ant3-5	ACC	HE858238	RID/ANT
				CA1307	rid3-8	ant3-5	ACC	HE858238	
				CA1308	ant3-5	ant3-5	ACC	HE858238	ANT
				CA1309	rid3-8	ant3-5	ACC	HE858238	RID/ANT
				CA1310	ant11-7	ant3-5	ACC	HE858238	ANT
	Tefenni	37.2333	29.7113	YECA15144	ant2-1	ant10-1	ACC	ACC	ANT
				YECA15145	ant4-3	ant10-1	ACC	ACC	
				YECA15146	ant2-1	ant4-3	ACC	ACC	
				KYECA15147	ant2-1	ant4-3	ACC	ACC	
				KYECA15149	ant3-5	ant10-5	HE858238	ACC	
				MAHACA15151	ant3-5	ant3-5	HE858238	HE858238	
				MAHACA15152	ant3-5	ant2-1	HE858238	ACC	

Table 3.3. (continued).

Turkey	Tekirdağ-Bıyıkali lake	41.0114	27.3930	CA1508	ant11-7	rid2-1	ACC	ACC	RID/ANT
				CA1509	ant11-7	rid1-2	ACC	ACC	
				CA1510	ant7-2	ant11-7	ACC	ACC	ANT
				CA1511	ant11-7	ant11-7	ACC	ACC	
				CA1512	ant11-7	ant10-4	ACC	ACC	
	Tekirdağ-Kepenekli dam	41.1121	27.5519	CA1513	ant11-7	ant11-7	ACC	ACC	ANT
				CA1514	ant11-7	rid1-2	ACC	ACC	RID/ANT
				CA1515	ant7-3	rid1-3	ACC	ACC	
				CA1516	ant11-7	rid1-3	ACC	ACC	
				CA1517	ant11-7	ant11-7	ACC	ACC	ANT
				CA1518	ant7-3	ant11-7	ACC	ACC	
	Tekirdağ-Yazır lake	40.9330	27.398	CA1503	ant7-3	ant7-3	ACC	ACC	ANT
				CA1504	ant7-3	rid3-4	ACC	ACC	RID/ANT
				CA1505	ant11-7	rid1-2	ACC	ACC	
				CA1506	ant11-7	rid1-7	ACC	ACC	
				CA1507	ant11-7	ant11-7	ACC	ACC	ANT
	Tokat-Avlunlar stream	40.5114	36.7342	CA1070	ant11-7	ant3-2	ACC	ACC	ANT
				CA1071	rid2-1	ant3-2	ACC	ACC	RID/ANT
				CA1072	rid2-1	ant3-2	ACC	ACC	
	Tokat-Çördük plataeu	40.2207	36.5622	CA1079	ant11-7	ant11-7	ACC	ACC	ANT
				CA1080	ant11-7	ant3-5	ACC	HE858238	
				CA1081	ant11-7	ant3-2	ACC	ACC	
				CA1082	ant11-7	ant11-7	ACC	ACC	
	Tokat-Kömeç Yeşilırmak	40.3396	36.4605	CA1055	ant11-7	ant11-7	ACC	ACC	ANT
				CA1059	ant11-6	ant3-2	ACC	ACC	
	Tokat-Yalancı stream	40.4106	36.7153	CA1062	ant11-7	ant7-3	ACC	ACC	ANT

Table 3.3. (continued).

Turkey	Tokat-Yalancı stream	40.4106	36.7153	CA1063	ant11-7	rid2-1	ACC	ACC	RID/ANT
				CA1064	ant11-7	ant7-3	ACC	ACC	ANT
				CA1065	ant11-7	ant7-3	ACC	ACC	
	Tokat Yusufoğlan	40.3421	36.9325	KO60318	ant11-6	rid2-1	ACC	ACC	RID/ANT
				KO60319	ant11-7	ant11-6	ACC	ACC	ANT
				KO60320	ant3-5	ant7-3	HE858238	ACC	
	Trabzon-Arsin	40.9515	39.9009	CA792	ant11-6	ant6-2	ACC	ACC	ANT
				CA793	ant11-6	ant6-2	ACC	ACC	
				CA795	ant6-2	ant6-2	ACC	ACC	
	Trabzon-Darıca	41.0718	39.5113	CA782	ant11-7	ant6-2	ACC	ACC	ANT
				CA783	ant11-7	ant11-7	ACC	ACC	
				CA787	ant11-7	ant7-3	ACC	ACC	
	Trabzon Derecik	41.0558	39.3900	RYDCA61256	ant7-3	ant6-2	ACC	ACC	ANT
	Trabzon-Söğütlü	41.0064	39.6310	CA790	ant11-7	ant7-3	ACC	ACC	ANT
				CA791	ant11-7	ant11-2	ACC	ACC	
	Türkoğlu	37.3808	36.8764	OBMBCA46373	cil1-4	bed1-5	HE858225	ACC	CIL/BED1
				OBMBCA46374	cil1-4	cil2-1	HE858225	ACC	CIL
				OBMBCA46376	cil1-4	cil2-1	HE858225	ACC	
				OBMBCA46377	cil1-4	ant3-5	HE858225	ACC	CIL/ANT
				OBMBCA46378	cil1-4	cil1-4	HE858225	HE858225	CIL
	Yalova-Altınova stream	40.7084	29.4730	CA1562	ant7-2	ant7-3	ACC	ACC	ANT
				CA1563	ant7-2	ant7-3	ACC	ACC	
				CA1565	ant9-1	ant7-2	ACC	ACC	
				CA1567	ant7-2	ant7-3	ACC	ACC	
	Yalova-Taşköprü	40.6801	29.3907	CA1568	ant7-2	ant7-3	ACC	ACC	ANT
				CA1570	ant7-3	ant7-3	ACC	ACC	

Table 3.3. (continued).

Turkey	Yalova-Taşköprü	40.6801	29.3907	CA1572	ant7-3	ant11-7	ACC	ACC	ANT
				CA1573	ant7-2	ant7-3	ACC	ACC	
	Yeşilova	37.5348	29.6473	ISCA1579	ant3-5	ant4-3	HE858238	ACC	ANT
				ISCA1580	ant3-5	ant4-3	HE858238	ACC	
				ISCA1581	ant10-1	ant10-1	ACC	ACC	
				ISCA1582	ant2-1	ant10-1	ACC	ACC	
				ISCA1583	ant10-4	ant10-4	ACC	ACC	
				ISCA1584	ant4-4	ant10-1	ACC	ACC	
				ISCA1585	ant4-3	ant11-7	ACC	ACC	
				ISCA1587	ant2-1	ant8-5	ACC	ACC	
				ISCA1588	ant10-1	ant10-1	ACC	ACC	
				ISCA1589	ant4-3	ant2-1	ACC	ACC	
	Yozgat-Gedikhasanlı	39.5720	35.1373	CA1111	rid2-1	ant3-2	ACC	ACC	RID/ANT
				CA1112	ant11-7	ant3-5	ACC	HE858238	ANT
				CA1113	ant11-6	ant7-3	ACC	ACC	
				CA1114	ant11-7	ant11-6	ACC	ACC	
	Yozgat-Mükremin lake	39.8030	35.2215	CA1117	rid2-1	ant3-5	ACC	HE858238	RID/ANT
				CA1119	ant11-7	ant11-7	ACC	ACC	ANT
				CA1120	rid2-1	ant11-7	ACC	ACC	RID/ANT
				CA1121	rid2-1	ant11-7	ACC	ACC	
	Yozgat-Sorgun	39.8042	35.2035	CA1105	ant11-7	ant11-7	ACC	ACC	ANT
				CA1106	ant11-7	ant11-6	ACC	ACC	
				CA1107	ant11-7	ant11-6	ACC	ACC	
	Yozgat-Yerköy Delice river	39.6117	34.5031	CA1124	ant11-7	ant11-7	ACC	ACC	ANT
				CA1125	ant11-7	ant11-7	ACC	ACC	
				CA1126	ant3-2	ant3-5	ACC	HE858238	

Table 3.3. (continued).

Turkey	Yozgat-Yerköy Delice river	39.6117	34.5031	CA1127	ant10-4	ant3-5	ACC	HE858238	ANT
	Yumurtalık	36.6925	35.6288	TBCASE0154	cil1-4	cil2-2	HE858225	ACC	CIL
				TBCASE0155	cil1-4	cil1-4	HE858225	HE858225	
				TBCASE0157	cil1-4	cil1-2	HE858225	ACC	
				TBCASE0158	cil1-5	cil1-7	ACC	ACC	
				TBCASE0160	cil1-4	rid3-8	HE858225	ACC	CIL/RID
				TBCASE0161	cil1-4	cil1-4	HE858226	HE858226	CIL
				TBCASE0163	cil1-4	cil1-8	HE858225	ACC	
				TBCASE0164	cil1-4	cil2-1	HE858225	ACC	
				TBCASE0165	cil1-4	cil1-5	HE858225	ACC	
	Van-Edremit Çiçekli	38.3443	43.1881	CA638	ant11-7	ant3-5	ACC	HE858238	ANT
				CA639	ant11-8	ant11-8	ACC	ACC	
				CA641	ant3-5	ant3-5	HE858238	HE858238	
				CA642	ant11-8	ant3-5	ACC	HE858238	
	Van-Gevaş	38.3079	43.1232	CA645	ant11-7	ant11-7	ACC	ACC	ANT
				CA647	ant11-8	ant3-5	ACC	HE858238	
				CA649	ant11-7	ant11-4	ACC	ACC	
				CA651	ant11-8	ant11-8	ACC	ACC	
	Van-Muradiye Bendimahı River	38.9366	43.6611	CA652	rid3-8	ant3-5	ACC	HE858238	RID/ANT
				CA653	rid3-8	rid3-8	ACC	ACC	RID
				CA654	rid3-8	ant3-5	ACC	HE858238	RID/ANT
				CA656	ant11-9	ant3-5	ACC	HE858238	ANT
	Uşak-Gediz river	38.7878	29.2243	CA1732	ant10-1	ant10-4	ACC	ACC	ANT
				CA1733	ant4-3	ant11-7	ACC	ACC	
				CA1734	ant11-7	ant10-1	ACC	ACC	
				CA1735	ant11-7	ant11-7	ACC	ACC	

Table 3.3. (continued).

Turkey	Uşak-Gediz river	38.7878	29.2243	CA1736	ant11-7	ant10-1	ACC	ACC	ANT
	Uşak-Göğen lake	38.7207	29.5563	CA1742	ant1-4	ant3-2	ACC	ACC	ANT
				CA1743	ant7-3	ant10-1	ACC	ACC	
				CA1744	ant11-7	ant10-4	ACC	ACC	
				CA1745	ant3-2	ant11-7	ACC	ACC	
				CA1746	ant7-3	ant11-7	ACC	ACC	
				CA1747	ant11-7	ant10-1	ACC	ACC	
	Uşak-Karakoç lake	38,6542	29,3336	CA1737	ant10-4	ant10-4	ACC	ACC	ANT
				CA1738	ant11-7	ant10-1	ACC	ACC	
				CA1740	ant11-7	ant10-1	ACC	ACC	
				CA1741	ant10-1	ant10-1	ACC	ACC	
	Zonguldak	41.4271	31.7268	FGCA67251	ant3-2	ant3-2	ACC	ACC	ANT
				FGCA67252	ant12-1	rid1-7	ACC	ACC	RID/ANT
	Zonguldak-Alaplı	41.1515	31.3521	CA1013	ant11-7	ant10-1	ACC	ACC	ANT
				CA1014	ant11-7	ant7-3	ACC	ACC	
				CA1016	ant11-6	ant11-6	ACC	ACC	
	Zonguldak-Kilimli	41.4005	31.6837	CA1003	ant11-7	ant11-6	ACC	ACC	ANT
				CA1004	ant7-3	ant7-2	ACC	ACC	
				CA1006	ant7-3	ant7-3	ACC	ACC	
	Zonguldak-Şirinköy	41.5065	31.9726	CA996	ant11-6	ant7-3	ACC	ACC	ANT
				CA997	ant11-7	ant12-1	ACC	ACC	
				CA998	ant7-3	rid1-7	ACC	ACC	RID/ANT
				CA1000	ant11-6	ant12-1	ACC	ACC	ANT
				CA1001	ant11-3	ant11-6	ACC	ACC	
Ukraine	Crimea-Theodosia town	45.0458	35.3716	42-1	ant6-2	ant6-2	ACC	ACC	ANT
				42-2	ant6-1	rid2-5	ACC	ACC	RID/ANT

Table 3.3. (continued).

Ukraine	Crimea-Theodosia town	45.0458	35.3716	42-3	ant7-3	rid2-5	ACC	ACC	ANT
				42-4	ant6-2	ant6-1	ACC	ACC	
				42-5	ant6-2	ant6-1	ACC	ACC	
				42-7	ant6-1	ant6-1	ACC	ACC	
				42-8	ant6-1	rid2-5	ACC	ACC	RID/ANT
	Kharkiv-Chepel	49.2666	36.9166	57-1	ant8-2	rid1-5	ACC	ACC	RID/ANT
	Kharkiv-Gaidary village	49.6205	36.3286	44-01	rid1-5	rid1-5	ACC	ACC	RID
				44-02	ant8-2	rid1-5	ACC	ACC	RID/ANT
				44-3	ant7-3	rid2-5	ACC	ACC	
				44-8	ant7-3	rid1-5	ACC	ACC	
				44-9	ant7-3	ant7-3	ACC	ACC	ANT
				44-10	ant7-3	rid1-5	ACC	ACC	RID/ANT
				44-12	ant8-2	rid1-5	ACC	ACC	
				44-13	ant7-3	rid1-5	ACC	ACC	
				44-25	ant7-3	ant7-3	ACC	ACC	ANT
	Kharkiv-Krasnokutsk	50.0527	35.1494	46-01	ant7-3	ant7-3	ACC	ACC	ANT
				46-2	ant7-3	ant7-3	ACC	ACC	
				46-4	ant7-1	ant7-1	ACC	ACC	
				46-6	ant11-7	ant7-3	ACC	ACC	
				46-7	rid2-5	ant7-3	ACC	ACC	RID/ANT
				46-8	ant7-3	ant7-3	ACC	ACC	ANT
	Kharkiv-Kolomak	49.8166	35.2833	54-1	ant7-3	rid1-5	ACC	ACC	RID/ANT
				54-2	ant8-2	ant8-2	ACC	ACC	ANT
				54-3	ant7-3	ant7-3	ACC	ACC	
	Kharkiv-Liptsi village	50.2291	36.3955	45-01	ant7-3	ant7-3	ACC	ACC	ANT
				45-02	ant8-2	rid1-5	ACC	ACC	RID/ANT

Table 3.3. (continued).

Ukraine	Kharkiv-Liptsi village	50.2291	36.3955	45-3	ant8-2	rid1-5	ACC	ACC	RID/ANT
				45-7	ant7-3	ant7-3	ACC	ACC	ANT
				45-8	ant7-3	rid1-5	ACC	ACC	RID/ANT
				45-9	ant8-2	rid1-5	ACC	ACC	
				45-12	ant8-2	rid1-5	ACC	ACC	
				45-14	ant8-2	rid1-5	ACC	ACC	
Uzbekistan	Andijan-near Khanabad village	40.7999	72.9666	4-01	sp nov-3	sp nov-3	ACC	ACC	SP NOV
	Karakalpakistan-Takhtakupyr town	43.0333	60.25	14-12	ter-4	ter-4	ACC	ACC	TER
	Kashkadarya-near Dehkanabad village	38.3300	66.5000	10-10	ter-1	ter-1	ACC	ACC	TER
	Samarkand	39.6833	67.0666	7-8	sp nov-2	sp nov-2	ACC	ACC	SP NOV
				7-12	ter-2	ter-2	ACC	ACC	*TER*
	Tashkent-Novyi Chinaz village	40.9166	68.7166	6-29	sp nov-4	sp nov-4	ACC	ACC	SP NOV
Outgroups									
Greece	Demati/Crete	35.0333	25.2833	Hotz19856/ZMB56960	cre-2	cre-3	FN432374	FN432375	*CRE*
	Skinias/Crete	35.0632	25.3083	Hotz19852/ZMB56959	cre-1	cre-1	FN432376	FN432376	
Greece	Igoumenitsa	39.5000	20.2666	Hotz19421	epe-1	epe-1	FN432369	FN432369	*EPE*
	Lechena/Peloponnese	37.9174	21.2667	Hotz19552	epe-2	epe-2	FN432370	FN432370	
Italy	Metaponto	40.3737	16.8028	No.6311	ber-1	ber-1	FN432381	FN432381	*BER*
	Tarsia	39.6166	16.2666	Hotz19586	ber-2	ber-2	FN432382	FN432382	
Italy	Carbonare	45.9333	11.2166	-	les-1	les-1	FN432384	FN432384	*LES*
Germany	Berlin-Stechlin			3466	les-1	les-1	FN432384	FN432384	
				3467	les-1	les-1	FN432384	FN432384	

Table 3.3. (continued).

Montenegro	Lake Skutari	42.2410	19.1061	16863	shq-1	shq-1	ACC	ACC	SHQ
				16861	shq-2	shq-2	ACC	ACC	
				16914	shq-1	shq-1	ACC	ACC	
France	Ligagnaeu	43.5333	4.7500	Lib11	per-1	per-1	FN432377	FN432377	*PER*
Algeria	Abadla	31.0197	-2.7360	Hotz16704	sah-1	sah-1	FN432380	FN432380	*SAR*
	El Golea	30.5732	2.8920	Hotz16737	sah-2	sah-2	FN432379	FN432379	

Table 3.4. Calculation of genetic distance among mitohondrial subgroups, main haplogroups, and outgroup species. Arithmetic means and standart deviations of Tamura-Nei distances (Tamura and Nei, 1993) within (blue) and between (black) main haplogroups (MHG1-8), outgroups (gray coloured) and subgroups of MHG6 and MHG2, estimated with a gamma distributed shaped parameter (G = 0.325) and rate heterogeneity among groups in the program MEGA 5.10 (Tamura et al., 2011). Subgroups of MHG6 and MHG2 did not compare with each other because only the amount of genetic distance within MHGs was tried to estimate.

	MHG6a	***MHG6b***	***MHG6c***	***MHG6d***	***MHG2a***	***MHG2b***
MHG6a	**0.008** **±0.001**					
MHG6b	**0.025** ±0.004	**0.003** **±0.001**				
MHG6c	**0.019** ±0.003	**0.017** ±0.003	**0.007** **±0.001**			
MHG6d	**0.024** ±0.004	**0.023** ±0.004	**0.017** ±0.003	**0.006** **±0.001**		
MHG2a	-	-	-	-	**0.009** **±0.002**	
MHG2b	-	-	-	-	**0.022** ±0.003	**0.008** **±0.002**

Table 3.4. (continued).

1. MHG1	**0.008 ±0.001**															
2. MHG2	**0.079** ±0.010	**0.014 ±0.002**														
3. MHG3	**0.099** ±0.012	**0.093** ±0.011	**0.005 ±0.001**													
4. MHG4	**0.085** ±0.011	**0.080** ±0.010	**0.081** ±0.011	**0.003 ±0.001**												
5. MHG5	**0.092** ±0.011	**0.088** ±0.011	**0.087** ±0.010	**0.041** ±0.006	**0.007 ±0.001**											
6. MHG6	**0.080** ±0.010	**0.079** ±0.009	**0.076** ±0.010	**0,046** ±0.007	**0.046** ±0.006	**0.014 ±0.002**										
7. MHG7	**0.094** ±0.011	**0.086** ±0.010	**0.086** ±0.011	**0,054** ±0.008	**0.053** ±0.007	**0.032** ±0.005	**0.009 ±0.001**									
8. MHG8	**0.102** ±0.012	**0.095** ±0.011	**0.096** ±0.012	**0.063** ±0.008	**0.057** ±0.008	**0.052** ±0.007	**0.058** ±0.008	**0.001 ±0.001**								
9. P.cretensis	0.183 ±0.021	0.159 ±0.019	0.178 ±0.019	0.167 ±0.020	0.179 ±0.021	0.176 ±0.021	0.181 ±0.021	0.197 ±0.022								
10. P.epeiroticus	0.253 ±0.030	0.269 ±0.032	0.279 ±0.036	0.294 ±0.036	0.259 ±0.031	0.260 ±0.032	0.284 ±0.034	0.267 ±0.034	0.315 ±0.036							
11. P.lessonae	0.283 ±0.035	0.269 ±0.032	0.255 ±0.029	0.265 ±0.030	0.227 ±0.024	0.255 ±0.027	0.274 ±0.030	0.264 ±0.030	0.321 ±0.037	0.343 ±0.041						
12. P.bergeri	0.302 ±0.037	0.279 ±0.033	0.253 ±0.030	0.257 ±0.029	0.236 ±0.026	0.244 ±0.027	0.257 ±0.029	0.245 ±0.028	0.330 ±0.041	0.349 ±0.043	0.050 ±0.008					
13. P.shqipericus	0.300 ±0.038	0.267 ±0.032	0.288 ±0.034	0.286 ±0.035	0.262 ±0.033	0.278 ±0.032	0.292 ±0.035	0.273 ±0.033	0.313 ±0.037	0.336 ±0.043	0.120 ±0.016	0.109 ±0.015				
14. P.perezi	0.367 ±0.044	0.333 ±0.039	0.357 ±0.043	0.349 ±0.041	0.348 ±0.040	0.354 ±0.042	0.370 ±0.043	0.357 ±0.044	0.398 ±0.045	0.453 ±0.055	0.397 ±0.050	0.387 ±0.047	0.374 ±0.046			
15. P.saharicus	0.457 ±0.054	0.406 ±0.046	0.475 ±0.054	0.435 ±0.049	0.402 ±0.046	0.433 ±0.050	0.439 ±0.049	0.424 ±0.048	0.449 ±0.048	0.457 ±0.053	0.462 ±0.054	0.440 ±0.052	0.447 ±0.049	0.342 ±0.039		
16. P.nigromaculatus	0.520 ±0.062	0.490 ±0.057	0.526 ±0.061	0.501 ±0.061	0.516 ±0.064	0.506 ±0.058	0.510 ±0.061	0.530 ±0.061	0.523 ±0.058	0.593 ±0.068	0.525 ±0.063	0.513 ±0.061	0.490 ±0.059	0.436 ±0.050	0.463 ±0.046	

Table 3.5. Calculation of genetic distance among nuclear subgroups, main allele groups and outgroup species. Arithmetic means and standart deviations of the Tamura-3-parameter (T92) model (Tamura, 1992) within (blue) and between (black) main allele groups (Anatolia, Asia and Ridibundus), *P.bedriagae 2*, *P.cypriensis*, outgroups (gray coloured) and subgroups of Anatolia MAG and allele groups of Asia and Ridibundus MAGs estimated with a gamma distributed shaped parameter (G = 0.622) in the program MEGA 5.10 (Tamura et al., 2011).

ANATOLIA MAG

	MAGa	***MAGb***	***MAGc***	***MAGd***	***MAGe***
MAGa	**0.003** **±0.001**				
MAGb	**0.013** ±0.003	**0.003** **±0.001**			
MAGc	**0.013** ±0.003	**0.006** ±0.002			
MAGd	**0.014** ±0.003	**0.007** ±0.002	**0.005** ±0.002	**0.004** **±0.001**	
MAGe	**0.018** ±0.004	**0.010** ±0.002	**0.009** ±0.002	**0.010** ±0.002	**0.003** **±0.001**

ASIA MAG

	CIL1	***CIL3***	***TER***	***SP NOV***	***BED1***
CIL1	**0.002** **±0.001**				
CIL3	**0.004** ±0.001	**0.001** **±0.001**			
TER	**0.005** ±0.002	**0.005** ±0.002	**0.001** **±0.001**		
SP NOV	**0.010** ±0.003	**0.007** ±0.002	**0.011** ±0.003	**0.001** **±0.001**	
BED1	**0.007** ±0.002	**0.005** ±0.002	**0.008** ±0.003	**0.011** ±0.003	**0.003** **±0.001**

RIDIBUNDUS MAG

	RID1	***RID2***	***RID3***	***KUR***
RID1	**0.004** **±0.001**			
RID2	**0.006** ±0.002	**0.002** **±0.001**		
RID3	**0.010** ±0.003	**0.005** ±0.002	**0.001** **±0.001**	
KUR	**0.013** ±0.003	**0.009** ±0.003	**0.011** ±0.003	**0.002** **±0.001**

Table 3.5. (continued).

	1	***2***	***3***	***4***	***5***	***6***	***7***	***8***	***9***	***10***	***11***	***12***	***13***
1. Anatolia MAG	**0.010 ±0.002**												
2. Asia MAG	**0.040** ±0.006	**0.006 ±0.001**											
3. Ridibundus MAG	**0.039** ±0.006	**0.013** ±0.003	**0.007 ±0.001**										
4. Levant MAG (bed2)	**0.050** ±0.007	**0.043** ±0.007	**0.046** ±0.007	**0.001 ±0.001**									
5. Cyprus MAG	**0.039** ±0.006	**0.034** ±0.006	**0.038** ±0.006	**0.041** ±0.007	**0.002 ±0.001**								
6. P.cretensis	0.035 ±0.006	0.033 ±0.006	0.036 ±0.006	0.035 ±0.006	0.021 ±0.005								
7. P.epeiroticus	0.025 ±0.005	0.025 ±0.005	0.025 ±0.005	0.042 ±0.007	0.041 ±0.007	0.037 ±0.006							
8. P.lessonae	0.038 ±0.010	0.025 ±0.008	0.033 ±0.009	0.029 ±0.009	0.031 ±0.009	0.030 ±0.008	0.029 ±0.009						
9. P.bergeri	0.041 ±0.010	0.028 ±0.008	0.036 ±0.010	0.032 ±0.009	0.034 ±0.009	0.033 ±0.009	0.032 ±0.010	0.006 ±0.004					
10. P.shqipericus	0.054 ±0.008	0.044 ±0.007	0.042 ±0.007	0.041 ±0.007	0.054 ±0.008	0.045 ±0.007	0.044 ±0.007	0.044 ±0.011	0.050 ±0.012				
11. P.perezi	0.070 ±0.009	0.056 ±0.008	0.058 ±0.008	0.070 ±0.010	0.064 ±0.009	0.062 ±0.009	0.061 ±0.009	0.042 ±0.010	0.045 ±0.010	0.077 ±0.011			
12. P.saharicus	0.072 ±0.009	0.061 ±0.009	0.063 ±0.009	0.076 ±0.011	0.067 ±0.010	0.068 ±0.010	0.064 ±0.009	0.053 ±0.011	0.056 ±0.012	0.080 ±0.011	0.031 ±0.006		
13. P.nigromaculatus	0.130 ±0.020	0.113 ±0.018	0.120 ±0.018	0.113 ±0.019	0.116 ±0.020	0.111 ±0.019	0.125 ±0.020	0.127 ±0.023	0.126 ±0.023	0.146 ±0.025	0.108 ±0.018	0.125 ±0.020	

Table 3.6. Group specific unique molecular variations for nuclear SAI-1+*Rana*CR1 gene.

Groups		*Unique molecular variations*	*Allele Groups*			
ANATOLIA MAG	***MAGa***	-	***ANT1***	***ANT2***	***ANT3***	-
		C: 122	A or C: 434	A: 434		
		G: 137	T: 524	C: 524		
		C: 155	A: 1053	C: 1053	A: 1053	
		C: 162	T: 1069	C:1069	T:1069	
		C: 184				
		G: 450				
		T: 732				
		4G: 514-517				
		5CA: 738-747				
		6T: 1135-1140				
	MAGb	-	***ANT4***	***ANT5***	-	-
		G: 541	T: 1057	C: 621		
		G: 641				
		5G: 514-518				
		5CA: 738-747				
		6T: 1135-1140				
	MAGc	C: 605				
		A: 641				
		4G: 514-517				
		5CA: 738-747				
		6T: 1135-1140				
	MAGd	-	**ANT6**	**ANT7**	**ANT8**	-
			A : 9	T: 780		
			T: 23	A: 851		
			C: 68	C: 905		
		A: 300	C: 255	8 bp deletion: 938-947		
		5CA: 738-747	C: 410			
			A: 514	A: 970		
			A: 580			
			4G: 514-517	4G: 514-517	3-4G: 514-517	
			6T: 1135-1140	5T: 1135-1139	5-6T: 1135-1140	
	MAGe	-	***ANT9***	***ANT10***	***ANT11***	***ANT12***
		G: 319	A: 471	C: 384		T: 759
		T: 527				
		C: 532				
		A: 533				
		C: 584				
		3G : 514-516				
		5CA : 738-747				
		6T: 1135-1140				

Table 3.6. (continued).

Groups	*Unique molecular variations*	*Allele Groups*				
ASIA MAG	-	***CIL1***	***CIL3***	***TER***	***SP NOV***	***BED1***
		A or G: 762	C or T: 697	A: 469	C: 174	A or C: 384
				A: 483	C: 379	T or C: 411
	3G: 514-516				C: 390	A: 413
	5T: 1135-1139				G: 438	G: 419
					T: 478	
					T: 506	
		6CA: 738-749	6CA: 738-749	6CA: 738-749	6CA: 738-749	4-6CA: 738-749
RIDIBUNDUS MAG	-	***RID1***	***RID2***	***RID3***	***KUR***	-
		G or T: 316	G or A: 538	G: 63	T: 186	
		A: 413	A or G: 569	T or C: 446	A: 202	
	3G: 514-516	G: 419	A or G: 733	A or G: 489	A: 415	
		A or C: 899	T or C: 740	T: 759	124 bp deletion : 758 - 890	
				A: 1014		
					C: 1057	
		5-6CA: 738-749	6-7CA: 738-751	8-10CA: 738-757	6CA: 738-749	
		5T: 1135-1139	5-6T: 1135-1140	6T: 1135-1140	6T: 1135-1140	

CHAPTER 4

CONCLUSIONS

In the first manuscript;

✓ In the 5' region of the water frog serum albumin gene, several potential regulatory elements were identified. These were TATA box, hepatocyte-specific promoter element, CAT box, amphibian downstream element, ADEI and ADEII, which could be involved in tissue specific expression.

✓ In the 3' region of the water frog serum albumin gene, several conserved cis-regulatory elements were found: poly(A)-limiting elements a and b (PLEa, PLEb), U-rich upstream element 1 (USE1), poly(A) signal (PAS), U-rich upstream element 2 (USE2), polyadenylation site (PAS), and GU-rich downstream element (GU-rich DSE).

✓ In contrast to strong length conservation in protein coding exons among distinct vertebrate species, intron lenghts in the albumin gene of *P. lessonae* showed a considerable variation, and were quite longer than those in other vertebrate species especially 3,4, 5, 8, 10, 11 and 13.

✓ Retroelements (belonging distinct classes of LTR, non-LTR elements, DNA transposons, and simple repeats) found upstream of the 5' UTR, downstream of the 3' UTR and within individual albumin introns could be one of the important drivers of the albumin gene evolution.

- ✓ Particularly Tc1 like elements (TLE) has 11 truncated copies in the serum albumin gene representing seven distinct intact TLEs, which could have an important impact on not only serum albumin gene but also genome evolution.

- ✓ Derived consensus elements of these seven TLE obtained from several truncated copies in the *P. lessonae* genome indicated that some of them could be recently transferred horizontally to the *P. lessonae* genome since some of them had several long copies and a few active copies in the genome such as PL Tc1-1Ory and PL Tc1-DR1 elements.

- ✓ In contrast, others could be potentially very old elements since they have several short truncated copies, very long insertion and deletions in both left and right ITRs or the transcriptional regulatory region, and none of copies has an intact ORF such as PL Tc1-10Xt, PL Tc1-RT, PL Tc1-PP and PL Tc1-FR3.

- ✓ All these had ITRs varying in size from 29 bp to 221 bp which contained DRs in their extremities. The size of the transcriptional regulatory region changed from 72 bp (PL Tc1-FR3) to 187 bp (PL Tc1-RT). Except PL Tc1-DR1 and PL Tc1-FR3, they all contained a TA duplication at the end of ITRs.

- ✓ In addition to TLEs, six truncated hAT-like elements (HLE), representing three distinct HLE were identified in the serum albumin gene. These were named as PL hAT-2-TS, hAT-2-ET, hAT-2-OG elements that all could be ancient elements because they had indels in both ITRs, the transcriptional regulatory region or ORF.

- ✓ Phylogenetic analysis of nucleotide and aa sequences of albumin gene exons gave similar topological results except the position of *P. epeiroticus* which formed a sister group to *P. ridibundus.*

In the manuscript 2,

- ✓ mtDNA and nuDNA markers revealed discordances in the tree topology, the level of genetic differentiation, the number of genetic stocks, the times of divergence and the patterns of geographic distribution.

- ✓ mtDNA tree represented several well diverged monophyletic groups while nuDNA tree contained both weakly supported and some well supported groups.

- ✓ In the mtDNA tree, *P. bedriagae* (MHG2) indicated an ingroup species, clustering with *P. ridibundus* (MHG1) as a sister group, whereas in the nuDNA tree it (Levant MAG5) formed a clade within the outgroup species *P. shqipericus/P. lessonae/ P. bergeri.*

- ✓ *P. cretensis* showed a divergence earlier than *P. cypriensis* in the mtDNA tree, but these two formed sister species in the nuDNA tree. The estimated time of divergence for mtDNA indicated divergence of P. cretensis before 9 Ma while the estimated time of divergence for nuDNA indicated the same divergence time both for P. cypriensis and P. cretensis about 6-5 Ma.

- ✓ *P. epeiroticus* split off before *P. cretensis/P. cypriensis* in the mtDNA tree, but in the nuDNA tree was more closely related with the Anatolia and Asia/Rid MAGs.

- ✓ *P. ridibundus* in the mtDNA tree formed a sister group with *P. bedriagae* from the Levant whereas in the nuDNA tree it clustered with the Asia MAG2, including groups from Central Asia, central-southern Turkey and the Levant (BED1) which indicated very recent divergence (2.0-1.7 Ma).

- ✓ In contrast to the well diverged Cilician (MHG4 and 5) and Central Asia (MHG7 and 8) monophyletic groups in the mtDNA tree about 3.5-4.5 Ma, their relationships within the Asian MAG2 were not fully resolved. nuDNA findings indicated a very shallow divergence among these groups about 1.5-0.5 Ma.

CURRICULUM VITAE

PERSONAL INFORMATION

Surname, Name: Akın Pekşen, Çiğdem
Nationality: Turkish
Date and Place of Birth: 9 September 1980, Edirne
Marital Status: Married
Phone: +90 312 210 50 45
Fax: +90 312 210 79 76
E-mail: cerigensis@gmail.com

EDUCATION

Degree	Institution	Year of Graduation
M. Sc.	METU Biology	2007
B. Sc.	Gazi University Biology	2002

WORK EXPERIENCE

Year	Place	Enrollment
2003-2015	METU Biology	Research Assistant

FOREIGN LANGUAGES

Advanced English

PUBLICATIONS

Theses:

M. Sc. Thesis: Detection of species boundaries in the *Rana ridibunda* complex of Southwestern Turkey using mitochondrial ND3 marker.

Research Articles:

1. Plötner, J., Baier, F., Akın, Ç., Mazepa, G., Schreiber, R., Beerli, P., Litvinchuk, S.N., Bilgin, C.C., Borkin, L., Uzzell, T. (2012) Genetic data reveal that water frogs of Cyprus (genus Pelophylax) are an endemic species of Messinian origin. *Zoosystematics and . Evolution.* 88: 261-283.

2. Akın, Ç., Bilgin, C.C., Beerli, P., Westaway, R., Ohst, T., Litvinchuk, S.N., Uzzell, T., Bilgin, M., Hotz, H., Guex, G.-D., Plötner, J. (2010b). Phylogeographic patterns of genetic diversity in eastern Mediterranean water frogs were determined by geological processes and climate change in the Late Cenozoic. *Journal of Biogeography* 37: 2111-2124.

3. Akın, Ç., Bilgin, M. & Bilgin C.C. (2010) Discordance between ventral colour and mtDNA haplotype in the water frog *Rana* (*ridibunda*) *caralitana*, 1988 Arıkan. *Amphibia-Reptilia* 31: 9-20.

International Congress Presentations:

Oral presentations:

1. Akın, Ç., Bilgin, C.C., Hotz, H., Beerli, P., Westaway, R., Ohst, T., Guex, G.-D., Litvinchuk, S.N., Uzzell, T., Bilgin, M., Plötner, J. (2009). Use of genetic divergence in water frogs to constrain geodynamics and landscape development in the eastern Mediterranean Region. Abstract: International Workshop on Active Tectonic Studies and Earthquake Hazard Assessment in Syria and Neighboring Countries, Arab School of Science and Technology – Damascus – Syria, 17-19 November, pp, 92-93.

2. Çilingir, F.G., Akın Pekşen, Ç., Ambarlı, H., Beerli, P., Bilgin, C.C. (2014) Brown bears from Turkey show exceptionally high maternal lineage diversity. Ecology and Evolutionary Biology Symposium (12-13 July, İstanbul), pp: 13-14.

3. Akın Pekşen, Ç, Bilgin, C.C., Beerli, P., Westaway, R., Schreiber, R., Mazepa, G., Uzzell, T., Plötner, J. (2014) Do discordant mitochondrial and nuclear distribution patterns indicate introgression following secondary contact between Anatolian water frog lineages (Pelophylax cf. bedriagae) and European water frog lineage (Pelophylax ridibundus) in Anatolia? Ecology and Evolutionary Biology Symposium (12-13 July, İstanbul), pp: 19.

Poster presentation:

1. Akın, Ç., Bilgin, M., Kaya, B., Bilgin, C.C. (2007) Discordance between ventral color and mtDNA haplotype in the water frog *Rana (ridibunda) caralitana*. Abstract (poster presentation): Origin and Evolution of Biota in Mediterranean Climate Zones – Zurich – Switzerland, 14-15 July, pp, 14.

National Congress Presentations:

Oral presentations:

1. Akın, Ç., Bilgin, M., Bilgin, C.C. (2006) Rana *(Ridibunda) caralitana* Arıkan 1988 (Amphibia: Ranidae) taksonunun yayılış sınırlarının moleküler yöntemlerle saptanması. 18. Ulusal Biyoloji Kongresi (26-30 Haziran, Aydın). Bildiri Kitabı Sayfa: 75.

2. Akın, Ç., Bilgin, C.C., Hotz, H., Beerli, P., Westaway, R., Ohst, T., Guex, G.-D., Litvinchuk, S.N., Uzzell, T., Bilgin, M., Plötner, J. (2010). Anadolu su kurbağalarının (Pelophylax (Rana)) mitokondriyal DNA genetik çeşitliliğinin geçmiş jeolojik olaylarla şekilllenmesi. 20. Ulusal Biyoloji Kongresi (21-25 Haziran, Denizli). Bildiri Kitabı Sayfa: 165-166.

3. Akın, Ç. Kılıç, A., Kürüm, V., Plötner, J., Bilgin, C.C. (2011) Anadolu su kurbağaları (Ranidae: Pelophylax) ticaretinin ekolojik etkileri. 10. Ulusal Ekoloji ve Çevre Kongresi (3-7 Ekim, Çanakkale). Bildiri Kitabı Sayfa: 24.

4. Kunduz, E., Akın, Ç., Bilgin, C.C. (2011) Moleküler yöntemlerle kuşlarda eşey tayini. 10. Ulusal Ekoloji ve Çevre Kongresi (3-7 Ekim, Çanakkale). Bildiri Kitabı Sayfa: 25.

5. Çilingir, F.G., Akın, Ç., Ambarlı, H., Bilgin, C.C. (2012) Zor yakalanan hayvan gruplarından boz ayıların (Ursus arctos) dışkı, kıl, ve postlarından girişimsiz genetik örnekleme başarısı. 21. Ulusal Biyoloji Kongresi (3-7 Eylül, İzmir).

Poster presentation:

1. Kunduz, E., Akın, Ç., Bilgin**,** C.C. (2012) Kuşlarda moleküler yöntemlerle eşey belirlenmesinde kullanılan üç primer sisteminin sonuçlarının kıyaslanması. 21. Ulusal Biyoloji Kongresi (3-7 Eylül, İzmir).

Book Chapter:

1. Plötner, J.**,** Uzzell, T., Beerli, P., Akın, Ç., Bilgin, C.C., Haefeli, C., Ohst, T., Köhler, F., Schreiber, R., Guex, G.-D., Litvinchuk, S.N., Westaway, R., Reyer, H.-U., Pruvost, N., Hotz, H (2010). Genetic divergence and evolution of reproductive isolation in eastern Mediterranean water frogs. In: Glaubrecht M (Ed). Evolution in Action. Case studies in Adaptive Radiation, Speciation and the Origin of Biodiversity. Special volume originating from contributions to the Priority Programme SPP 1127 “Radiations: Origins of Biological Diversity” of the DFG. Springer, Heidelberg, Berlin, pp. 373-403.

PROJECTS:

1. Investigation of population biology and the effect commercial trade on eastern Mediterranean water frog populations (*Pelophylax* spp). TUBITAK TBAG 112T913.

2. Detection of genetic diversity in the eastern, southeastern Anatolia, Black Sea and east of Central Anatolian water frog populations. TUBİTAK TBAG 111T584.

3. Genetic divergence and evolution of reproductive isolation in Eastern Mediterranean water frogs. Complementary action among German, Switzerland and Turkey, financed by DFG (Germany) (2002-2009).

4. Detection of species boundaries in the *Rana ridibunda* complex of Southwestern Turkey using mitochondrial ND3 marker. (BAP-08-11-DPT.2002K120510-DK-14). OYP-DPT Project.

RESEARCH ACTIVITY:

1. Studies on molecular markers at Museum für Naturkunde, Berlin, Germany (supervised by Dr. Jörg Plötner)
i. Application of ITS2 markers on the southwestern Anatolian water frog populations for three months in 2006
ii. Application of a new nuclear marker on Anatolian water frogs for three months in 2009
iii. Application of SAI-RanaCR1 marker on eastern Mediterranean water frog complex and learning new methods about whole genome and bioinformatic tools for 9 months in 2012-2013.

2. Genetic analysis of ungulate populations (fallow deer) data derived from microsatellites at ISPRA (Department of Conservation Biology and Genetics, Laboratory of Genetics) , Bologna, Italy for 4 weeks in 2012 (supervised by Dr. Ettore Randi)

AWARDS/GRANTS:

1. First Honor in B. Sc., Gazi University University, June 2002
2. Training course grant for Conservation Genetics: Assessing populations structure and dynamics through the use of molecular markers and novel computational models", Château Liblice, Czech Republic, 1-7 September 2008.
3. German Academic Exchange Service (DAAD): Research grants and Study Scholarships (10/06/2009 - 08/09/2009)
4.. TÜBİTAK International Scientific Publication Awards, 2010
5. METU Scientific Publication Award, 2010
6. ÖYP Grant for 9 months research in Museum für Naturkunde, Berlin, Germany, 2012-2013.