



3rd Ecology and Evolutionary Biology Symposium, Turkey

August 31 - September 1, 2016

Symposium Programme

&

Abstract Book

Hacettepe University

Ankara, 2016

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Symposium Program

August 31st - September 1st, 2016

August 31st

07:30 - 09:30 | Registration

09:45 - 10:00 | Opening ceremony

Keynote Speaker

10:00 - 10:45 | Alexey S. Kondrashov - "Evidence for evolution: XXI century perspective"

10:45 - 11:15 | Tea/coffee break

Session 1 - (Chair: Mehmet Somel)

11:15 - 11:30 | Alexey Yanchukov - "A general framework to study genome-wide associations in hybrid zones with high-resolution genome coverage: example of gene Copy Number Variant data"

11:30 - 11:45 | Oleksandr I. Zinenko - "Phylogeny, phylogeography, taxonomy and evolution of small European vipers: why we need all types of markers"

11:45 - 12:00 | Eren Ada - "A new insight into the phylogeography of the European Green Lizard"

12:00 - 13:30 | Symposium Lunch

Keynote Speaker

13:30 - 14:15 | Matteo Fumagalli - "Detecting adaptive evolution in the high-throughput sequencing era"

Session 2 - (Chair: Gürkan Semiz)

14:15 - 14:30 | C. Can Bilgin - "First molecular findings for the Anatolian Leopard (*Panthera pardus tulliana*) imply an extended range eastwards and a reassessment of subspecies level taxonomy"

14:30 - 14:45 | Kahraman İpekdal - "Detection of hybridization from microsatellites: a case study using the genus *Thaumetopoea* (Lepidoptera)"

14:45 - 15:00 | Ferhat Kaya - "Late Miocene biogeography of the Old World savanna mammals and the origins of the East African savanna biome!"

15:00 - 15:15 | David Tarkhnishvili - "Combination of modeling and genetic data for allocation of Tertiary refugia in the Caucasus"

15:15 - 15:30 | Tamer Albayrak - "Phylogeography and genetic diversity of Anatolian avifauna: A mtDNA perspective"

15:30 - 16:30 | Poster Session (including tea/coffee)

16:30 - 18:30 | Panel and discussion on the conservation of biodiversity in Turkey (in Turkish)

19:30 - 21:00 | Annual General Assembly of Ecology and Evolutionary Biology Society of Turkey (in Turkish)

September 1st

Keynote Speaker

09:15 - 10:00 | Anders Götherström - "The demography of the neolithisation, the greatest story in our history."

Session 3 - (Chair: S. Bülent Alten)

10:00 - 10:15 | Alexander Gavashelishvili - "Glacial human refugia and landscape permeability explain the current genetic structure of human populations better than language or ethnicity"

10:15 - 10:30 | Emre Keskin - "Environmental DNA MetaBarcoding approach in biodiversity Assessment of a lake ichthyofauna"

10:30 - 10:45 | Mehmet Somel - "Autism spectrum disorder in context of human brain evolution"

10:45 - 11:00 | Mine Altınlı - "The effect of *Wolbachia* genetic diversity on the prevalence of *Culex pipiens* densovirus (CpDV) in natural *Cx. pipiens* populations in Tunisia"

11:00 - 11:30 | Tea/coffee break

Session 4 - (Chair: Nüzhet Dalfes)

11:30 - 11:45 | Anıl Soyumert - "The lynx in the Western Black Sea Region of Anatolia: An update on local distribution"

11:45 - 12:00 | Nur Filiz - "How phytoplankton community response to extreme temperature and nutrient stressors: using a heated mesocosm experiment"

12:00 - 12:15 | Korhan Özkan - "Danish lake plankton: opportunities of analysing long term monitoring datasets"

12:15 - 12:30 | Remzi Atlıhan - "Assessment of temperature-mediated changes in predation rates: A case study of the green lacewing, *Chrysoperla carnea*, at different temperatures"

12:30 - 14:00 | Poster Session (including lunch)

Session 5 - (Chair: Utku Perktas)

14:00 - 14:15 | Raşit Bilgin - "The intertwined effects of geographic barriers, palaeoclimate and life history on the distribution of genetic diversity: A case study with two marine species in the eastern Mediterranean"

14:15 - 14:30 | Dilan Saatoğlu - "Genetic diversity of gazelles (*Gazella marica* and *Gazella gazella*) in Southeast Turkey: Special emphasis on ongoing conservation studies of *Gazella marica* in Turkey"

14:30 - 14:45 | Mert Kükreler - "Adaptive traits of Turkish honeybee subspecies in response to climate: A survey and a test of niche overlap"

14:45 - 15:00 | Uğur Işkın - "Zooplankton community structure under the impact of heat waves and nutrient enrichment: A mesocosms approach"

15:00 - 15:30 | Tea/coffee break

Session 6 - (Chair: Ayşegül Birand)

15:30 - 15:45 | Erol Akçay - "Social inheritance in animal social networks and its consequences"

15:45 - 16:00 | İsmail Bekar - "The role of anthropogenic and natural factors in shaping recent fire regimes in Mediterranean ecosystems"

16:00 - 16:15 | Özge Tutar - "Oxidative stress response of *P. oceanica* and *C. nodosa* to short-term heat stress"

16:15 - 16:30 | Ezgi Özkurt - "Genome evolution of the fungal grass pathogen *Zymoseptoria pseudotritici* following homoploid hybrid speciation"

Closing Session

17:00 - 18:00 | Poster & oral presentation awards, concluding remarks, and closing ceremony

KEYNOTE TALKS

Evidence for evolution: XXI century perspective

Alexey S. Kondrashov¹

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The hypothesis that humans and apple trees shared a common ancestor is so astonishing that it should not be accepted without strong evidence. In physics, a hypothesis is tested by comparing its quantitative predictions with the data. However, theory of evolution of life is generally incapable of generating such prediction, with the marked exception of the case of neutral theory. By contrast, there are a lot of qualitative predictions,. The hypothesis of past evolution is supported by suboptimality of modern species, their similarities not forced by adaptation, hierarchical joint distributions of multiple traits, a number of scenario-based inferences, and a number of patterns in spacial distributions of modern species.

Keywords: evolution, evidence, homology, hierarchy, neutral theory.

Detecting adaptive evolution in the high-throughput sequencing era

Matteo Fumagalli¹

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High-throughput sequencing machines are now providing researchers with massive amount of DNA data. I will discuss how the recent availability of large-scale genomic data from many species of interest is providing novel insights and advances into (i) evolutionary genomics, (ii) human genetics, and (iii) bioinformatics.

(i) The relatively low cost of whole-genome sequencing experiments is allowing researchers to study previously neglected species. By analyzing more than one hundred genomes of bears, I will show how signatures of adaptation to cold and a lipid-rich diet are present in the genome of polar bears. I will then discuss how isolation and low population size have drastically affected the genomic variability in worldwide bears, with notable consequences for conservation.

(ii) Detecting signatures of natural selection in the human genome has a twofold meaning. Apart from unveiling traces of our past history, variants targeted by selection are candidate to hold important functionality to the carrier. I will discuss how, by analyzing the genomes of human populations locally adapted to the Arctic environment, we were able to identify genetic variants strongly associated with anthropometric phenotypes, with direct clinical relevance. I will then present some ongoing research on the evolution of a family of human proteins involved in glucose transport. We show how selection might have dramatically affected the genetic diversity of such family, with implications for protein functionality at the cellular level.

(iii) Data produced by high throughput sequencing machines is typically affected by large errors and uncertainty. Recently, we introduced statistical methods that take genotype uncertainty into account, allowing for an accurate estimation of nucleotide diversity from noisy data. However, most of the available approaches are based on assumptions of random mating and diploid genomes. I will present a novel statistical framework to estimate ploidy from sequencing data, taking into account base qualities and depth. We also show how this method can be adopted to perform variant and genotype calling under an arbitrary number of ploidy.

Keywords: Next-generation sequencing, population genetics, natural selection, human genetics, polyploidy

The demography of the neolithisation, the greatest story in our history

Anders Götherström¹

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In the beginning of last century archaeologists started to piece the puzzle on the spread of farming together. Vere Gordon Child described a pattern where the earliest remains indicating a transition from a hunter-gatherer lifestyle to a farming one were found in Anatolia. Almost a century of debate followed on how the farmer-expansion occurred. There were just not enough evidence to conclude what part migration played. Until 2012, when we were able to directly compare genomic data from early farmers and late hunter-gatherers in northern Europe. The four years that have since followed has seen a number of reports on the subjects from us and several of our colleagues. There are many particulars. The genetic make-up are different in early farmers and late hunter-gatherers in Europe and the western parts of Asia, as is the genetic variability. Through a number of studies we are now able to follow the farming technology, and the people who carried it with them, all the way back to central-southern Anatolia. The early phase seems to have been a dynamic period in Anatolia, where techniques were refined and genetic elements from external groups were picked up and adsorbed. Whereafter the whole package expanded out from Anatolia and into Europe with recurrent geneflow. An average Swedish modern genome can trace about 40% of its genes back to this expansion, while certain areas of the northern coastal Mediterranean are almost complete genetic descendants of the farming groups that once left Anatolia. The effect the process had on our societal development can not be exaggerated, and it also is the stuff of one of the most beautiful stories of our common history.

Keywords: Neolithisation, aDNA, demography, migration

ORAL PRESENTATIONS

A general framework to study genome-wide associations in hybrid zones with high-resolution genome coverage: example of gene Copy Number Variant data

Alexey Yanchukov^{1,2}, Zusanna Hiadlovská³, Zeljka Pezer⁴, Milos Macholan³, Jaroslav Pialek² and Stuart J.E. Baird²

¹ Department of Biology, Faculty of Arts and Sciences, Bülent Ecevit University, Turkey ² Institute of Vertebrate Biology, AS CR, Czech Republic ³ Institute of Animal Physiology and Genetics, AS CR, Czech Republic ⁴ Laboratory of Evolutionary Genetics, Ruđer Bošković Institute, Croatia ⁵ Max-Planck Institute of Evolutionary Biology, Germany

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Hybrid zones have long been described as ‘windows on the evolutionary process’, a statement becoming ever more significant with the advance in the genome analysis tools. The hybrid zone between two subspecies of the house mouse (*Mus musculus musculus* and *Mus m. domesticus*) is a unique mammalian model system to study fine scale interactions of recently diverged genomes. Recently, 252 individuals both from the hybrid zone and the allopatric populations were genotyped for ~500k SNPs and the population of origin (i.e. *musculus* or *domesticus*) of every SNP allele was determined in the admixed individual genomes (Baird et al., in prep.). This dense marker coverage coupled with large sample size allows us to explore genome-wide associations of various traits that distinguish the two mouse subspecies and thus may play an important role in the speciation process. I present a general framework for the per-SNP association test for any quantitative trait in principle and apply it to the Copy Number Variation (CNV) data of the five genes that clearly differentiate the *musculus* and *domesticus* sides of the hybrid zone. In three cases the highest and/or outlying levels of association were observed at or close to the position of the gene amplicon as annotated in the mouse genome reference, demonstrating the power of our approach in confirming the reference locations of copy number variants. Notably, several other reference locations were recognized as positive outliers in association with particular CNV genes, possibly representing the extra gene copies and/or their epistatic interaction sites.

Keywords: MDA-SNP, house mouse, CNV, GWAS, hybrid zone

Phylogeny, phylogeography, taxonomy and evolution of small European vipers: why we need all types of markers

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Small European vipers of subgenus *Pelias* constitute a monophyletic group with divergent views on numbers and relationships between species in the group. We used different markers (mitochondrial and nuclear genes sequences, microsatelliteelites, RADseq) and methods (Maximum Likelihood, Bayesian Inference, Maximum Parsimony, coalescent reconstructions of phylogeny and effective population number, mismatch analysis, Bayesian clustering, ABBA/BABA statistics) to address questions related to evolution, phylogeny, speciation and hybridization, dating evolutionary events and systematics. Our results support monophyly of the group and its division into three subgroups – *V. ursinii*-*V. renardi* meadow and steppe vipers, *V. berus*-*V. seoanei* group of temperate “forest” species and endemic of Caucasus region *V. kaznakovi* group. At the same time, every single type of marker introduces its own bias, connected with such phenomena as high magnitude of variation (morphology), genetic drift (mitochondrial and nuclear genes), presence of nuclear copies of mitochondrial genes, mitochondrial genome capture through hybridization, interspecific gene flow and formation of stable hybrid populations, other peculiarities of evolution of single locus connected with adaptive evolution and different demographic history. Many morphological species described from isolated populations in fact show low levels of genetic divergence and should be synonymized. Different species of small vipers are often allopatric and are prone to hybridization in contact zones due to weak isolation mechanisms. Hybridization may play an important role in their evolution during Quaternary, when dynamic landmass reformations and climate oscillations were frequent.

Keywords: Genetic markers, phylogeny, phylogeography, evolution, *Vipera*

A new insight into the phylogeography of the European Green Lizard

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The late Quaternary climatic oscillations have always been an important actor for genetic differentiation within species. These differentiation patterns can be informative to understand species' historical demographic structure. There are a number of studies showing that many species distributed in the temperate zone have experienced range expansions and contractions. Therefore, some southern regions have been identified as glacial refugia for many species. Asia Minor is one of these glacial refugia and has been underrepresented in many studies that concern European phylogeographic patterns. In this study, we re-evaluated historical demography of *Lacerta viridis* (European Green Lizard), using ecological niche modelling and molecular phylogeography. Recent studies suggest that Anatolia was an important refugium for one lineage within species. In addition, we added three new mtDNA haplotypes, and found that Anatolia was the refugial area for another lineage, too. The results suggest that Anatolia is not a single homogeneous southern refugium but rather a more complex one than we thought before.

Keywords: Phylogeography, demography, last glacial maximum, climate change, lizard

First molecular findings for the Anatolian Leopard (*Panthera pardus tulliana*) imply an extended range eastwards and a reassessment of subspecies level taxonomy

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As a highly adaptable species, leopard is the most wide-ranging of the large felids. However, in most of western Asia their numbers have declined during the last century. The enigmatic Anatolian Leopard continues to remain emblematic for the Turkish public yet it is considered either already extinct or critically endangered by experts. On the other hand, there is genetic research claiming a single subspecies, *Panthera pardus saxicolor* in all of western Asia (except for Arabia). Yet no samples from Turkey were ever analyzed and published to support this claim while rules of zoological nomenclature were incorrectly applied during lumping several former subspecies into one.

Here we present the first genetic findings on Anatolian leopards. DNA from five tissue samples were amplified from old pelts at museums and private collections. Additional genetic material was obtained from 13 specimens from northeastern Turkey, Afghanistan, Armenia, Azerbaijan, Iran and Turkmenistan. We amplified and sequenced NADH-5 and CR regions of the mitochondrial genome, and combined our results with published sequences to determine the phylogenetic position of Turkish leopards. Leopard samples from the Aegean coast to the Caspian littoral formed a separate cluster compared to samples from further south and east, and possessed population specific mtDNA haplotypes. Our findings suggest that *tulliana* is not restricted to western Anatolia but ranges throughout Turkey, the Caucasus, northern Iran and Turkmenistan. We discuss whether the evidence is sufficient to subsume *saxicolor* under *tulliana*, and the consequences of such a taxonomic decision for species conservation in the region.

Keywords: Anatolian Leopard, mtDNA, taxonomy, *Panthera pardus*, subspecies

Detection of hybridization from microsatellites: a case study using the genus *Thaumetopoea* (Lepidoptera)

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Thaumetopoea pityocampa (TP) and *T. wilkinsoni* (TW) are two important forest pests in the Mediterranean. They exhibit highly similar habitat requirements and reproductive behavior. TP occurs in Europe, western North Africa, and northwestern Turkey, and TW in Turkey, and the Middle East. They are known to have a contact zone in Turkey but due to lack of sufficient genomic data, no further questions could be asked related to this contact zone.

We used 12 microsatellite loci along with sequence data from a mitochondrial and two nuclear genes. The questions we addressed are: (i) what is the extent of the contact zone that was previously determined, (ii) what is the extent of ongoing hybridization in this contact zone? For taxonomical identification, we used sequence comparisons, p-distances, phylogeny trees, and haplotype networks. Microsatellite data were analyzed for the population genetic structure first by performing principal component analysis and then by calculating membership coefficients (q) and hybrid indices of each individual in the dataset using STRUCTURE, NEWHYBRIDS, and INTROGRESS softwares. In order to determine q thresholds for each analyses, we simulated a hybridization scenario using the software HYBRIDLAB. For this purpose we determined 50 parental individuals from the two species according to their q scores and produced 100 and 1000 hybrid individuals per each of the four hybrid classes (i.e. F1, F2, backcross with each parental species).

We found 37 hybrid individuals out of 216 samples (0 F1, 6 F2, 11 backcrosses, 20 mt-nuc discordants). We also found that all of the individuals having the discordant pattern had a "*pityocampa*" mitochondrial haplotype. In the contact zone, where the populations of the two species are living together, we found that hybridization was not the common characteristic. While some populations had traces of introgression, others did not have any trace."

Keywords: Hybridization, microsatellite, *Thaumetopoea*, pine processionary moth

Late Miocene biogeography of the old world savanna mammals and the origins of the east African savanna biome!

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In spite of the long-running history of studies on the late Neogene mammal communities of the Old World, biogeographical relationships of African, Indian, and mainland Eurasian faunas within the framework of paleoenvironmental changes have remained obscure. We assembled the most recent data from the Old World Neogene mammal fossil record to map biogeographical development of chronofaunas in association with paleoenvironmental conditions, using genus-level faunal similarity and mean ordinated hypsodonty paleoprecipitation proxy analysis. In addition to the hypsodonty proxy we used late Miocene paleoclimate modeling to reconstruct global scale paleoenvironmental conditions. The map patterns reveal that savanna biomes developed as a result of the middle Miocene global cooling and aridification, spread of open habitats that connected vast continental areas during the early late Miocene. The Old World savanna biome, which flourished during the progressive drying of the late Miocene, and fragmented to Eurasian and African branches by increased aridification of North Africa and Arabia probably due to joining effect of major paleoenvironmental changes occurred during the latest Miocene. The Eurasian branches, the Pikermian and Baodean chronofaunas, became extinct at the end of the Miocene. The East African branch, the Nawatian chronofauna, survived and eventually contributed to the development of Plio-Pleistocene African savanna fauna, including its early hominins, through increasing East African endemism under the influence of intensified aridification of East Africa. The modern African savanna fauna is therefore an effectively surviving component of the Old World savanna biome, which at its peak covered much of the Old World.

Keywords: Fossil mammals, late Miocene, paleoclimate, African savannah, faunal similarity

Combination of modeling and genetic data for allocation of Tertiary refugia in the Caucasus

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Tertiary refugia maintain large portion of non-tropical biodiversity through geological time. The knowledge of the exact geographic position of the refugia is important because this helps to (1) better concentrate conservation efforts, (2) better design sampling for evolutionary and biodiversity studies, (3) identify source populations of threatened species. Traditionally, position of the refugia was inferred from extant biodiversity pattern and paleovegetation data. This approach leads to imprecise geographic pattern, because high species diversity can be of secondary origin (climates may spatially displace) and because availability of fossils depends on the current climate and landscape. We apply combination of two approaches for reconstruction the refugia: first, projecting GIS-based suitable habitat models on grids describing ancient climate; second, comparing these models and phylogenies of clonally inherited genes of organisms with low dispersal abilities. This approach allowed us to conclude that (a) there are multiple cryptic refugia beyond ones inferred by geo- and palaeobotanists, and (b) the known refugia were in fact discontinuous “meta-refugia”, supporting high local genetic diversity. West-Caucasus (“Colchis”) forest refugium at the eastern coast of the Black Sea provides an example of such complex spatial structure. Both modelling and phylogeography of various organisms (lizards, amphibians, snails, trees) revealed that individual areas with mild climates, separated by non-suitable areas of few tens of kilometers, supported isolation of multiple evolutionary lineages for millions of years. At the moment, we can make a firm conclusion on the presence of four more or less isolated refugia within the area referred as Colchis.

Keywords: Tertiary Refugia, phylogeography, GIS modeling, ancient climate, biomes

Phylogeography and genetic diversity of Anatolian avifauna: a mtDNA perspective

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Understanding the evolutionary processes in Anatolian populations has been a central theme in avian evolution. Though Anatolia has internationally recognized avian biodiversity with more than 470 bird species, phylogeography of the species are not well known. Five species, Kruper's Nuthatch, Chaffinch, Great Tit, Blue Tit, and Blackbird, were caught in six localities which covered the throughout Anatolian peninsula. To infer the genetic diversity of the species; we analyzed partial sequences of the mitochondrial cytochrome oxidase subunit I gene (COI) and NADH dehydrogenase 2 (ND2). The species showed geographic structuring or a low level of genetic differentiation in Anatolia. Different haplotypes were found among populations of the species in Turkey. The genetic structures are consistent with the isolation of these populations in different glacial refugia followed by establishing secondary contact after glacial retreat. Our results show that the level of the genetic diversity in Turkish avifauna is important and that resident forest species should be treated as separated conservation units.

Keywords: Anatolia, avifauna, mitochondrial DNA, conservation

Acknowledgments: This study was supported by TUBITAK (113O271).

Glacial human refugia and landscape permeability explain the current genetic structure of human populations better than language or ethnicity

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Our research attempts to provide an explicit explanation of human-biome interactions during the last glacial period and how these and landscape complexity have influenced the current human population genetics at the global scale.

Using climate, terrain, hydrographic, fossil pollen and plant macrofossil data we developed a model of the distribution of biomes during climate deteriorations of the last glacial period. Subsequently, we analyzed current human genetic structure, the origins of genetic lineages and Palaeolithic human sites in relation to the inferred biomes as well as landscape permeability.

Our analyses indicated that: (1) current human Y-DNA diversity, the places of origin of Y-DNA lineages and the distribution of Palaeolithic human settlements are best explained by distance from savanna and dry woodland during a series of glacial maxima, (2) during periods of relatively benign climate conditions, humans dispersed through areas of high primary productivity while avoiding dense forest cover and (3) there is a strong correlation between genetic differentiation among the populations and landscape permeability to human migrations. The permeability is determined by the combination of terrain ruggedness, forest cover, and snowiness.

In a metapopulation of Palaeolithic humans, the biome of savanna and dry woodland supported source populations and other biomes acted as sinks. Present-day genetic differences are largely related to landscape permeability between human source populations, and in the post-glacial period there has not been enough time for displacements and admixture of human populations to completely blur these differences.

Keywords: *Homo sapiens*, ice age, biome, refugium, terrain

Environmental DNA metaBarcoding approach in biodiversity assessment of a lake ichthyofauna

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Over exploitation and anthropogenic impacts are the main factors related to species extinction as the freshwater habitats become the most threatened ecosystems. It is a known fact that globally, more than 25% of freshwater animal species were under threat or already extinct. The main bio-indicators in monitoring of a healthy freshwater ecosystem is considered to be the fish species as they constitute the main vertebrate species with the highest intraspecific diversity. Identification of many taxa at once through complex and degraded DNA samples is the most novel approach on biodiversity assessment field and this approach is known as eDNA MetaBarcoding. This approach enables to determine a complete list of organisms from the target taxon without any need for a prior knowledge on the inhabiting species. Within this design, the success of pyrosequencing from environmental samples was tested in terms of determining the fish fauna of a deep tectonic lake (Lake Iznik). Primers, targeting a short fragment of cytochrome b gene of the mitochondrial genome were tagged according to sampling grids and used to enhance the specificity of eDNA metabarcoding approach. A total of 23 fish species were identified and five of them were found out to be reported for the first time. Results analyzed from pyrosequencing raw data was indicating that short fragments of sequences from cytochrome b gene made species level identification possible. The potential of this approach in monitoring biodiversity of species, especially rare and non-native ones in freshwater habitats is promising.

Keywords: eDNA, pyrosequencing, cytochrome b, metabarcoding, freshwater fish

Autism spectrum disorder in the context of human brain evolution

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Humans and chimpanzees display distinct cognitive differences, and one the most striking divergence lies in human social abilities and learning prowess. Our previous work comparing human, chimpanzee and macaque brain transcriptomes throughout postnatal development had identified candidate processes that distinguish humans from other primates. The most conspicuous candidate was synaptic development, which at a delayed and extended fashion compared to the other two species. This feature was suggested as key to elevated human learning abilities and possibly social skills. Notably, autism spectrum disorders (ASD), which affect about 1 in 100 individuals, involve disruption in social abilities and communication. Here we studied brain development in autism using RNA sequencing of postmortem brains of healthy and ASD individuals and compared expression shifts in autism with those identified among species. Our results indicate that the same synaptic development pathways that underwent a human-specific shift in hominin evolution are altered in autism.

Keywords: Autism, human evolution, brain, synapse, development

The effect of *Wolbachia* genetic diversity on the prevalence of *Culex pipiens* densovirus (CpDV) in natural *Cx. pipiens* populations in Tunisia

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Densoviruses are small, non-enveloped, single-stranded DNA viruses. They mainly infect arthropods causing epizootics in insects and crustaceans. In mosquitoes, they cause denosucleosis resulting in deformation, inhibition of the development, paralysis and host death. In this study, we focus on *Culex pipiens* densovirus (CpDV), initially discovered in *Cx. pipiens* mosquitoes, which are competent vectors of several arboviruses, as well as filarial nematodes and avian Plasmodia. All the mosquitoes of this species complex have always been found associated with a variety of strains from the wPip *Wolbachia* clade. Being a vertically transmitted endosymbiont, *Wolbachia* manipulates their hosts' reproduction to spread in the population. Additionally, recently, *Wolbachia* gained scientific interest due to their protective effect against several viruses in several arthropod hosts. Both densoviruses and *Wolbachia* are considered as possible vector control strategies due to their pathogenicity against mosquitoes and protection against viruses, respectively, even though our knowledge about the interactions between densoviruses and *Wolbachia* within the same host environment is limited. To discover these interactions in natural populations a detection test of CpDV by PCR amplification of NS2 protein coding region has been established. CpDV was found to be widespread in the tested larvae samples from Tunisia where two genetically different *Wolbachia* types co-exist. Moreover, CpDV prevalence was affected by *Wolbachia* type and sampling year. The next step in our study is to investigate the effect of *Wolbachia* amount and genetic diversity on host survival, virus load and diversity to better understand the dynamics of host-symbiont-pathogen interactions in natural *Cx. pipiens* populations.

Keywords: Densovirus, *Culex pipiens* complex, *Wolbachia*, vector ecology

The lynx in the Western Black Sea Region of Anatolia: An update on local distribution

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Western Black Sea Region of Anatolia has a worldwide importance in accordance to large mammal community. The region involves many large mammal species including brown bear (*Ursus arctos*), grey wolf (*Canis lupus*), Eurasian lynx (*Lynx lynx*), red deer (*Cervus elaphus*), wild boar (*Sus scrofa*) and roe deer (*Capreolus capreolus*). Camera-trapping studies in the region has been conducted since 2007 in the provinces of Bartın, Karabük and Kastamonu. The study consists of 242 camera-trap stations and over 50.000 camera-trap day in total at 15 different study areas including five wildlife reserves and one national park. The results indicate that the distribution map of Eurasian lynx is required to be updated. According to the previously existing maps, lynx has a wide distribution throughout the region, but the recent data obtained from the present study reveal that the lynx positive stations are located in Ilgazdağı, Gavurdağı and Elekdağı Wildlife Reserve Areas situated in the southern and eastern parts of Kastamonu, whereas the species could not be detected in the northern part of the Western Black Sea Region.

Keywords: Wildlife ecology, camera-trapping, large mammals, lynx

How phytoplankton community response to extreme temperature and nutrient stressors: using a heated mesocosm experiment

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Phytoplankton are short-lived organisms responding fast and directly to environmental fluctuations which make them useful indicators of deterioration in lake ecosystems to stressors. Due to climate change, extreme events including heat waves and flooding will be more common in the future and such changes also augment eutrophication, a problem lakes already is facing today.

To understand the effects of temperature and nutrient stressors on phytoplankton taxonomic groups and size diversity we conducted a mesocosm experiment in Silkeborg, Denmark a system which has been already continuously operated for 11 years. There are 24 mesocosms (1.9 m in diameter, 1.5 m in total depth, imitating a shallow lake) simulating two nutrient levels (unenriched and enriched with additional nitrogen and phosphorus) and three different temperature scenarios (ambient, IPCC A2 scenario and A2+%50) with 4 replicates. Heat wave was imitated for 1 month by rising the temperature 5°C (from 1st July till 1st August 2014). During this period samplings were done twice a week, and later less frequently. Phytoplankton was identified, biovolume and size diversity calculated. Using also physico-chemical variables from the mesocosms, the effects of the extreme heatwave on the phytoplankton community and structure at contrasting nutrient levels will be analysed and discussed.

Keywords: Phytoplankton, mesocosm, nutrient, heatwave

Danish lake plankton: opportunities of analysing long term monitoring datasets

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A monitoring programme for Danish lakes has been initiated in 1980's to understand the effect of eutrophication and climate change on Danish lakes. Approximately 400 lakes have been monitored with varying sampling intensity. The spatial analyses on a subset of these lakes (n: 195) have found driving role of water chemistry, especially total nitrogen on the patterns of phytoplankton richness with limited influence of land-use and climate. Due to uneven sampling intensity a stratified permutation and randomisation based statistical framework was used. Temporal analyses of another subset of these Danish lakes (n: 17, with two-decade bi-weekly time series) showed similar patterns. Lakes, which were previously eutrophicated and experienced a decline in their nutrient concentrations, had a strong corresponding decline in phytoplankton biomass and a recovery of plankton composition. Notably, a widespread positive trend in plankton richness was observed coinciding with widespread nutrient reductions mostly due to the better agricultural practices. However, no strong response in plankton was observed reflecting the trends in climate. Long term monitoring also provides unique opportunities to understand the effect of complex ecological dynamics like trophic interactions. For example, Lake Engelsholm was biomanipulated to reinforce its recovery from eutrophication. Long term monitoring showed that biomanipulation led a 10-fold decrease in phytoplankton biomass with substantial reduction of nutrient concentrations and an increase in plankton diversity. Long-term monitoring programmes are essential to understand the response of the ecosystems to changing environment. The scarcity of long-term monitoring programmes in Turkish ecological science is an important limitation.

Keywords: Community composition, phytoplankton, plankton diversity, trophic interactions, zooplankton

Assessment of temperature-mediated changes in predation rates: a case study of the green lacewing, *Chrysoperla carnea*, at different temperatures

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Temperature is one of the most important environmental variables influencing the efficiency of biological control agents in agricultural ecosystems. This study examines the effect of temperature on the functional response of third instar larvae of green lacewing, *Chrysoperla carnea* (Stephens), to different densities of dusky-veined walnut aphid, *Panaphis juglandis*. Experiments were carried out on walnut leaf discs (30 mm in diameter) placed in petri dishes (100x150 mm) at four different temperatures (18, 23, 28, and 32 °C), 60 ± 5% RH and a photoperiod of 16: 8 (L:D) h (5000 Lux) under laboratory conditions. Six prey densities (4, 8, 16, 32, 64, and 128) were used in the experiments. Logistic regression model was used to determine the functional response type of the predator. Results showed that temperature did not alter the functional response type, and third instar larvae of the predator exhibited a Type II response on dusky-veined walnut aphid at each temperature tested. However, the mean number of prey consumed (killed) increased with temperature. This finding suggested that warmer conditions may increase effectiveness of green lacewings for biological control of its hosts including dusky-veined walnut aphid.

Keywords: Functional response, *Chrysoperla carnea*

The intertwined effects of geographic barriers, palaeoclimate and life history on the distribution of genetic diversity: A case study with two marine species in the Eastern Mediterranean

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Understanding the allopatric isolation and evolutionary processes in the marine realm can be particularly difficult due to the high dispersal and gene flow potential of pelagic planktonic stages. Straits can be potential barriers to gene flow in the marine environment, resulting in the isolation of populations on either side. In addition to such physical barriers, paleoclimate and life history characteristics of species also contribute to genetic differentiation. In the eastern Mediterranean, the Turkish Straits System (TSS), comprising two straits (the Dardanelles and the Bosphorus Strait) and the Sea of Marmara forms the only connection between the Black Sea and the Mediterranean. TSS is also interesting from a paleoclimatic perspective, having been closed and opened multiple times during the last ice age. The effect of TSS as a barrier and/or corridor to gene flow has been proposed, but not extensively tested using genetics, previously. Here, using mitochondrial DNA (mtDNA) and nuclear markers, we tried to understand the effect of the TSS on the population structure of the Mediterranean mussel, *Mytilus galloprovincialis* and the rock shrimp, *Palaemon elegans*, both with pelagic larvae, but with sessile and non-sessile adult stages, respectively. We analyzed samples collected from the entire distribution of the two species around Turkey, encompassing the Black Sea, the TSS and the Aegean/Mediterranean. Results of the mtDNA analyses suggest that, in both species, the Black Sea populations were isolated and differentiated from the Aegean populations during the last ice age, and subsequently were able to colonize the Sea of Marmara and Aegean, with larval transport *via* the surface currents of the TSS. The gene flow was one-way for the most part, however, as the TSS did not allow the dispersal of the planktonic larvae of the Aegean haplotypes northwards. This is also where we see idiosyncracies due to the different life histories of the two species. Individuals with haplotypes of the Aegean origin in *P. elegans*, due to their non-sessile adult stages were able to recolonize the TSS at a higher frequency than their counterparts in *M. galloprovincialis*. The nuclear analyses, however, do not reflect the mtDNA differentiation observed among the Black Sea and the Aegean populations, and provide no genetic resolution. The discordance between

mitochondrial DNA and microsatellites suggest that although the isolation between the Black Sea and the Aegean populations of the two species resulted in the formation of two mitochondrial entities, it did not last long enough to promote nuclear differentiation and reproductive isolation.

Keywords: Allopatric barriers, paleoclimate, life history, intraspecific differentiation, *Mytilus galloprovincialis*, *Palaemon elegans*, Turkish Straits System

Genetic diversity of gazelles (*Gazella marica* and *Gazella gazella*) in Southeast Turkey: Special emphasis on ongoing conservation studies of *Gazella marica* in Turkey

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In the present study, we analysed samples from two captive gazelle populations at the Kızılkuyu State Farm (n=48) and the Erikçe State Farm (n=25) in Turkey using nuclear, mtDNA and Y-chromosome markers. A comparative sequence analysis of the mtDNA partial cyt-b region has confirmed that they belonged to *Gazella marica*. The structure analysis differentiated between these two populations and revealed wild population originated samples. We have also analysed four samples from a recently discovered *Gazella gazella* population in Hatay employing the same markers. The INRA126 locus on the Y-chromosome was sequenced from both *Gazella gazella* and *Gazella marica* species, for the first time in this study. Both the mtDNA partial cyt-b region RFLP analysis using HaeIII and HinfI endonucleases and the sequence analysis of the Y-chromosome INRA126 locus distinguished the two gazelle species from each other. Among the 17 autosomal microsatellite loci analyzed, 12 (RT1,ETH10, OARFCB304, BM848, BMC1009, INRA40, BM4505, INRABERN172, TGLA122,ILSTS005, BM757 and CSSM43) were found to be informative based on their polymorphic information content (PIC) estimates that can be employed in future studies.

Based on microsatellites, the effective population sizes were estimated as 9.7, 8.9 and 6.4 for the Kızılkuyu, Erikçe and Hatay populations, respectively. When the Kızılkuyu and Erikçe populations (where severe inbreeding depressions seems to be occurring already) were pooled, the estimated Ne was 24.5. Unfortunately, all these effective population sizes are too small for the sustainability of either individual or pooled populations in nature or even in captivity.

Keywords: *Gazella*, conservation, microsatellites, mtDNA, Y-chromosome

Adaptive traits of Turkish honeybee subspecies in response to climate: A survey and a test of niche overlap

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There are over 24 subspecies or “geographic races” of honeybees in the world. These races differ in morphology, biogeography and behavior and appear to have diversified following reproductive isolation during the Pleistocene glaciation. Research on their genetics suggest a model where Turkish races belong mostly to the same lineage, but evolved in extremely different habitats. Habitat-specific features such as daily temperature, abundance and phenology of nectar flow, length and severity of winter, or predator pressure are expected to influence foraging strategy, honey storage, production of young, overwintering success, swarming behavior or aggression in different races.

We surveyed potentially adaptive behavioral traits for each genetic component identified by microsatellite-based STRUCTURE analysis, and explored relations with climatic conditions prevalent where those components are geographically concentrated. To overcome restrictions of limited sampling, we used ecological niche modeling to estimate distributional ranges and identify possible climatic drivers of adaptation for four subspecies and one ecotype.

Our survey revealed a number of life history traits that were shown or hypothesized to be related to certain climatic features, and that most honeybee forms have morphologies or behave as predicted. Despite low sample size, niche modeling produced ranges for each subspecies/ecotype that roughly correspond with particular ecoregions in Turkey. Precipitation in warmest or coldest quarter, precipitation and temperature seasonality, mean temperature of wettest quarter and annual mean temperature explained more than other variables in the best models. We discuss adaptive values of the traits of honeybees and suggest hypotheses to test these associations.

Keywords: *Apis mellifera* subspecies, adaptive traits, ecological niche modeling, climate, distributional range

Zooplankton community structure under the impact of heat waves and nutrient enrichment: A mesocosms approach

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Shallow lakes, besides being the most widespread inland water bodies in the world are very sensitive to external perturbations, including land use and climate change. Today, unprecedented rates of warming threaten the functioning of lakes, especially when combined with additional multiple stressors as climate change itself also exacerbates the effects of stressors, especially eutrophication. Lately, extreme events e.g. -heat waves or flooding further complicate the impacts of stressors on ecosystem structure and functions. To elucidate the effects of nutrients and heat waves on zooplankton community structure and functioning we used 24 flow-through mesocosms (1.9 m in diameter, 1.5 m in total depth, imitating a shallow lake) located in Lemming, Denmark. The mesocosms simulate two nutrient levels, unenriched for control group and enriched with additional Nitrogen (N) and Phosphorus (P) combined with three different temperature scenarios (ambient, IPCC climate scenario A2, A2 + %50). Each of these treatment combinations were replicated four times. The heat wave treatment applied during a full month from 1st July 2014 till 1st August 2014. During this period zooplankton community was sampled more frequently, after the treatment period, sampling frequency extended over time. Total sampling period is from 19th June to 9th October. Collected zooplankton samples are being identified, counted and measured for further analysis. Impact of treatments on the community structure of zooplankton will be discussed using several community parameters such as biomass, biodiversity, size diversity, richness etc.

Keywords: climate change, freshwater, global warming, shallow lakes, stressors

Social inheritance in animal social networks and its consequences

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The social network structure of animal populations has major implications for survival, reproductive success, sexual selection, and pathogen transmission of individuals. But as of yet, no general theory of social network structure exists that can explain the diversity of social networks observed in nature, and serve as a null model for detecting species and population-specific factors. Here we propose a simple and generally applicable model of social network structure. We consider the emergence of network structure as a result of social inheritance, in which newborns are likely to bond with maternal contacts, and via forming bonds randomly. We compare model output to data from several species, showing that it can generate networks with properties such as those observed in real social systems. Our model demonstrates that important observed properties of social networks, including heritability of network position or assortative associations, can be understood as consequences of social inheritance.

Keywords: Social inheritance, social networks, heritability, assortment, social structure

The role of anthropogenic and natural factors in shaping recent fire regimes in Mediterranean ecosystems

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Although climatic factors are the main agents driving fire regimes during the most of the Holocene, many anthropogenic factors are responsible for the changes in fire regimes during the last century. The aim of this study is to investigate the relative roles of the anthropogenic and natural drivers shaping fire regimes in Mediterranean-type ecosystems of Turkey. Fire data gathered from NASA. BIOCLIM variables, NDVI, PET, and geographic variables were used to investigate the effect of natural factors on fire regimes. Data on road network, human population size, agricultural and husbandry activities were included in anthropogenic factors. The data was analyzed by binomial and zero-inflated negative binomial GLMs. Results showed that among all variables temperature and NDVI were the most explaining factors for fire regimes (respectively, %13.6 and %3.6). None of other factors has explained deviance higher than %1. Elevation had serious impact on the relative role of the drivers of fire regimes. Further analyses showed that considering agricultural lands in natural fire regime researches may have a potential of misleading the results. Our findings suggest that despite the intense anthropogenic pressure, natural factors are still the main drivers of fire regime in the study area. This study contributes to close the gap in our knowledge on fire regimes in the eastern Mediterranean Basin. As climate is the most influential driver shaping current fire regimes in the study area, the climate change may have profound effects on future fire regimes.

Keywords: Pyrogeography, fire ecology, fire regime, zero inflated data, climate

Oxidative stress response of *P. oceanica* and *C. nodosa* to short-term heat stress

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Posidonia oceanica and *Cymodocea nodosa* are marine angiosperms widely distributed in the Mediterranean Sea. As habitat builders, they have crucial importance for coastal ecosystems; however because of human activities and environmental changes populations are in regression. Studies indicate that increased maximum annual seawater temperature leads to increased seagrass mortality. High temperature induces oxidative stress and causes damage to proteins, lipids and DNA. Even though heat-stress induced oxidative stress is studied in some model species, there is a lack of knowledge for seagrasses, which actually can help to understand the response of species to global warming. Scope of this study was to understand the response of two important seagrass species to a realistic heat-wave simulation. Four different genotypes of *P. oceanica* and *C. nodosa* were collected from shallow and deep habitats in Murcia, Spain and exposed to short-term heat stress in mesocosms. Samples were collected at three time points and RNA was extracted by adult leaves. Gene expression analyses were performed by RT-qPCR. Antioxidant and stress responsive genes expression levels identified interspecific and intraspecific differences in the response to heat stress conditions. *P. oceanica* individuals are more affected by temperature increase compared to *C. nodosa*. The deep population of *P. oceanica* reacts to heat exposure later than the shallow one and does not show a real recovery. The more responsive genes in *Posidonia* are molecular chaperones, SOD and PrxQ. These results are opening questions for further studies considering the adaptation of seagrasses to global warming and their response at genotypic level.

Keywords: oxidative stress, heat stress, seagrass

Genome evolution of the fungal grass pathogen *Zymoseptoria pseudotritici* following homoploid hybrid speciation

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Hybridization is proposed to be a major force in the speciation of fungal plant pathogens. The ascomycete grass pathogen *Zymoseptoria pseudotritici* emerged recently from an interspecific cross between yet unknown parental species. In a previous study, the genomes of five individuals of *Z. pseudotritici* were sequenced and revealed a peculiar nucleotide diversity pattern: The genome consists of segments of high nucleotide diversity but comprising only two diverged haplotypes (2-3% nucleotide divergence). The other segments comprising more than 40% of the genome are completely depleted of variation. This particular genome structure results from a cross between only two parental individuals that gave rise to a hybrid swarm that has recombined but never back-crossed to the parental species. *Z. pseudotritici* provides a unique model system to study genomics of a young hybrid species. Hence we set out to investigate patterns of selection and distribution of derived mutations by sequencing additional 22 individuals. Re-analyzing the new sequence alignment, we could confirm the diversity patterns of the genome as found among only five individuals. Moreover, two parental haplotypes diverge from each other by 2.2%. This result reaffirms that the hybridization occurred between two close *Zymoseptoria* species, but after the divergence of the *Z. tritici* lineages. In the variable segments, 98% of the SNPs segregate as two alleles among the 27 individuals. The sites harbouring three or four alleles represent those sites in the genome where new mutations accumulate in the hybrid population. We assessed the site frequency spectrum to further investigate the distribution of variation in our population sample. The distribution of the allele frequencies was found to be remarkably different from the pattern in close relative species *Z. tritici* reflecting the different evolutionary histories of the species. Moreover, we assessed genome-wide signatures of positive selection by computing dN/dS ratios. 77 of the 5478 genes were identified to be evolving under positive selection. Gene ontology analyses showed that 14 of the positively selected genes encode secreted proteins, and are putative effector candidates involved in host-pathogen interactions. We are currently applying additional analyses to estimate age the hybridization and the amount of variation in the whole population.

Keywords: Hybrid speciation, fungal genome evolution, pathogen evolution

POSTER PRESENTATIONS

The effects of three different heavy metal (zinc, copper, nickel) on some biological and biochemical properties of the *Hyphantria cunea* larvae infected by *Bacillus thuringiensis* subsp. *kurstaki*

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In this study, we examined the synergistic effects of *Hyphantria cunea* larvae, which were infected with *Bacillus thuringiensis* subsp. *kurstaki*, on catalase (CAT), glutathione peroxidase (GSH-Px) and oxide dismutase (SOD) enzymes, total number of hemocytes, amount of pupae protein and lipid when they were fed with some artificial foods that were prepared by adding some heavy metals (Ni, Zn ve Cu) at different concentrations (% 4, 8, 12).

It was found that zinc (Zn), copper (Cu) and nickel (Ni) inhibited glutathione peroxidase, while they activated catalase and superoxide dismutase. According to these results, it was determined that heavy metals and infection of larvae into the bacteria cause oxidative stress by affecting the activity of enzymes such as CAT and SOD. When compared to the control diet, number of hemocytes was high only in the diet in which 8% Zinc (Zn) was added, and was low in all other groups. Pupal protein and lipid amount was lower in other diet groups compared to the control diet. Also, pupae weights were low in all the groups when they were compared to the control diet.

Keywords: Heavy Metal, *Bacillus thuringiensis* subsp. *kurstaki*, hemocyte, enzyme; catalase, glutathione peroxidase, superoxide dismutase

Salmonids in Georgia--conservation status and taxonomic questions

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Salmonids in Georgia, wild and farmed varieties, are a valuable resource and important to the regional aquatic ecology. However, the current status of wild populations, especially anadromous varieties, and the effects of widespread non-native rainbow trout (*Oncorhynchus mykiss*) on native species, are unknown. Anecdotally, harvest declines and the increasing scarcity of larger individuals suggests that native anadromous and riverine salmonid populations are in decline, but there is no hard data to confirm or refute this suspicion. We have initiated a study to assess the current status of native salmonids in Georgia, to determine whether these populations persist, where they persist, and what kinds of protection measures they might need to ensure a stable future for these fish. In addition, there is a persistent taxonomic question, whether the anadromous populations, which spawn in Georgian rivers but mature in the Black Sea, represent a distinct species, or whether the anadromous behavior is facultative, driven by ecological imperatives, rather than genetic predisposition. Our study uses molecular population genetics data (microsatellites and DNA sequence) to measure population parameters and gene flow among salmonid populations, and phylogenetic analysis to address phylogenetic and taxonomic questions. Preliminary mitochondrial sequence data (Tarkhnishvili and Ninua, unpublished data) indicate a clear separation of a Mediterranean/Ponto-Caspian clade of *Salmo trutta* from Atlantic *S. trutta*, but within-clade relationships of populations from Turkey, Georgia, and Eastern Europe are unresolved, as is the question of anadromy.

Keywords: Salmonid, *Salmo*, molecular taxonomy, Caucasus, Black Sea, anadromous

Phylogeography and molecular systematics of the rabbitfishes (*Siganus*) from the Western Indian Ocean

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Accurate species identification is essential for biodiversity studies and conservation of economically important species. By definition, traditional morphology-based taxonomy may be insufficient to identify cryptic species in a species complex. Rabbitfishes are an important resource for artisanal fisheries across the Indo-Pacific region, however their identification to species level is in some cases challenging. We aim to investigate the evolution of rabbitfishes and resolve taxonomic and systematic problems in the genus by using DNA barcoding and population genetic approaches. Hence, the project has been built around three objectives: 1) the development of a DNA barcoding library for the genus that includes 30 valid species, 2) the evaluation of the utility of this tool in addressing the taxonomic challenges (species misidentification, cryptic species and hybridisation) 3) a specific population genetic survey of *Siganus sutor*, a commercially exploited rabbitfish species in the Western Indian Ocean (WIO). Preliminary results revealed that the genus still has taxonomic issues, hybridisation and cryptic species. To address these challenges, we developed a multi-locus barcoding approach including nuclear genes. This is also helpful to the accurate identification of larvae and juveniles of *Siganus* spp. in the WIO. Using 17 microsatellites that we recently developed for *S. sutor*, two populations with limited gene flow were identified in the WIO. The outcomes of the project include the development of molecular resources for *Siganus* spp. at both phylogenetic and population genetic level, in addition to a multi-locus barcode library.

Keywords: *Siganus*, complex taxonomy, multiple-locus barcoding, microsatellites

A preliminary comparative skeletochronological analysis on cervical vertebrae, tibiotarsus and phalanges of Eurasian eagle-owl, *Bubo bubo* (Linnaeus, 1758)(Strigiformes: Strigidae)

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Skeletochronology is a widely used method for determining age of ectothermic animals as fishes, amphibians and reptiles. In addition, there are some skeletochronology studies on the endothermic animals (birds and mammals) which provided reliable informations about longevity. Our purpose was to compare different types of bones (cervical vertebrae, tibiotarsus and phalanges) using the skeletochronology method on a bird species which is predicted as road mortality killing Eurasian Eagle-owl, *Bubo bubo* (Linnaeus, 1758). The material used for this study was consisted of a male (1 ♂) specimen from *Bubo bubo* was killed by a car at Çanakkale-Çan highway in April 2014. *B. Bubo* was listed "Least Concern (LC)" but the population trend is decreasing recently. Different parts of the skeleton; cervical vertebrae, tibiotarsus and phalanges were investigated by skeletochronology method. First of all, parts of skeleton were dissected from the body and preserved in 70% ethyl alcohol for subsequent analysis. The bones, exposure to 5% nitric acid solution for decalcification for 3-15 hours depending on the bone size and thickness. For removing acid from the bones, the bones were rested in slow flowing water for 12 hours in order to remove the acid residuals. Then they were dehydrated through a series of concentrated ethanol solutions from 70% to absolute degree. Then the bones were washed with xylene and were embedded into paraffin. 12 µm thick cross-sections, were extracted via rotary microtome, stained with toluidine blue and haematoxylin for the examination under light microscope. The investigated bones of *Bubo bubo* specimen, skeletochronology method were performed with cervical vertebrae, tibiotarsus and phalanges and the age was estimated as 4 years. Examinations on all bone tissues (cervical vertebrae, tibiotarsus, and phalanges) were given equal numbers of LAG's (Lines of Arrested Growth). Best areas for examination LAG's were those on axis (first of cervical vertebra) and phalanges. As a result, skeletochronology is a common method for cold blooded animals even so this study reveals that skeletochronology methods might be used for estimation of ages on endothermic animals such as birds.

Keywords: Skeletochronology, *Bubo bubo*, age, longevity

Acknowledgements: We wish to thank Alper Bodur for providing the specimen (*Bubo bubo*), and thanks to Utku Şahin for performing a work on this study.

Temperature - dependent life table demography and population growth rate of green lacewing (*Chrysoperla carnea*)

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Temperature is one of the most important environmental parameters influencing all the biological processes and functions of poikilothermic organisms, like insects. It profoundly influences the population growth rate of insect pests of crops, as well as their natural enemies. Population growth parameters of green lacewing *Chrysoperla carnea* (Stephens), which is commercially available and is among the most commonly released predators, were evaluated at four different temperatures (18, 23, 28, and 32 °C), 60 ± 5% RH and a photoperiod of 16: 8 (L:D) h (5000 Lux) under laboratory conditions. Developmental time, survival and fecundity data were analyzed using the age-stage, two-sex life table to take the variable developmental rate among individuals and male population into consideration. The developmental rate was fitted to the equation $y = a + bx$ by using linear regression, where y is the developmental rate (1/d) and x is the temperature. Results indicated that population growth rate of green lacewing increased as temperature increased. Due to shorter immature developmental time, the higher total fecundity and earlier peak in fecundity, the predator had the highest performance at 28 and 32 °C. These results demonstrate that the lethal high temperature for green lacewing is over 32 °C

Keywords: Functional response, *Chrysoperla carnea*

Seasonal variations on the wing morphology of a natural population of *Phlebotomus tobbi* Adler and Theodor 1930 (Diptera: Psychodidae), the proven vector of cutaneous leishmaniasis in Turkey

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Phlebotomus tobbi, is the predominant sandfly species and the proven vector of cutaneous leishmaniasis (CL) in Turkey. In this study, we aimed to investigate the phenotypic variations of a natural *P. tobbi* population collected from Cukurova region during active season and determine the temporal environmental factors affecting the morphology. Sandflies and microclimatic data were collected monthly from May to October in 2011 from five locations in six villages. Variation of wing morphology of *P. tobbi* specimens collected each month was analyzed using geometric morphometric tools. Two distinct groups were observed based on the wing shape variance of the male specimens. First group included the specimens collected in May and June, while the second one included the specimens from August; September and October. Specimens from July collection were found to be distributed between these two groups. Although similar grouping patterns were observed for females, specimens collected in October were found to be represented as the third distinct group. Wing size of female specimens collected at the beginning of the season was significantly bigger. Males collected at the end of the season were found to have smaller wings. Wing morphology of females were correlated with average temperature and relative humidity, while the morphology of male specimens were correlated with the average relative humidity. No correlations were observed between wing morphology and seasonal population density of *P. tobbi*. These results may improve our understanding of *P. tobbi* and its vectorial capacity considering its important role for CL epidemiology in Turkey.

Keywords: Sandfly, *Phlebotomus tobbi*, geometric morphometry, wing, seasonal variation

Computational analysis of cytosine methylation patterns in archaic human genomes

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Ancient DNA (aDNA) research on archaic human genomes has great potential to provide new insight into the genetic composition, as well as environmental conditions of archaic human populations. Post-mortem chemical damage, inflicted on DNA for millennia, causes structural changes that can be interpreted as nucleotide misincorporation during sequence analysis. The most outstanding damage appears to be cytosine deamination: deamination of unmethylated cytosine residues creates uracil residues, and deamination of methylated cytosine (mC) residues creates thymine residues. When uracil-DNA-glycosylase (UDG) and endonuclease VIII (endoVIII) treatment are used to repair aDNA by removing post-mortem-created uracil residues, ancient cytosine methylation can be detected as mC->T mis-incorporations. The aim of this study is to determine aDNA methylation levels of archaic individuals from published UDG-treated aDNA datasets. In preliminary analysis, we used genomic sequence from 8,000-year-old individuals and predicted methylation signatures at CpG sites. Notably, these putative ancient methylation signatures are significantly correlated with methylation signatures from modern-day tissues, including osteoblasts ($\rho > 0.20$, p -value < 0.00001). We thus show that, even with low coverage data, reliable aDNA cytosine methylation signatures can be captured. Reconstructing methylome diversity maps for archaic humans arising from a diversity of regions and periods will yield significant information about epigenetic changes and their environmental correlates in human prehistory.

Keywords: Ancient DNA, DNA methylation, archaic human

Comparing species delimitation methods based on single-locus data: A case study on the genus *Halictus* Latreille, 1804 (Halictidae: Apoidea: Hymenoptera)

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The diversity of life is the basis of all biological studies and species diagnosis is the first step in determining questions such as detection of biological diversity, ecological, biogeographical and evolutionary problems. Due to the restrictions on the morphology-based identification of species, more effective methods for species identification have become inevitable. DNA barcoding was originally developed for fast and reliable identification of species using a short DNA sequence and COI is accepted as the universal DNA barcode region for the animal kingdom. Such short sequence data would be useful for other kind of DNA-based methods to delineate operational taxonomic units (OTUs). In this study morphology-based delimitation of the species boundaries were compared with DNA-based methods (Parsimony networks, Automatic Barcode Gap Discovery-ABGD, General Mixed Yule Coalescent-GMYC) with the samples from the genus *Halictus*. The study was carried out with 25 species which were identified according to morphological characters. As a result of this comparison, ABGD initial partition method gave 25 OTUs parallel to morphology-based identification but delimitation boundaries of OTUs were not match with morphology in terms of specimens. Parsimony networks with 95% cut-off value and GMYC with single threshold model gave 32 OTUs but differ in two OTUs and these results were higher than the morphology-based species delineation. Integrating three different DNA-based results with morphology-based results suggests that parsimony network and GMYC outperformed ABGD. Overall, our study suggests that all DNA-based methods should be considered together with and these results might be integrated to morphology-based results for obtaining efficient results.

Keywords: DNA Barcoding, *Halictus*, integrated taxonomy, species delimitation

How can we evaluate ecological status of a river basin depend on Water Framework Directive?: An example of Fırat-Dicle Basin (Turkey)

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Fırat-Dicle Basin was studied for evaluation of ecological status of a river basin based on WFD. Macroinvertebrate samples were collected at totally 81 stations within 2014. Some environmental parameters (temperature, pH, dissolved oxygen, ammonium nitrogen, nitrate nitrogen and total phosphorus) also were measured. BMWP, ASPT and Margalef indices were used at evaluation of Fırat-Dicle Basin ecological status. Consequently, totally 52 taxa were determined in Fırat-Dicle Basin. The highest dominance taxa are meso and polysaprob Oligochaeta (27.28%) and Chironomidae members (21.76%) and betamezosaprob Gammaridae (15.82%), respectively. Gökçe River (Bingöl district) has highest taxonomic diversity in basin with 17 taxa; followed by Fırat River (Erzincan) with 15 taxa and Sultansuyu River (Malatya) with 14 taxa. The values of Margalef Index are varied between 0-3,56; BMWP and ASPT score classes are varied between II-V and I-IV, respectively. Water quality of Fırat-Dicle Basin were determined as between high quality water (Class I in 19 stations) and polluted (Class IV in 12 stations) in by YSKYY (Regulation on the Management of Surface Water Quality). Some stations were found highly polluted according to BMWP and ASPT values while water quality had high quality according to environmental parameters. As results show, we should evaluate macroinvertebrate data and environmental parameters together. Because environmental parameters give us results at measured time, but macroinvertebrate show long term results in water.

Keywords: Fırat-Dicle Basin, benthic macroinvertebrate, Water Framework Directive

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Genetic analysis of north-eastern Mediterranean populations of green sea turtle and loggerhead sea turtle

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Globally threatened species *Chelonia mydas* (Green turtle) and *Caretta caretta* (Loggerhead turtle) nest in the Mediterranean. Beaches in Turkey are recognised as the most important nesting areas for Mediterranean Green turtles and the second most important for Mediterranean Loggerhead turtles. It is important to understand the genetic relationships and gene flow between nesting populations along the Northeastern Mediterranean in order to determine efficient conservation and management strategies. To achieve this, we sampled from dead hatchling turtles and late embryos obtained during nest excavations from the nesting beaches of Erdemli, Belek, Samandağ and North Cyprus. From the sampling areas 170 individuals from 108 Loggerhead nests and 154 individuals from 87 Green turtle nests were sampled in total during the 2015 nesting season. The mitochondrial D-loop and nuclear intron R35 finger protein were chosen as markers, considering the reproductive biology of both species. By means of these two markers, it is possible to compare nesting populations in the Northeastern Mediterranean and elucidate their phylogenetic relationships. Thus, intraspecific, interspecific and inter nesting population diversity can be defined regardless of the number of individuals along the nesting beaches leading to more effective conservation studies. This study is carried out through monitoring and conservation studies by the METU Institute of Marine Sciences at the Erdemli Campus beach host nesting of both species in collaboration with the North Cyprus Society for Protection of Turtles, Hacettepe and Cumhuriyet Universities. Since the analyses are in progress, the results will be discussed in the presentation.

Keywords: *Caretta caretta*, *Chelonia mydas*, conservation, genetic, mitochondrial DNA D-loop, nuclear intron R35

Predicting breeding woodpecker species distributions based on ecological niche modeling: a historical biogeography perspective

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The late Quaternary glacial–interglacial cycles caused shifts in the distributions of species. Although some species expanded their distributional ranges, most of the species in the Palearctic ecozone had to narrow their distributions into refugial areas to survive. The Last Glacial Maximum, which happened approximately 22,000 years ago, caused many bird species to narrow their ranges into refugial areas (Iberia, Italy, Balkans and Anatolia) as documented by several phylogeographic studies. In this study we tested whether refugia within refugia hypothesis existed for four sympatric woodpecker species (*Picus viridis*, *Dendrocopos major*, *Dryobates minor* and *Leiopicus medius*) in Anatolian Refugium that expanded their distributions currently when compared to their distributions on The Last Glacial Maximum by using ecological niche modelling approach. We also focused on current distribution predictions of these woodpecker species. Then, we discussed our results by comparing the outcomes of this study with phylogeographic studies that we did before for some of these species.

Keywords: Quaternary Climatic oscillations, ecological niche modelling, *Picus viridis*, *Dendrocopos major*, *Dryobates minor*, *Leiopicus medius*

Assessment of taxonomic binning methods on ancient DNA metagenomic samples

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Ancient DNA datasets are rarely from a single species. Usually the host's DNA constitutes less than 5% of the mix. In other words, over 95% of the reads correspond to the environmental exposure of the specimen through all its history. This information has its own value: it tells us about the pathogens that affected the specimen, its diet, the plants she had access—and the climatic condition she was exposed. However, aDNA analysis present its own particular challenges: it is highly fragmented (average length below 100bp), degraded by post-mortem decay (such as deamination on the 5' side), and possibly contaminated with modern DNA.

From the genomic point of view these sets of reads can be seen as a metagenomic sample. Several tools are available to detect, classify and quantify the taxonomical diversity present in metagenomic samples. Nevertheless it is not evident if these tools can be applied on aDNA. Some tools are based on sequence comparison versus a database of known genomes, but this approach can only find previously-known species. Other tools are based on the statistical composition of the reads, and can provide a putative partial taxonomical classification (e.g. phylum level) even for unknown organisms. However, their success rate is low for short reads, such as the ones on aDNA.

In this work we propose a methodology to assess and compare the characteristics of composition-based tools when applied to in silico simulated communities. We present the results of applying this methodology to nine widely used tools.

Keywords: Ancient DNA, metagenomics, composition-based binning methods, protocol assessment

mtActinopterygii: Analyzing evolution of mitogenomes belonging to the most dominant class of vertebrates

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Mitochondrial DNA data has widely been used for phylogenetic and population genetic analyses and becomes a potential tool in our understanding of vertebrate evolution regarding its properties such as maternal inheritance, low effective population size, lack of recombination and high evolutionary rates compared to the nuclear DNA. The main complication underlying in mitochondrial analyses are mostly based on substitution rates of the extreme variations among different sites and difficulties in estimation of pairwise distance related with parallel mutations, which makes phylogenetic inferences controversial. In order to enhance the basic information gathered from mitochondrial DNA studies of vertebrate evolution, we focused on the global mtDNA diversity in Actinopterygii (ray-finned fishes) which is known as the most dominant class of vertebrates comprising nearly 99% of 33.888 fish species. Thirteen protein coding genes and two ribosomal RNA genes of 348 families with diverse origins were analyzed to provide a concurrent view on vertebrate evolution. Size of the mitogenomes shows a great deal of variance from 15.725 base pairs (Drepaneids) to 23.152 base pairs (Protanguillidae) long. Most conserved regions were found out to be 12S and 16S rRNA with a genetic distance of 0,148 and 0,169 for respectively. Cytochrome c oxidase I gene of the four armed frogfish from Tetrabrachiidae family consist 28 major deletions which is highly unexpected for this region known as the barcoding gene. Findings of this study will provide data for comparison of mitochondrial genes used in conservation biology, evolutionary genetics and molecular phylogenetic studies in fish species and vertebrates.

Keywords: mtDNA, Actinopterygii, phylogenetics, evolution, vertebrates

Two new records to the suctorian ciliate fauna of Turkey with ecological notes: *Dendrosoma radians* (Ehrenberg, 1837) and *Heliophyra rotunda* (Hentschel, 1916)

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In this study, two remarkable suctorian ciliate, *Dendrosoma radians* and *Heliophyra rotunda* were studied in details.

All the samples for this study were collected from lakes by using 10 µm plankton net and artificial substrates. Morphological characters were identified by live observation and observation with impregnation methods. The species were defined by the evaluation of morphometric measurements and counts which were performed digitally by IM50 image manager system and Q-win measurement program. Illustration of the specimens were by free-hand sketches and micrographs.

Dendrosoma radians, size in vivo up to 4mm height, irregularly shaped body directly attach to the substrate posteriorly, fingerlike actinophores arise from body with capitat shaped single bundle tentacles at their ends. Macronucleus irregular in shape with broad ramifications. Several randomly located contractile vacuoles in cytoplasm. *Heliophyra rotunta*, disk shaped body 50-60 µm size in vivo. Distinct tentacles bundled, up to 100 µm length and distally bubble shape to spherical. Macronucleus disk shape and almost centrally located. Approximately 10-12 disorganised contractile vacuoles.

The present study reports two new records for the Turkish Ciliate Fauna, adding taxonomic details from original drawings and pictures, and adds geographic distribution of these species with ecological notes.

Keywords: Anatolia, Ciliophora, habitat

Status and structure of breeding gull populations in North eastern Mediterranean island

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Seabirds are located at the top of the food web of coastal ecosystems. Therefore, the distribution and abundance of seabird populations is an important indicator of well-being of the marine ecosystems and the anthropogenic impacts on them. Audouin's gull (*Larus audouinii*) has experienced a sharp population decline in 1960's. Although its Western Mediterranean population size has recently recovered; Audouin's gull population is still not stable and there is not enough information on dispersal and status of its breeding populations in the Eastern Mediterranean coasts.

The aim of our study is to survey breeding Audouin's gull colonies along the coasts of Turkey and to elucidate the genetic structure of these populations, gene flow among each other and relationship with Western Mediterranean populations by using microsatellite loci and mitochondrial D-Loop region.

We surveyed all 21 islands and islets along the South East coastline of Turkey from Taşucu, İçel to Gazipaşa, Antalya in late May 2016 and recorded their habitat characteristics and breeding bird colonies. One colony of Audouin's Gull and seven colonies of Yellow-legged gull (*Larus michahellis*) has been recorded and feather samples were taken from the chicks for genetic analyses. The relationship between habitat characteristics and abundance and distribution of breeding gull colonies will be discussed. Heterozygosity levels, phylogeny and gene flow among populations will be elucidated by using fragment analysis data of microsatellite markers and sequence data of D-Loop region. Moreover, signatures of genetic bottleneck and also phylogeography of Audouin's gull in the whole Mediterranean will be analyzed.

Keywords: Population Genetics, phylogeography, yellow-legged gull, Audouin's gull, conservation

Effect of altitude-related ecological factors on mitochondrial ND6 and ATP8 genes in Anatolian *Cephus pygmeus* (Cephidae, Hymenoptera) populations

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Altitude dependent environmental conditions are an effective force on shaping population structure. Populations of widespread insect species are exposed to independent and variable impacts of different selection pressures during the altitudinal gradient. Therefore, it is expected that different selection pressures lead to local adaptation within species. If the selection power weaker than gene flow, the genetic variation between populations will be homogenized, otherwise, the genetic differentiation will be balanced between gene flow and selection. Bioenergetic requirements which are limiting factor on organism adaptation to different environmental conditions depending on the lifestyle of the populations, cause differences in mitochondrial characteristics. Conformation of mitochondrial genome caused by the varied ATP needs in different geographical and climatic zones, are regarded as an adaptive feature of it. In this study, *Cephus pygmeus* was used as an model organism. *C. pygmeus* is distributed worldwide especially in Northern hemisphere and pest on cereals. 182 individuals was sampled from 56 localities ranged from 10m to 1971m altitudes. ATP8 and ND6 genes was sequenced for each individuals. Genetic variations and effects of environmental factors on mitogenome of *C. pygmeus* populations were examined. It is found that genetic variation much higher at low altitudes than high altitudes. Also, haplotype diversity is higher at mid altitudes. Consequently, selection pressure caused by altitude dependent environmental factors leads differentiation of *C. pygmeus* populations.

Keywords: Altitudinal gradient, *Cephus pygmeus*, ATP8/ND6, genetic structure.

Evidence of relaxed selection in evolution of mitogenome for holometabolous insects

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The mitochondrial genome have been the focus of evolutionary studies for many years because of containing both variables conserved gene regions. Mitogenome covers different characteristics: evolve faster than nuclear genome (about 10 times), originated from bacteria and controlled by nuclear genome. It has been expected to conserved by purifying negative selection because of coding important enzyme complexes in ETS. However, a recent study showed that mitogenome can be evolve by positive Darwinian selection. It has been proposed that this effect will be stronger in invertebrates than vertebrates. In this context, evolutionary patterns of holometabolous insects was examined via mitogenome data considering with invertebrate diversity. In the study, data set was prepared from 576 individuals belong to 11 holometabolous insects order. Footprints of evolution was examined primarily on protein coding genes and overall in total nucleotide sequences. As a result, a prevalent relaxed selection was found on some gene cluster and non-coding region depending on copy number of mitogenome and co- evolution with nuclear genome. We can conclude that both the necessity of being conserved and high mutation rate of mitogenome which cannot be explained by neither mutational pressure nor selective forces, can be explained by this explanation.

Keywords: Relaxed selection, holometabolous insects, mitogenome, dN/dS

Seabird mortality rates in the Aegean Sea long-line fishery: Results from interview survey of fishermen

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Fisheries by-catch, referring to unintentional capture of non-target species is one of the major current threats to the seabirds at sea. Turkey holds a wide diversity of seabird species and a large artisanal fishing fleet, but level of seabird mortality from long-line fisheries is unknown. In this study, seabird by-catch rate in the Aegean Sea long-line fishery is assessed through interviews with fishermen. The average catch per unit effort was 0.02 birds per fishing event. Yelkouan shearwater (*Puffinus yelkouan*) was the most common by-caught species reported. Serious limitations were experienced when sampling the fishermen and collecting data on fisheries effort and seabird by-catch rates. Therefore the interview data are suspected of underestimating seabird by-catch rate due to the sample size and self selecting sample of fishermen. Although more and reliable data is needed to calculate robust by-catch rates in the Aegean Sea, the interview data suggest that the impact of long-line fishery by-catch on the populations of globally threatened Yelkouan shearwater might be high and therefore long term monitoring of seabird by-catch in the Aegean Sea is urgently required to collect robust data.

Keywords: Fishery by-catch, conservation, seabirds, Yelkouan shearwater (*Puffinus yelkouan*), Aegean Sea

Preliminary results of evaluation of the Anatolian *Drosophila* species' distribution

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Anatolia is at the exact center of Africa, Middle East and Europe. The country is the meeting place of three phyto-geographical regions: Euro-Siberian, Mediterranean and Irano-Turanian. Their distinctive vegetation reflects differences in climate, geology, topography, soils and floristic diversity, including endemism. Since Turkey has a diverse ecology and is estimated to host around 10,000 plant species and at least 33% are endemic. Knowing the diversity of plants in our country, it is very essential to determine the diversity invertebrates living on them. Endemic plant species in different habitats can be at host position for endemic invertebrates.

Knowledge of diversity of a particular invertebrate in Anatolia and its morphological, taxonomical and genetical data provide the filling of the information gap in terms of biogeographical position within its distribution. In addition, discovery and protection new species also means increase biological diversity in this region. Discovery of new species means not only contribution to biogeographical information or richness of biological diversity. If these are new species, like *Drosophila*, as an important model organism for human biology and human disease, so it is vitally important. Although recorded more than 3000 *Drosophila* species up to now, our knowledge of the species *Drosophila* in Anatolia is almost none.

Anatolia is the only country covered almost entirely by three of the World's 37 phyto-geographical regions. The Anatolian Diagonal extending from north eastern Anatolia to the Mediterranean Toros mountains has been critical for plant diversification. As regards to *Drosophila*, it's an organism which has won thousands of years struggle for existence through plants. Knowing natural history of many Drosophilid, which live in extreme environment contributes to detect novel resistance mechanisms and novel dietary adaptations and reproductive strategies. In brief, revealing richness of Anatolian *Drosophila* species is the subject of this review.

Keywords: Drosophilidae, Anatolia, biological diversity, *Drosophila* species, distribution, morphological and molecular description

The list of the *Lactarius* species from Turkey's Aegean Region

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Turkey has a great biological diversity because of different geographical features and climate ranges. These features provide to grow variety of mushroom species and Aegean region has generally Mediterranean climatic properties and big mixed forests.

In our study, 22 *Lactarius* species are given with morphological properties and distribution of Turkey which has done between 2013-2015 years. According to literature datas, 8 *Lactarius* species (*L. chrysorrheus* Fr., *L. deliciosus* (L. : Fr.) Gray, *L. deterrimus* Gröger, *L. quieticolor* Romagn., *L. salmonicolor* R. Heim & Leclair, *L. sanguifluus* (Paulet) Fr., *L. semisanguifluus* R. Heim & Leclair, *L. vellereus* (Fr. : Fr.) Fr.) are recorded in the region before.

Except these species, 14 *Lactarius* species that are *L. blennius* (Fr. : Fr.) Fr. *L. controversus* (Pers. : Fr.) Fr., *Lactarius musteus* Fr., *L. piperatus* (L.: Fr.) Pers., *L. porninsis* Rolland., *L. pyrogalus* (Bull. : Fr.) Fr., *L. quietus* (Fr. : Fr.) Fr., *L. scrobiculatus* (Scop. : Fr.) Fr., *L. torminosus* (Schaeff. : Fr.) Gray, *L. volemus* (Fr. : Fr.) Fr., *L. zonarioides* Kühner & Romagn., *L. zonarius* (Bull.) Fr., *Lactifluus bertillonii* (Neuhoff ex Z. Schaeff.) Verbeken, *Lactifluus rugatus* (Kühner & Romagn.) Verbeken were founded in Turkey according to literature but these species are determined for the first time at Aegean region by our research.

Keywords: *Lactarius*, Aegean region, Turkey

First ancient genomic data from Anatolian sheep

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Based on archaeological evidence, sheep is believed to have been domesticated about 12,000 years before present (BP), in an area that extends from Central Anatolia to the Zagros Mountains. In the present study, we aim to understand the history of sheep domestication using ancient DNA from some of the first domestic sheep populations found in the Near East. For this purpose, we built 24 whole genome sequencing libraries from 21 sheep bone and tooth samples from Tepecik Çiftlik (n=11, 12 libraries), Hallan Çemi (n=2, 4 libraries) and Çatalhöyük (n=8, 8 libraries) archaeological sites, located at the periphery of the core zone of sheep domestication in Anatolia. The age of these samples ranged between 10,000 and 7800 years BP. Whole genome shotgun sequences were obtained using Illumina HiSeq 2500 platform for 20 high quality libraries, and mapped to the sheep genome (Oar_v3.1). Five of the libraries showed evidence for authentic ancient DNA based on postmortem damage and read length distributions. We will next compare these ancient sheep samples to the published data from OvineSNP50 BeadChip (Illumina) for 671 sheep individuals from 37 populations. We expect our results to illuminate the demographic changes involved in sheep domestication.

Keywords: Ancient DNA, sheep, Anatolia, domestication, population genomics

***Noccaea* s.l. versus *Noccaea* s.str: Does sampling strategy affect phylogenetic reconstruction?**

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The genus *Thlaspi* L (*Thlaspi* s.l.) is one of the most problematic genera of the cabbage family (Brassicaceae=Cruciferae). Historically, it has been considered as one of the largest genera until Meyer (1973) divided the genus into 12 segregate genera and retained only six species in *Thlaspi* s. str. Subsequent molecular studies clearly showed that this complex includes at least three different genera (*Thlaspi* s.str, *Noccidium* and *Noccaea*) which are not related. The main problem is the generic circumscription of *Noccaea*. Some authors consider it as a large lineage with ca. 120 species (*Noccaea* s.l. including all other segregates except *Thlaspi* s.str, and *Noccidium*), whereas others argue for a narrow concept supporting Meyer's *Noccaea* s.str. We argue that the main pitfall in most studies is insufficient taxon sampling. We used a broad taxon sampling (representing all *Thlaspi* s.l. segregates), and inferred phylogenetic trees from nuclear ITS and plastidic trnL-F and rps16 regions. Our results clearly show that *Noccaea* s.str (sensu Meyer) is polyphyletic. Instead, our data support a broadly defined *Noccaea* s.l., comprising all *Thlaspi* s.l. segregates (except *Thlaspi* s.str., and *Noccidium*), characterized by profound differences in fruit architecture. It has been well documented in the Brassicaceae that species with dramatically different fruits may be very closely related, implying that developmental processes controlling fruit shape and structure are extremely plastic in evolution. As a consequence, we argue that the delimitation of the genus *Noccaea* should follow a molecular phylogenetic approach.

Keywords: Noccaeeae; Brassicaceae; Phylogeny, *Noccaea*, sampling.

Characterization of the mitochondrial genome of *Syrista parreyssi* and *Hartigia linearis*

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Insects have been able to adapt quite different ecosystem. This has been achieved by development of different life-history strategies through evolution. Environmental stress causes differences in the rate of change in mitochondrial genome depending on their life-history strategies. Particularly gene rearrangements are remarkable facts in evolutionary process of mitochondrial genome. The rearrangements are common in Hymenoptera order, mitochondrial genomes of Symphyta suborder especially in bounded by tRNAs A-T rich region/ND2, ND2/COI, COII/ATP8 and ND3/ND5 regions. Also it was determined that the rearrangements that occurred in genes that overlap are not random, unlike exhibit a pattern. The mitochondrial genomes of *Hartigia linearis* and *Syrista parreyssi* species were investigated in the study. The mitochondrial genome sequence of the species was drawn by means of reference mitogenome with BWA and SAMtools programmes from sequence data that was obtained with Illumina Hi-seq method. The mitochondrial genome organization of the species was determined by characterizing obtained mitochondrial genome sequences. After all, the gene rearrangement trends that are particularly common in the Hymenoptera mitogenome, were found in these two species too. The radical and conserved changes that are exhibited by protein coding genes were found meaningful by related species. The prolongations that are observed especially in Cephidae family in small subunit of rRNA genes were determined in these two species. The prolongations and iterative sequences in noncoding A+T rich region were determined and correlated with replication and transcription processes.

Keywords: Gene rearrangement, mitochondrial genome, *Syrista parreyssi*, *Hartigia linearis*

Morphological relationships among *Campanula hakkiarica* P.H.Davis, *C. karakuschensis* Grossh. and *C. bornmuelleri* Nabelek.

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The genus *Campanula* L. comprises ca 420 species, widely distributed in temperate areas in the Northern Hemisphere (Lammers 2007). In Turkey, the genus *Campanula* is represented by ca. 120 species with an endemism ratio of ca 50% (Guner et al, 2012). According to Damboldt (1978), there are six subgenera of *Campanula* in Turkey. One of them is sect. *Rupestres* (Boiss.) Charadze. *C. hakkiarica* P.H.Davis, *C. karakuschensis* Grossh. and *C. bornmuelleri* Nabelek are members of this section. These species are rather close species in each other. The closeness of these species has caused many taxonomic problems. Surprisingly, Kolakowsky (1991) changed the status of *C. hakkiarica* as synonym of *C. karakuschensis* but under new genus *Theodorovia* Kolak. ex Ogan. as *T. karakuschensis* (Grossh.) Kolak. According to our revisional study on *Campanula* subgen. *Campanula* in Turkey based on morphological and molecular studies, we concluded that the transfer of *C. karakuschensis* and *C. hakkiarica* is not acceptable in a separate genus *Theodorovia*. However, *T. karakuschensis* are accepted instead of *C. karakuschensis* by Lammers (2007) in "World checklist of selected plant families". Although there are some morphological differences in type materials, after the detailed morphological and molecular studies we decided that these three species are same species. Finally, we proposed *C. karakuschensis* and *C. hakkiarica* as synonyms of *C. bornmuelleri*.

Keywords: *Campanula*, *Campanula hakkiarica*, *Campanula karakuschensis*, *Campanula bornmuelleri*, synonym, sect. *Rupestres*.

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Investigation of zooplankton community and size structure in different nutrient and water level among latitudinal gradient: a mesocosm experiment

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Higher temperature could have severe impact on ecosystem function as consequences of community changes. Thus lakes are very sensitive to warming. We assessed the effects of nutrient and water level changes on zooplankton community composition and size structure in different climate zones by running a standardised controlled six-month experiment in six countries. The mesocosms were established with two different nutrient levels and two depths, all run with four replicates. We analysed pooled zooplankton samples originating from monthly samplings of each mesocosm throughout the study period. We found a significant effect of temperature on the community composition and size structure of the zooplankton. However, no water depth and nutrient effect appeared. In all countries except for Greece, zooplankton community biomass was mostly dominated by cladocerans. The normalised size spectrum (NSS) slope increased with temperature but did not differ among depths or nutrient levels. The slope of NSS was shallower in Greece than in the other countries. Neither taxonomic diversity nor size diversity showed clear pattern at different nutrient or depth level along temperature gradient. However, genus richness decreased through warmer regions. Our experiment generally

supports current evidences that ongoing temperature increase at the existing rate may result in lower genus richness and lower abundance of large-sized grazers and, consequently, trigger eutrophic conditions.

Keywords: Climate change, water level change, zooplankton, size structure, mesocosms

Assesing the impact of environmental variables together with a short extreme wind event on metabolism Lake Eymir using high frequency data

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Lake metabolism includes the collective fixation and mineralization of carbon by all organisms. Balance between gross primary production (GPP) and respiration (R), net ecosystem production (NEP) is efficient estimate for trophic classification of lakes provided that the estimation based on high frequency data. The high frequency lake motoring system was used to estimate lake metabolism for Lake Eymir where is located in cold dry step climate. Of the central Anatolia, Turkey. The system consist of two sonde at 1.5 meter and 4.5 meter, thermostat chain consisting of 7 thermo-probes through the water column and meteorological station. Using high frequency data, metabolism of Lake Eymir was estimated by using diel dissolved oxygen measurement. In spring, the lake metabolisms was autotrophic with positive NEP probably caused by increased chl-a concentration. In summer, the metabolism of Lake Eymir swung between heterotrophy and autotrophy but generally it was heterotrophic with negative NEP. It appears that there was a positive correlation between NEP, GPP and R with TP concentrations. An extreme wind event took placed in autumn broke up the thermal stratification and mixed the whole water column that led to anoxic conditions with consequence of fish kill. Through this mixing event, the NEP estimated from the both of the sonde at 1.5 m and 4.5 m had the close values and were negative. Thus the whole water column was heterotrophic. The impact of this extreme wind event will be further analyzed and discussed in relation to the environmental factors.

Keywords: Climate change, lake metabolism, extreme weather event, wind speed

Comparison of recent past and present states of Turkish shallow lakes by using Cladocera sub-fossil remainings

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Order Cladocera (small crustaceans) has an important place in lake ecosystems as they are both consumers of primary producers and prey for larger predator species. As a result, their abundance is a strong indicator of ecological conditions in a lake at a certain time. Cladocera body parts, such as headshields, shells, etc.) are largely silica based and can be preserved inside the lake sediment for long periods of time. Sedimentary sub-fossil records of Cladocera remains allow us to understand past and more recent conditions. Our aim is to determine changes in lake ecological status over time by using abundances of Cladocera sub-fossils at top (present) and bottom(recent past) centimeters of the sediment cores taken from 28 shallow lakes of Turkey. Comparison of the recent past and present states were carried out using Similarity/Dissimilarity Analysis. Furthermore the results were assessed exploring the changes took place in a specific lake through time.

Keywords: Cladocera, sub-fossil, shallow lakes, lake sediment, similarity/dissimilarity analysis

An evolutionary approach to polycystic ovary syndrome

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Polycystic ovary syndrome (PCOS) is a common and complex genetic disorder associated with increased risk of infertility and metabolic diseases including type-2 diabetes, dyslipidemia, and cardiovascular disease. High incidence and prevalence rates throughout the world populations is considered as an evolutionary paradox. To investigate evolutionary forces acting on the determinants of PCOS, we adopted an evolutionary population genetics approach. Firstly, we examined the (clinical) phenotypes associated with PCOS and listed the most informative traits (phenotypes) with high heritability. Then we compared and contrasted the distribution of selected traits among Caucasians, Asians, and Africans in light of the demographic history and recent life style changes in these populations. Secondly, based on published genetic studies we identified the most influential genetic factors and related biological pathways associated with PCOS. We investigated the evolutionary past of the PCOS related genes, and the distribution of PCOS risk alleles among Caucasians, Asians, and Africans. Our results suggest that PCOS is an ancient disorder and genetic risk factors were already present in the ancestors of humans. The risk factors for PCOS in modern times might have been advantageous for survival in our ancestors. However, one cannot exclude the role of genetic drift in shaping the genetic architecture of traits associated with PCOS.

Keywords: Polycystic ovary syndrome, genetics, evolution, human population genetics

Differences of mitochondrial rRNA genes secondary structure prediction in Hymenoptera order

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Hymenoptera is one of the most important insect orders in terms of diversity of life history strategies and species richness. This order is potentially useful as a model group in determination of the numerous evolutionary and biogeographical patterns. Researches are increasingly applied to the molecular techniques to study evolution and molecular ecology. Mitochondrial DNA is also used as a molecular marker in these studies because of its several advantageous: relatively small genome size, abundance in a cell, relatively easy to isolate from tissue and mode of maternal inheritance.

The secondary structure predictions of mitochondrial DNA that ribosomal RNA (rrnL and rrnS) genes, which their nucleotide sequence and transcript have functional importance, obtain reveal important findings for the phylogeny of Hymenoptera, understanding the diversity and richness of species and understanding different life strategies they have developed. The domains present in the secondary structure that binds to the large subunit of the ribosome rrnL and binds to small subunit of ribosome rrnS genes transcripts obtained form the binding surfaces of ribosomal proteins, tRNAs', peptidyl transferase enzyme and many other molecules. The secondary structures of polymorphic helices were compared in secondary structures of ribosomal RNAs' that offer an opportunity to assess structural and functional aspects. The polymorphic helices, which are located in the secondary structure of rrnL and rrnS gene products in some species representing the Hymenoptera, were compared by making secondary structure predictions.

Keywords: Hymenoptera, mitochondrial genome, rrnL, rrnS, secondary structure prediction

Genetic relatedness estimation using ancient genomic data

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One distinct feature of these early Neolithic settlements in the Near East was their burial customs. Both in the Levant and in Anatolia, people dug graves inside their houses, and multiple individuals were buried in these intramural graves; a custom that reached its climax in Çatalhöyük. Archaeological evidence suggests that individuals buried in a house were socially related, which has motivated anthropologists to estimate biological relatedness among individuals who share the same grave. Such information, which could be obtained from ancient DNA data, could shed light on the social structure of these ancient sites/communities, and be valuable for archaeological studies. The challenge of working with ancient DNA is that it is highly degraded and usually in minute amounts, which results in limited DNA data availability. Importantly, in ancient DNA datasets usually only one allele can be detected per individual. There exist a number of methods to estimate genetic relatedness designed for modern high coverage genomic data, but their performance on ancient DNA data has not been tested. Here we run these methods on low coverage whole genome data from real family pedigrees, as well as ancient DNA data from simulated pedigrees. We further propose a new approach to calculate relatedness between ancient individuals, which would require minimal coverage and SNP numbers to accurately estimate relatedness. Our approach is expected to promote the application of ancient DNA to address new archaeological questions.

Keywords: relatedness, ancient, neolithic, genomic

Latitudinal variation of wing size, stress tolerance and climatic adaptation in *Drosophila melanogaster*

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Analysis of the genetic variability in natural populations is an important tool in the field of population, evolutionary, and ecologic genetics, together with *Drosophila* as a model for these studies. As a cosmopolite species, *D. melanogaster* shows a wide geographical distribution. This distribution is accompanied by latitudinal differences as well as genetic diversity. This indicates that local climate, particularly temperature is a selective factor in this diversity. Latitudinal clines are found in morphological and stress related traits that affect fitness. Fitness-related genetic variations along a geographical transect is a result of adaptive evolution. Parallel clines in different geographic transects is an important source for local adaptations. Increase in stress tolerance is to ensure a high adaptation success under selection pressure created by environmental factors. This study aimed to assess latitudinal variations in wing size and thermal tolerance among *D. melanogaster* populations.

Inbreed lines were created from different populations, each of them belongs to different latitudes, collected from Moscow, Kiev and Ankara. Body size was determined by linear measurement of the wings, recovery time from chill-coma was measured and survival numbers from heat-shock were counted.

In addition to sexual dimorphism were seen in wing lengths, as expected, wing sizes were showed significant variation according to locations they collected. Differences in recovery times from chill-coma and survivals from heat-shock were also significant among populations. Results have revealed a clinal variation in body size and thermal resistance, as these variations may have emerged as a result of adaptation mechanisms of these populations.

Keywords: *D. melanogaster*, local adaptation, latitudinal cline, thermal tolerance, body size

Determinants of phytoplankton size structure in warm, shallow lakes

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Phytoplankton are the main primary producers in most aquatic ecosystems and responsible for nearly half of primary production on Earth. They are highly diverse group and range in size from picoplankton species with cell dimensions around 1-5 μm to some colonial or filamentous species that can be visible to the naked eye. Body size is an important characteristic of any organism because it affects physiological and morphological performance measures like fertility, population growth rate, and competitive interactions. In this study we sampled 46 mostly shallow and permanent lakes mostly located in Western Anatolian Plateau. We investigated the effects of 22 abiotic and biotic drivers including higher trophic levels on phytoplankton size in the community in Turkish lakes, to further our understanding of drivers that control phytoplankton size in warm regions. We used structural equation modelling, a multivariate statistical analysis method that detects interaction pathways and direct and indirect effects among numerous variables. According to our preliminary results only rotifers had direct positive significant effect on phytoplankton size. Moreover, total phosphorus, zooplanktivorous fish and salinity also has significant indirect effect on phytoplankton size structure. Our results highlight the sensitivity of the size structure to biotic and abiotic interactions and suggest that trait-based approaches, cell size in particular, can be used as a tool to assess ecological responses to climate change in aquatic ecosystems.

Keywords: Phytoplankton, cell size, trophic state, climate change

Inferring conductivity and eutrophication in Turkish shallow lakes by using subfossil Diatoms

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In recent years, paleolimnologists have the ability of making accurate environmental predictions using high quality data sets through the help of modern techniques and analytical methods for answering questions about past and present status of freshwater environments. Diatoms play an important role in freshwater ecosystems as being good indicators of water quality and they provide valuable information about current and past status of lakes due to their high sensitivity about shifts in trophic status of the environment.

In this study, 47 shallow lakes from Turkey were sampled for water chemistry and sediments along a latitudinal gradient using space for time approach. Due to preservation issues, 36 lakes were used during the analyses. According to Redundancy Analysis (RDA) via forward selection, conductivity, total phosphorus (TP) and percent plant volume inhabited (PVI%) were the most important environmental variables influencing the distribution of diatoms with total of 36% of the variance. Additionally, two shallow lakes (Karagöl-İzmir and Karagöl-Bolu) were selected for further ecological reconstruction of the past status. Passive plotting of the core data onto RDA graph and comparison of bottom core with every upper sample using Square Chord Distance (SCD) revealed the changes through time for both lakes. It is found out that although conductivity is the main driver for present time, eutrophication had a significant impact on whole core during past. Eutrophic taxa were dominant for both cores with only compositional change through time. Moreover, transition between planktonic to benthic taxa addressed changes for water level.

Keywords: Diatom, ordination, shallow lakes, eutrophication, ecological reconstruction

GC-biased gene conversion in smut fungi

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Gene conversion is copying one stretch of DNA into another; GC-biased gene conversion (gBGC) is favoring G & C alleles over other bases in this conversion process. gBGC is a mechanism that has been proven to be very important in shaping the genomic patterns of plants, mammals and even bacteria. However, little is known about its role in fungi. The group of study would include some species of basidiomycetes, the so-called "smut" fungi, which contain the model species *Ustilago maydis*. It is known for being the species where the mechanism of recombination are discovered by Robin Hollyday. Because it has a very efficient recombination rate, it can incorporate almost any piece of DNA and can easily be transformed. This is why it has also become a model species for the study of host-pathogens interactions. Here we interested in the recombination patterns of these species, and notably their putative influence on the nucleotide composition of the genome via the mechanism of gBGC. We are able to see the signs of the gBGC in 11 smut fungi species. Moreover, our results suggest the relaxation in this biased gene conversion.

Keywords: Biased gene conversion, smut fungi, genome compartmentalization

Taxonomic status of *Campanula seraglio* Kit Tan & Sorger.

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The genus *Campanula* L. is the most diverse and species-rich genus of the Campanulaceae Juss. It comprises about 420 species. Turkey is an important diversity centre of *Campanula*. Approximately 120 species are distributed in Turkey and about half of these are endemic. One of the section of *Campanula* subgen. *Campanula* is sect. *Symphyandriiformes* (Fomin) Charadze (Damboldt 1978). This section include four high variable species. All these species are distributed in North Turkey. There are many taxonomic problems in this section because of the high variation range, especially *C. betulifolia* K.Koch is the most variable species in this group. The other species in sect. *Symphyandriiformes* is *C. choruhensis* Kit Tan & Sorger., *C. seraglio* Kit Tan & Sorger and *C. troegerae* Damboldt. These 4 species are very close according to morphological and also molecular studies. After our revisional studies especially based on morphological and molecular studies on *Campanula* subgen. *Campanula*, we concluded that *C. seraglio* is a synonym of *C. troegerae*. However, Kit Tan and Sorger (1984) separated the *C. seraglio* with some little morphological features such as much smaller corolla and less split corolla lobes than *C. troegerae*. It is a variant form of *C. troegerae*, adapted to high altitudes.

Keywords: *Campanula*, *Campanula seraglio*, *C. troegerae*, sect. *Symphyandriiformes*, Turkey.

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Modeling future ecosystem services of Lake Beyşehir

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Freshwater ecosystems serve various ecosystem services such as supplying water for different purposes and food as provisioning services, nitrogen retention, flood protection as regulating services and recreation as cultural services. Lake Beyşehir is the largest freshwater lake in Turkey and it is critically important in terms of supplying ecosystem services for the area including irrigation, drinking water to a certain extent, fisheries and recreation. In this study, we applied the eco-hydrological model SWAT (Soil and Water Assessment Tool), to evaluate the effects of potential land use changes and the projected future climate on water and nutrient runoff of Lake Beyşehir catchment. Climate change scenarios were based on IPCC 5th main scenarios (RCP 4.5 and RCP 8.5) derived from 2 regional climate models (GFDL-ESM2M and IPSL-CMA-LR) for 2 different time periods (2030s and 2060s). Outputs of eco-hydrological model and the climate models were subsequently used as input to two individual lake ecosystem models (PCLake, General Lake Model). Chlorophyll a, water level and cyanobacteria biomass was used as a proxy to determine whether Lake Beyşehir will continue to supply its ecosystem services in the future as well. Our preliminary results showed that climate change scenarios demonstrate great variability in terms of precipitation which caused higher uncertainty in predicting future water levels. In addition, increased temperature had strong effect on chlorophyll a and cyanobacteria biomass which deteriorate the water quality and may result in loss of drinking water value of Lake Beyşehir.

Keywords: Lake modeling, ecosystem services, SWAT, chlorophyll a

Analysis of Neanderthal introgression into Western Asian human populations show population-specific patterns

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Neanderthals contributed genetic material to the ancestors of present-day Eurasians via multiple admixture events. The initial introgression event mostly likely occurred in Western Asia during the out-of-Africa migrations of modern humans. A recent study shows that Arabs from present-day Qatar carry lower proportions of Neanderthal ancestry compared to present-day Europeans. It was hence suggested that additional introgression events might have occurred subsequent to the divergence of Near Eastern populations from other Eurasian populations. To test this, we sequenced genomes of 10 present-day humans, including North and Western Europeans, Mbuti Pygmies, and the Middle Eastern Druze at high read-depth (30X). We also integrated published whole genome data from the 1000 Genomes Project and 16 individuals from present-day Turkey. Consistent with the observations in the Qatari population, the Turkish population carried significantly lower proportions of Neanderthal ancestry compared to Europeans. However, we detected no difference in the Neanderthal introgression rates between Druze and European populations. We surmised that the observed variation in observed Neanderthal admixture levels among Western Asian populations could be related to more recent, population-specific migrations. Indeed, it has previously been shown that Western Asian populations show significant genetic structure, essentially creating a quilt pattern, which contrast the clinal patterns of genetic variation observed in Europe. To test whether such genetic structure can explain different levels of Neanderthal admixture among Western Asian populations, we identified the haplotypes in Turkish individuals introgressed from Neanderthals. Our results revealed distinct introgressed haplotypes that show more than expected population differentiation among Turkish individuals and in other Eurasian populations. Our study will further address whether complicated population history of Western Asian population, adaptive introgression, or both is responsible for the observed haplotype variation observed in the region.

Keywords: Neanderthal introgression, Western Asian Human populations, migration

Biodiversity assessment of Lepidoptera under the influence of climate change

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In recent years, climate change is causing major impact on nature and ecosystems, with steadily increasing harmful effects also to mankind. Considerable increase of temperature at global level, changes in rainfall patterns and extreme climatic events are the most striking examples for climate change. Both seasonal and long-term changes affect the fauna, flora and population dynamics of insects including Lepidoptera. Butterflies and moths are excellent indicators for studying the effects of climate change, being one of the most species-rich primary consumers, taxonomically (comparatively) well-studied, occupying a broad range of ecological niches, and last but not least enjoying a very positive public perception.

DNA barcoding provides an important tool to improve the quality and speed of botanical and zoological studies, while, at the same time, such studies contribute to the development of a global DNA Library which is becoming an important resource for the scientific community. From the very beginning, the Lepidoptera campaign of iBOL (international Barcode of Life) has provided a crucial contribution to demonstrate the efficiency of DNA barcoding. Lepidoptera are the second-most diverse order of insects with approx. 165,000 known species and likely as many still awaiting description. By May 2016, DNA barcodes have been generated for 51% of the global fauna, hence most species can be identified reliably and monitored by molecular assessments, now. Such monitoring can retrieve precious and objective information on altitudinal distribution, ecological plasticity and habitat preferences, sensitivity to abiotic influences (e.g. climatic change) and thus to potential extinction.

Key words: Climate change, Lepidoptera, biodiversity