EEBST 2019

Ecology and Evolutionary Biology Symposium

10-12 July 2019

ABSTRACT BOOK

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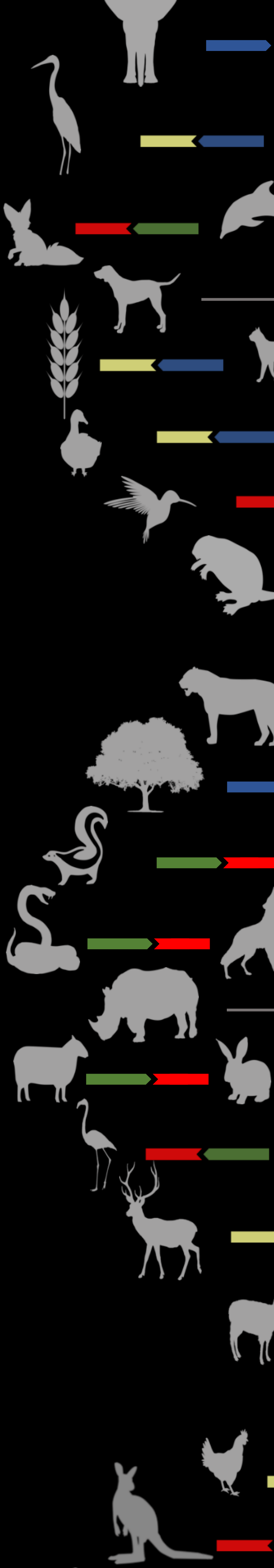

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Program

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		10.07.2019 Wednesday
08:30	08:45	Registration
08:45	09:00	
09:00	09:15	
09:15	09:30	Welcome: Emre Keskin
		Chair: TBA
09:30	10:30	Keynote Speech: *Olivia Roth* The Evolution of Male Pregnancy and the Remodelling of Vertebrate Adaptive Immunity
10:30	10:45	Mini-Break
10:45	11:00	Unraveling the extend of gene duplication in Arabidopsis thaliana using GWAS *Benjamin Jeagle, Mayela Soto, Gökce Aköz, Ilka Reichardt-Gomez, Magnus Nordborg*
11:00	11:15	Characterization of the Human Pathogen Peptidome and Specialization in Peptide Binding Among MHC Class-I Alleles *Onur Özer, Tobias L. Lenz*
11:15	11:45	Coffee Break
		Chair: TBA
11:45	12:00	Structural Organization and Standing Genomic Variation in the MHC of the Three-spined Stickleback *Malavi Sengupta, Panchal M, Samonte IE, Chain F, Eizaguirre C, Feulner CGD, Kalbe M, Bornberg-Bauer E, Reusch TBH, Milinski M, Lenz TL*
12:00	12:15	Genetic Structures of Salix alba and Salix excelsa Populations from Two Major River Systems in Turkey *Funda Özdemir Değirmenci, Pelin Acar, Zeki Kaya*
12:15	12:30	Not a generalist after all? Life history genomic regions explain differences in Atlantic salmon diet *Tutku Aykanat, Martin Rasmussen, Mikhail Ozerov, Eero Niemelä, Kjetil Hindar, Vidar Wennevik, Torstein Pedersen, Martin-A. Svenning, Craig R. Primmer*
12:30	13:30	Lunch

		Chair: TBA
13:30	13:45	Keynote Speech: *Dieter Ebert* Explaining species wide diversity: What shapes phenotypic and genotypic diversity across space?
13:45	14:00	
14:00	14:15	
14:15	14:30	
14:30	15:30	Poster Session & Coffee Break
		Chair: TBA
15:30	15:45	Species interactions captured in phylogeographic patterns *Emrah Coraman, Heliana Dundarova, Christian Dietz, Frieder Mayer*
15:45	16:00	Environmental DNA: a tool for estimation of fish biomass/abundance? *Ayşegül Er, Metehan Arıkan, Fuat Bilgin, Emre Keskin*
16:00	16:15	Seasonality effect on the demography of large mammal species in Northwestern Anatolia *A. Dilşad Dağtekin, Arpat Özgül, Alper Ertürk, Anıl Soyumert*
16:15	16:30	Changes in Waterbird Community Structure and Functional Diversity in Shallow Lakes: The Role of Water Level and Submerged Macrophytes *İbrahim Kaan Özgencil, Meryem Beklioğlu, Korhan Özkan, Çağatay Tavşanoğlu, Niccolo Fattorini*
16:30	16:45	Mini-Break
		Chair: TBA
16:45	17:00	Influence of Fish Predation on Size-based Interactions and Recovery of Zooplankton Communities in Freshwater Planktonic Food Webs: Examples from Mesocosm Experiments *Zeynep Ersoy, Mireia Bartrons, Thomas Mehner, Erik Jeppesen, Sandra Brucet*
		High Ecological Plasticity and Genetic Diversity of the Native Ponto-Caspian Gobies Suggests Establishment Success in Their Invasive Range *Ali Serhan Tarkan, Uğur Karakuş, Nildeniz Top, Esra Mine Ünsl, Erdi Gökhan Tepeköy, Emre Keskin*
17:00	17:15	Genetic similarities among diseases as a means of undertstanding ageing *Handan Melike Dönertaş, Matias Fuentealba Valenzuela,Linda Partridge, Janet M. Thornton*
17:15	17:30	Mesocosm Experiment on Effects of Microplastic on Freshwater Zooplankton Community *Dilvin Yıldız, Gülce Yalçın, Meryem Beklioğlu*

11.07.2019 Thursday

08:30	08:45	Registration
08:45	09:00	
09:00	09:15	
09:15	09:30	
		Chair: TBA
09:30	10:30	Keynote Speech: *Douglas Joel Futuyma* The Evolutionary Synthesis Then and Now: Accomplishments and Challenges
10:30	10:45	Mini-Break
10:45	11:00	Contributions of sperm and seminal fluid to ejaculate senescence, and its amelioration via insulin signalling *Irem Sepil, Ben Hopkins, Rebecca Dean, Eleanor Bath, Solomon Friedman, Ben Swanson, Harrison Ostridge, Norene Buehner, Mariana Wolfner e,q, Rebecca Konietzny, Marie-Laëtitia Thézénas, Elizabeth Sandham, Philip D Charles, Roman Fischer, Josefa Steinhauer, Benedikt M Kessler, Stuart Wigby*
11:00	11:15	Coevolution of female fidelity and male help under intra- and inter-locus sexual conflict *Xiang-Yi Li, Wolfgang Goymann*
11:15	11:45	Coffee Break
		Chair: TBA
11:45	12:00	Sex Ratio at Mating Does Not Modulate Age-Related Fitness Decline in Drosophila melanogaster *Zahida Sultanova, Pau Carazo*
12:00	12:15	Life history evolution under cancer risk: linking cell-level strategies to organismal traits *E. Yağmur Erten, Hanna Kokko*
12:15	12:30	Cultural Selection Shapes Network Structure *Marco Smolla, Erol Akçay*
12:30	13:30	Lunch

Chair: TBA

13:30	13:45	Distinguishing between recent balancing selection and incomplete sweep using deep learning *Ulaş Işıldak, Matteo Fumagalli*
13:45	14:00	Studying polyploidy with "right" genomes and "right" approaches *Gökçe Aköz, Magnus Nordborg*
14:00	14:15	Rigorous Model Ranking and Exhaustive topology Exploration Improve the Functionality of qpGraph *Eren Yüncü, Olga Flegontova, Piya Changmai, N. Ezgi Altınışık, Stephan Schiffels, Pavel Flegontov*
14:15	14:30	Empirically Tractable Antibiotics Time Machines *Burak Kocuk, Ali Rana Atılgan*
14:30	15:30	**Poster Session & Coffee Break**
15:30	15:45	Panel Gender Equality
15:45	16:00	
16:00	16:15	
16:15	16:30	
16:30	16:45	Mini-Break
16:45	18:30	EEBST Board Meeting

		12.07.2019 Friday
08:30	08:45	Registration
08:45	09:00	
09:00	09:15	
09:15	09:30	
		Chair: TBA
09:30	10:30	Keynote Speech: *Lucie Zinger* Macroecology of Microbial Communities
10:30	10:45	Mini-Break
10:45	11:00	The effect of salt concentrations on genome-wide mutation rate on halophilic archeon Halobacterium salinaru *Alp Mete Ümmet, H. Özgür Özdemirel, Dilara Ulusal, Hasan Ünal, Sibel Küçükyıldırım*
11:00	11:15	Assessment of Using Three-Way Interactions Between Plants, Microbes and Arthropods in Pest Management: A Case Study of the Three-Way Interaction Between Potato Plant, Mycorrhizal Fungi and Colorado Potato Bee *Remzi Atlıhan, Semra Demir, Mehmet Ramazan Rişvanlı*
11:15	11:45	Coffee Break
		Chair: TBA
11:45	12:00	The role of gene flow and hybridization in shaping genetic diversity structure of Populus nigra populations in Turkey *Asiye Çiftçi, Zeki Kaya*
12:00	12:15	Establishing National Early Warning and Monitoring System for Available and Potential Non-native Freshwater Species in Turkey *Esra Mine Ünal, Işılay Çelik, Ali Serhan Tarkan, Ozan Çiftçi, Ayşegül Er,* *Sevgi Kaynar, Hasan Hüseyin Atar, Emre Keskin*
12:15	12:30	Impact of Deep Sea Mining on Seafloor Ecosystems: A Baseline Study on Clarion-Clipperton Zone (Expedition SO268) *Batuhan Çağrı Yapan, Julia M. Otte, Yasemin Bodur, Jakob Barz, Elena Schiller, Freija Hauquier, Felix Janssen* *Frank WenzHöfer, Massimiliano Molari*
12:30	13:30	Lunch

		Chair: TBA
13:30	13:45	Keynote Speech: *Laurent Duret* The dark side of recombination: biased gene conversion in the tree of life
13:45	14:00	
14:00	14:15	
14:15	14:30	
14:30	15:30	Poster Session & Coffee Break
15:30	15:45	**Panel** Turkish Antarctic Expeditions and Future for Turkish EcoEvo Researchers to Conduct Fieldwork in Global Context
15:45	16:00	
16:00	16:15	
16:15	16:30	
16:30	16:45	Mini-Break
		Chair: TBA
16:45	17:00	Towards a More Comprehensive Approach for Delineating Priority Areas for Plant Conservation in Biodiversity Hotspots: The Case of Lebanon (Eastern Mediterranean) *Mohammad S. Al-Zein*, *Mariana Yazbek*
17:00	17:15	Structural Evaluation of DHFR Resistance Conferring Mutations Reveal Distinct Resistance Mechanisms at the Molecular Level Haleh Abdizadeh, Yusuf Talha Tamer, Erdal Toprak, Ali Rana Atılgan, *Canan Atılgan*
17:15	17:30	Determination of Culturable Free-Living Amoebae in the Biofilm in Formation Process Miray Ustunturk-Onan, Tuba Unsal, Esra Ilhan-Sungur
17:30	18:30	Closing Ceremony

Keynote Speakers

Douglas Joel Futuyma

Stony Brook University, Department of Ecology and Evolution, New York, USA

Douglas Futuyma's research interests in evolution focus primarily on speciation and the evolution of ecological interactions among species. He has been a Guggenheim and a Fulbright Fellow, the President of the Society for the Study of Evolution, the American Society of Naturalists, and the American Insitute of Biological Sciences, the editor of Evolution, and is a member of the National Academy of Sciences. He is editor of the Annual Review of Ecology, Evolution, and Systematics, and is the author of the successful textbooks Evolutionary Biology and Evolution.

Olivia Roth

Helmholtz Centre for Ocean Research GEOMAR, Kiel, Germany

Why males and females exist and how sex roles have evolved belong to the most controversial issues in evolutionary biology. Parental Investment and Immune Dynamics research group examine the evolution of male pregnancy in pipefishes and seahorses (syngnathids) by addressing its genetic basis and the modulations of the immune system. Insights into joint and distinct loss or recruitment of genes along with the establishment of novel genes for male vs. female pregnancy, will help to unravel convergent evolution of parental investment and pregnancy.

Laurent Duret

Université Claude Bernard, Laboratoire de Biométrie et Biologie Évolutive, Lyon, France

My principle research interest is to understand the processes that drive genome evolution. I try to analyze the relative contribution of selection, mutation, drift and biased gene conversion (BGC) to the evolution of genomic features. During my PhD and my postdoc I studied the evolution of non-coding sequences in vertebrate genomes. I discovered that many vertebrate genes contain long highly conserved sequences in their non-coding regions. I also started studying the isochore organization of vertebrate genomes. During the last 10 years, we found strong evidence that the evolution of these peculiar genomic landscapes is the consequence of recombination, via the BGC process.

Lucie Zinger

Institut de Biologie de l'École Normale Supérieure, Paris, France

Since then, my main research question has been how complex assemblages of elusive organisms, such as microbes or even invertebrates, do respond to – or interact with – their biotic and abiotic environment. More recently, I became also interested in their link with ecosystems functioning. To address these questions, I use both in situ and experimental approaches to study a diversity of systems, ranging from host-associated microbial communities to the whole soil biota.

Dieter Ebert

Universität Basel, Departement of Environmental Sciences, Basel, Switzerland

The main focus of the research group of Dieter Ebert are the evolution, genomics and ecology of host-parasite and host-mutualist interactions. Research topics include local adaptation, coevolution, evolution in metapopulations, the evolution of microbiota, the evolution of sex, genome evolution, trait mapping and genetic/genomic architecture. In the last years we developed a Diversity Panel of the crustacean Daphnia magna with the aim to understand species wide patterns of genomic and phenotypic diversity.

Abstracts

Unraveling the extend of gene duplication in *Arabidopsis thaliana* using GWAS

Benjamin Jaegle1*, Mayela Soto, Gökce Aköz, Ilka Reichardt-Gomez, Magnus Nordborg.
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Abstract

Around two thirds of genes in plant genomes are duplicated. In *Arabidopsis thaliana,* this is estimated to be between a half to two-thirds. Most of what we know has come from comparisons of gene duplicates (i.e. homologous genes) between reference genomes across species, but we currently know little about gene copy-number variation within species. Standard algorithms to such variation rely on changes in sequencing coverage or chimeric reads generated as mapping artefacts. Those approaches are often noisy and have low power in mapping the insertion of the duplicated genes.
Because *Arabidopsis thaliana* is largely selfing, most of the genome is expected to be homozygous. As mutations arise, the sequences of duplicated genes diverge, but often map to the same location, creating spurious heterozygous SNPs. Moreover, rare outcrossing events between two accessions will generate further spurious heterozygosity. Such SNPs can be considered as a signature for duplicated genes.Using presence/absence of heterozygous SNPs as a phenotype, we performed GWAS to map duplicated genes. We show that we can detect and map duplicated genes segregating in *Arabidopsis thaliana*. We have confirmed these results using de novo assemblies of five genomes using PacBio data. We found more than 2570 duplicated genes segregating in the 1001 genomes dataset. Gene Ontology analysis reveals a strong enrichment for genes involved in biological processes like response to UV-B, or to fungi and bacteria. This approach is applicable to other highly-selfing model species like *Lotus japonicus* or *Medicago truncatula*. In the future we hope to extend our analysis and detection of “spurious” heterozygous SNPs in obligate outcrossing species.

Keywords: Duplication, natural variation, GWAS

Characterization of the Human Pathogen Peptidome and Specialization in Peptide Binding Among MHC Class-I Alleles

Onur Özer1*, Tobias L. Lenz1

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Abstract

Classical molecules of the major histocompatibility complex (MHC) present pathogen-derived antigenic peptides to immune cells to trigger a pathogen-specific immune response. The excessive polymorphism observed at MHC genes is thought to result mainly from the need to recognize diverse pathogens, a process called pathogen-driven balancing selection. This process assumes that pathogens differ in their peptidomes – the pool of short peptides derived from the pathogen's proteome – so that different pathogens select for different MHC variants with distinct peptide-binding properties. However, the full diversity of the pathogen peptidome that a given host is facing has never been characterized, leaving a crucial gap in our understanding of the evolutionary dynamics that shape MHC variability in natural populations. Here we compiled a comprehensive dataset of >51 Mio 9mer peptides, derived from the proteomes of 36 representative human pathogens including viruses, bacteria and eukaryotic parasites, in order to quantify peptide diversity within and between pathogens. Intuitively, the amount of peptide sharing among pathogens decreases with increasing evolutionary distance. However, only 1.2 % of all peptides were found to be shared by two or more pathogens while the remaining peptides were unique to a single species. We also used computational binding prediction to characterize the binding specificities of 149 common human MHC class-I alleles and investigate quantitative differences among HLA alleles with regard to binding peptides from distinct pathogens. These results have profound implications for the study of MHC diversity, potentially identifying a key selection factor for the excessive allelic diversity observed in natural populations.

Keywords: major histocompatibility complex, MHC, HLA, allele promiscuity

MHC of the Three-spined Stickleback

Sengupta M.*[1], Panchal M. [1,2], Samonte I.E. [1], Chain F. [1,3], Eizaguirre C. [4], Feulner P.G.D. [1,5,6], Kalbe M. [1], Bornberg-Bauer E. [5], Reusch T.B.H. [7], Milinski M. [1], Lenz T.L.[1] .

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Abstract

Parasites have been found to be a major driver for the evolution of host nucleotide diversity, but less is known about their effect on structural variation in the host genome. The Major Histocompatibility Complex (MHC) is a genomic region essential to adaptive immunity and has many intriguing characteristics, such as high allelic variability and sequence divergence as well as potentially adaptive copy number variation (CNV) at some of its loci. Yet, the evolutionary factors and mechanisms that drive its structural variation are still elusive.

Here, we study the genomic organization of the MHC class II region in the three-spined stickleback (*Gasterosteus aculeatus*), for which we found a candidate region on Chromosome VII. We used BAC cloning and long-range sequencing to sequence several distinct CNV haplotypes of the MHC region, which we then assembled and annotated for genes, regulatory regions, and repetitive elements, thereby creating a reference map of this region. We also studied synteny in this region, and found indels that account for CNV and pseudogenization. Other genes of the MHC class II antigen presentation pathway-are scattered throughout the genome.

We are now combining these alternative reference sequences of the stickleback MHC region with WGS data from natural stickleback populations. Earlier work revealed local adaptation of MHC allele pools to distinct parasite communities, potentially contributing to ecological speciation, so we are testing the hypothesis that parasite-mediated selection causes divergence in this genomic region. We are also teasing apart different modes of selection that may be operating, and study the demographics of our local stickleback populations. More broadly, we aim to create a multi-layered understanding of the stickleback MHC region and its evolution: sequence, gene annotation, repeat annotation, population genomics, and demographics. Our ultimate goal is to understand how selection acts on SV’s, contributing to ecological speciation.

Genetic Structures of *Salix alba* and *Salix excelsa* Populations From Two Major River Systems in Turkey

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ABSTRACT

Salix alba (white willow) is an indicator species and an important component of an healthy riparian ecosystem with great renewable energy potential in Turkey. It is used as one of the most effective phytoremediation tool in the world for river cleaning and ecosystem rehabilitation efforts. Genetic structure of Salix alba populations in two river systems (Göksu and Kızılırmak Rivers) in Turkey were studied with the use of 20 microsatellites markers to provide information for effective conservation and breeding programs. Since Salix excelsa was used an a synonym of Salix alba and was not well differentiated from S. alba, 112 genotypes of S. alba belonging to the Göksu River from four populations and 147 genotypes belonging to the Kızılırmak River from five populations were sampled. Only some loci showed evidences of null alleles that are specific to a certain population. No significant linkage disequilibrium and clonal duplication were detected in populations. Genetic structure analysis clearly revealed that S. alba populations in two different river systems represent two different founder populations with very high membership values. All populations maintain moderate level of genetic diversity. The highest pairwise Fst values with the lowest number of migrants were obtained from the Kızılırmak downstream populations. Therefore, these populations were genetically most distant to the remaining populations. Cluster, Bayesian, PCoA analysis, and AMOVA clustered 259 genotypes from nine different locations of two rivers to two major groups because of high level of gene flow within river systems, but less gene flow between river systems. The genetic structure data of the studied river systems will be useful for future breeding programmes, efficient conservation, management and utilization of genetic resources of S. alba. Under increasing habitat deterioration and fragmentation, efficient in situ and ex situ conservation studies should utilize and conserve the species’ genetic resources.

Keywords: Genetic diversity, SSR, Population structure, *Salix*

Not a generalist after all? Life history genomic regions explain differences in Atlantic salmon diet.

Tutku Aykanat[1], Martin Rasmussen[2], Mikhail Ozerov[3,4], Eero Niemelä[5], Kjetil Hindar[6], Vidar Wennevik[7], Torstein Pedersen[2], Martin-A. Svenning[8*], Craig R. Primmer[1*]

1 Organismal and Evolutionary Biology Research Programme, University of Helsinki, Finland. 2 Department of Arctic and Marine Biology, UiT e Arctic University of Norway, Tromsø, Norway. 3 Department of Biology, University of Turku, Finland. 4 Kevo Subarctic Research Institute, University of Turku, Finland. 5 Natural Resources Institute Finland (Luke), Oulu, Finland. 6 Norwegian Institute for Nature Research (NINA), Trondheim, Norway. 7 Institute of Marine Research (IMR), Bergen, Norway. 8 Norwegian Institute of Nature Research (NINA), Arctic Ecology Department, Tromsø, Norway. * denotes equal share senior author.

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An ecological consequence of climate change is the alteration of food-web structures. Species with ontogenetic (age-dependent) diet variation, such as Atlantic salmon, may be more sensitive to food-web perturbations, which may exert age-dependent changes in survival, and subsequently, changes in demography. We have earlier shown that age structure in Atlantic salmon is influenced by a few major effect loci (*vgll3* and *six6*), but whether these regions are linked to diet is not known. We hypothesised that genetic variation in these life history genomic regions may govern age dependent resource utilization efficiency, whereby alleles linked to maturation deliver increased resource utilisation efficiency during different marine migration phases. Thus, we performed targeted genotyping by sequencing of Atlantic salmon sampled at sea on their return migration to fresh water, and quantified their diet via stomach content analysis. We present evidence that diet acquisition in Atlantic salmon (stomach fullness) is associated with *six6,* a gene previously shown to be potentially under divergent selection and correlated with age at maturity among populations. There was no association with *vgll3,* a gene having a large effect on maturation age. However, prey preference (proportional mass of each prey species in the stomach) was linked to both *six6* and *vgll3*. Our results suggest Atlantic salmon are not as generalist as previously thought and that genetic variation partly underlies resource utilisation variation among individuals. Given that this genomic region is spatially divergent across populations, we predict that populations will have diverse evolutionary responses to future changes in marine food-web structures.

Environmental DNA: a tool for estimation of fish biomass/abundance?

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Abstract

Environmental DNA has become popular method to detect living organism in aquatic and terrestrial habitats. Besides, eDNA can be used for estimation of fish biomass/abundance in freshwater. In our study we tested the relationship between eDNA and traditional method by comparing the eDNA read numbers of *Cyprinus carpio*, *Carassius gibelio* and *Sander lucioperca* with the traditional abundance/biomass estimation data in the Karataş lake. We designed seasonal field and simulated laboratory experiments for February, April, June and September. eDNA sampling was done from three stations of the lake and fishing was done for laboratory experiments. Before aquarium experiments, parameters of biomass were measured for each captured individual. In laboratory experiment, the effect of three different factors (duration, water temperature and fish biomass/abundance) on eDNA concentration was investigated. We set up three aquarium experiments using 250L fiber tanks. Target species were kept in for 1,2,3,6 and 9 days in experiment tanks. For temperature experiment, selected species were kept six days at 7, 15 and 25°C in experiment tanks. To evaluate target species abundance on eDNA concentration 1, 5, 10, 25 individuals were kept 6 days in experiment tanks. After these experiments, 500ml of water was filtered by using 0.22µm pore size filters. We obtained total 192 filters. DNA extractions were done by using optimized eDNA protocol and two-step PCR were done using universal fish primers MiFish-U-F/ MiFish-U-R with related high throughput sequencing platform adaptors with 500K read per sample.
According to bioinformatics analysis we found statistically correlated results between eDNA copy number and fish biomass/abundance estimated using traditional methods. Comparison of results from traditional and eDNA method for estimation of biomass/abundance of target species resulted with an average of %4 deviation. As a result, using eDNA metabarcoding can provide cost-effective, time-saving and rapid results similar to traditional methods to estimate species biomass/abundance in natural environments.

Keywords: Environmental DNA, Biomass, Abundance, Freshwater Fish, High Throughput Sequencing

Seasonality effect on the demography of large mammal species in Northwestern Anatolia

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Abstract

Large mammals act as keystone species shaping the biodiversity in many ecosystems. Understanding their habitat use patterns is important for determining the most effective management plans and conservation action. Additionally, most natural populations inhabit seasonal environments, and species' habitat use can change among seasons. Automated monitoring methods, such as camera trapping, are used commonly to investigate habitat-species interactions. However, imperfect detection, which can vary among species, habitats, and seasons, is an important consideration in the analysis of these type of data. Both imperfect detection and seasonal variation need to be accounted for to gain a better understanding of species' habitat use. Turkey, as an intersection between Europe, Central Asia, and Africa, hosts a rich diversity of large mammals. The extensive forests of Northwestern Anatolia are one of the few remaining undisturbed habitats for large mammals. In this study, using a dynamic occupancy modeling approach and 3 years of camera trapping data from 11 large mammal species in the Northwestern Black Sea Region, we investigated habitat use patterns for each species. We specifically looked at seasonal changes in habitat use and environmental and anthropogenic factors underlying the observed patterns. Our aim is to understand the species-specific habitat-use patterns and contribute evidence-based recommendations for the management of large mammals in the region.

Keywords: wildlife demography, seasonality, large mammals, hierarchical models, camera trapping

Changes in Waterbird Community Structure and Functional Diversity in Shallow Lakes: The Role of Water Level and Submerged Macrophytes

İbrahim Kaan Özgencil 1*, Meryem Beklioğlu 2, Korhan Özkan 3, Çağatay Tavşanoğlu 4, Niccolò Fattorini 5

1 Department of Biological Sciences, Middle East Technical University, Ankara, Turkey 2 Department of Biological Sciences, Middle East Technical University, Ankara, Turkey 3 Institute of Marine Sciences, Middle East Technical University,Mersin, Turkey
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Abstract

Water level (WL) and submerged macrophytes are critical elements of shallow lake ecosystems. We analyzed historical mid-winter waterbird survey data, water level measurements and submerged macrophyte records from sediment cores using generalized linear models to explore the effects of these two important factors on community structure and functional diversity of wintering waterbirds in Lake Beyşehir and Lake Uluabat, two shallow lakes in Turkey. A collection of response and effect traits was chosen to calculate functional diversity metrics. Null models were used to obtain standardized effect sizes for the calculated functional diversity measures. We discovered that abundances of omnivorous and herbivorous waterbirds were higher during macrophyte-dominated years. Conversely, abundance of fish-eating waterbirds was higher during turbid-water periods. The effect of WL was more pronounced in Lake Beysehir where low WL years attracted significantly more omnivorous and herbivorous waterbirds, and more waterbirds on average. WL didn't have any significant effect on community structure and diversity in Lake Uluabat, probably due to the weaker link between WL and submerged macrophyte coverage. We found that, other than functional richness, the functional diversity measures of the communities do not differ significantly from those of the randomly generated assemblies. Functional richness and functional dispersion of the communities were mostly lower than the expected values. Functional evenness and functional divergence showed no patterns. Functional dispersion was found to be significantly higher for low-macrophyte years for both lakes, which is in line with the recent findings of high functional dispersion in communities of disturbed and fragmented habitats. Our results suggest that macrophyte-dominated conditions in shallow lakes attract more wintering waterbirds, especially herbivorous and omnivorous species, some of which are globally threatened, and that the influence of abiotic and biotic community assembly processes changes with environmental conditions as shown by the higher functional dispersion under low-macrophyte conditions.

Keywords: community ecology, functional diversity, submerged macrophyte, water level, waterbird

Influence of Fish Predation on Size-based Interactions and Recovery of Zooplankton Communities in Freshwater Planktonic Food Webs: Examples from Mesocosm Experiments

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Planktivorous fish predation affects the community and size structure of zooplankton and this may indirectly cascade down to phytoplankton. Thus far, studies in trophic interactions have been centered in variations of community abundance and biomass. However, studies on individual size-based interactions, having an important role in ecosystem functioning, have been scarce. Moreover, the resilience of zooplankton communities to fish predation and the cascading effects on phytoplankton have not been explored thoroughly. We conducted two different mesocosm experiments in Lake Mývatn, Iceland and Lake Müggelsee, Germany in order to assess the cascading effects of fish predation on size-based interactions and resilience of communities after fish predation, respectively. The experimental set-up consisted of enclosures with fish and without fish, which were inoculated with plankton communities from natural lakes. By using parameters of size diversity, mean size, abundance and biomass of different groups, we studied changes in the community and size structure of zooplankton and phytoplankton communities. Our results from these experiments showed that fish predation negatively influenced zooplankton size diversity. The occurrence of cyanobacteria blooms in Lake Mývatn during the experiment, also resulted in a decrease in zooplankton size diversity as well as in energy transfer. In Lake Müggelsee, short-term fish predation weakened the resilience in zooplankton community by modifying community composition. We observed that the small zooplankton dominated and some of the large zooplankton such as calanoids did not appear again after fish predation. This caused higher phytoplankton yield, thus low water quality in the fish enclosures than in the controls. In conclusion, both top-down and bottom-up controls influence of planktonic communities, and thus ecosystem functioning. Understanding size-based interactions and resilience are essential for trophic cascade studies and phosphorus ratio) (Chlorophyll-a: Total the community and size structure restoration and management strategies of aquatic ecosystems to better predict responses to global warming.

Keywords: fish predation, zooplankton, phytoplankton, trophic interactions

High Ecological Plasticity and Genetic Diversity of the Native Ponto-Caspian Gobies Suggests Establishment Success in Their Invasive Range

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Abstract

Risk assessments of invasive species are relying on ecological and molecular data that help the predictions of whether a non-native species will adapt to new environment. Thus, relevant data from the native range of potential invaders can assist these assessments. Here, we aim to provide baseline data and fill a remarkable knowledge gap in our understanding of factors influencing the invasiveness of two Ponto-Caspian gobiid, monkey goby *Neogobius fluviatilis* and Western tubenose goby *Proterorhinus semilunaris* in four natural lakes in their native range (the Marmara Region – NW Turkey). Populations of both species were generally characterised by slow somatic growth rates, being the slowest reported across all the native and non-native ranges of *N. fluviatilis*. Across all lakes studied, there was considerable variability in sex ratios and reproductive traits including size at maturity and fecundity for *N. fluviatilis*, whereas they did not significantly differ between lakes for *P. semilunaris*. Isotopic (mixing models) and traditional (stomach contents) dietary analyses of both species suggests considerable inter- specific dietary differences amongst the lakes. This was also the case for habitat preferences of both species being highly variable amongst the lakes and seasons, with *P. semilunaris* more flexible in habitat choice. These two species and populations were identified using DNA barcoding. The results obtained by analysing the data set was in accordance with the taxonomic classification performed according to the morphological definitions created by FAO. Phylogenetic models and Median Joining network analyses results are indicating a single haplotype for monkey goby populations while a clear diversification was detected in western tubenose goby populations. The data obtained from the study clearly reveal the effectiveness of COI barcodes in the identification of freshwater fish species even at population level. These reference COI barcodes for aquatic organisms in our country will constitute an important molecular resource for future studies. Overall, all of the obtained data in this study suggest that both *N. fluviatilis* and *P. semilunaris* have considerable plasticity in the expression of its life history traits and genetic structure, which provides both species considerable adaptive capacity following introductions and facilitate the ability to establish in novel conditions.

Keywords: Monkey Goby, Western Tubenose Goby, Niche Plasticity, Phylogenetic Relationship, Natural Lakes

Genetic similarities among diseases as a means of understanding ageing

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Abstract

Ageing is a major risk factor for many diseases. With the rise in life expectancy, the overall burden of ageing-related diseases increases. The ultimate causes of ageing and its molecular link with ageing-related diseases, however, still await discovery. In this study, we test weather diseases with similar age-of-onset share a genetic component that is also implicated in ageing. We further characterise the evolutionary history of these genetic associations at the level of SNPs, genes and pathways. More specifically, we perform GWAS on UK Biobank data, which includes genomic, medical and lifestyle measures for almost 500,000 participants and test for overlaps across diseases using novel computational approaches. In order to explore the link between ageing and these diseases, we combine our results with publicly available datasets for ageing, such as age-series gene expression profiles and lifespan assays using model organisms. Analysing associated variants for the diseases with different age- of-onsets, we can also test the two most attributed evolutionary theories of ageing, i.e. mutation accumulation and antagonistic pleiotropy. We hope that our novel approach can help both to elucidate the ultimate causes of ageing and to target multiple age- related pathologies through shared genetic components.

Mesocosm Experiment on Effects of Microplastic on Freshwater Zooplankton Community

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Abstract

Microplastic (MP) pollution is a major environmental concern globally. MPs are emerging threat both for marine and freshwater ecosystems. However, studies for the impact of MPs on freshwater ecosystems is significantly less than MP focused studies on marine ecosystem. The impact on freshwater lake ecological communities remain unknown, so outdoor mesocosm experiment gives environmentally realistic research option to understand the fate of freshwater lake species exposed MP. Especially, zooplankton has the key role among the other species to evaluate the impact of MPs on lake ecosystem. In this study, impacts of MPs on freshwater species were assessed outdoor mesocosm experiment with an environmentally relevant concentration of microplastic in all surface, water column and sediment were considered. Experiment were conducted 12 cyclindrical-shape mesocosms (4 control, 4 low MP content, 4 high MP content) for 2 months on a floating platform in the middle of the lake. Each mesocosms were inoculated with phytoplankon, zooplankton, macro-invertebrates (snail, dragon flies and mayflies). Zooplankton were analysed for microplastic ingestion. The study shows that functional groups of zooplankton community being exposed to different MP concentrations shifts.

Keywords: Microplastic, mesocosm, freshwater, zooplankton

Contributions of sperm and seminal fluid to ejaculate senescence, and its amelioration via insulin signalling

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Abstract

Understanding the causes of variation in male ejaculate performance is of widespread importance for diverse fields, ranging evolutionary biology to assisted reproduction. Age-related declines are of particular immediacy given current trends for later fatherhood and decreased male fertility in many countries. However, the causes and consequences of ejaculate senescence, for example the relative sperm and seminal fluid, and how they impact ejaculate function, opaque. Here we address this problem using label-free quantitative proteomics and fluorescent sperm labelling in the *Drosophila* model. We show that age and frequent-mating reduces ejaculate performance, which is mediated by changes to both sperm and seminal fluid, but via different mechanisms. Sperm production declines with age, while repeated mating depletes sperm reserves and reduces sperm viability. In contrast, seminal proteins maintain their abundance, or accumulate in sexually abstinent males, but display evidence of age-related qualitative changes. Finally, we reveal that ablation of insulin-like peptide-producing cells in males can ameliorate aspects of ejaculate senescence. Collectively our data show that the causes of age-related declines in male ejaculate performance are multi-faceted, but that lifespan-extending interventions may provide co-benefits by delaying ejaculate senescence.

Keywords : sperm, ejaculate senescence, Drosophila, lifespan extension

Coevolution of female fidelity and male help under intra- and inter-locus sexual conflict

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Abstract

In many species of monogamous birds, females commit extra-pair mating and male also actively try to obtain opportunities for siring extra-pair offspring. In some of these species, pairs perform elaborated and well-coordinated courtship rituals such as duets or pas-de-deux. Taking a female perspective, it has been argued that these displays help females evaluate the commitment of their male partners to invest in the pair-bond and paternal care of offspring. However, taking a male perspective, we wonder how males that invest in building a strong pair-bond with a female by coordinating duets or pair-displays can be sure that the female is equally committed to the pair-bond and does not seek extra-pair copulations with other males? The problem is further complicated by intralocus sexual conflict. When males and females have different trait value optima, high-condition males may sire attractive sons but low fecundity daughters, and vice versa. In this work, we study the coevolution of female fidelity and male help under the present of both types of sexual conflict. We show that the effectiveness of mate-guarding of males (as a by-product of helping with parental care) plays crucial role in the coevolutionary dynamics. When mate-guarding is effective, stable polymorphism evolves in the male population, so that most males are highly helpful to their partners while a small proportion forgo pair formation completely and try to obtain paternity solely from extra-pair mating. When mate-guarding is ineffective, the degrees of female fidelity and male help can fluctuate in cycles.

Keywords: sexual conflict, extra-pair mating, mate guarding, parental care, mathematical modelling

Sex Ratio at Mating Does Not Modulate Age-Related Fitness Decline in *Drosophila melanogaster*

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Abstract

Investigating the effects of male and female age on reproductive success is vital to understand the evolution of life history traits and sex-specific ageing. Considering that sexes have different strategies to optimize their fitness, social context has the potential to modulate age effects on reproductive success in a sex-specific manner. Yet, studies of reproductive senescence so far have mainly focused on how pre/post-meiotic ageing processes might lead to a decline in the pre- and post-copulatory abilities of both males and females. In contrast, how age effects on reproductive success might be modulated by the social context has been largely overlooked. In this study, we explored whether social context (in terms of sex ratio at mating) can modulate age effects on male and female reproductive success by using *Drosophila melanogaster* as a model organism. As expected, male and female age caused a decline in reproductive success across male-biased and female-biased social contexts but, contrary to previous findings, sex ratio at mating did not modulate such age-related fitness decline in either of the two sexes. We discuss these results in the light of how social context might modulate pre/post-copulatory abilities that are involved in inter- and intra-sexual competition in *D. melanogaster*. Finally, we suggest that the effects of social context on these processes might be species specific.

Keywords: sex ratio, ageing, reproductive success, fitness, senescence

Life history evolution under cancer risk: linking cell-level strategies to organismal traits

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Abstract

Multicellular organisms require cell divisions to attain their body sizes, maintain their tissues, and to reproduce. Each cell division occurs with a probability of mutations that could lead to uncontrolled growth, which could ultimately cause cancer and end an organism's life. Intuitively, this means cancer risk should increase with the number of cell divisions. However, despite requiring more cell divisions, large-sized and long-lived organisms seem to avoid a high cancer incidence (Peto's Paradox). This suggests that they have evolved ways to lower their mutation accumulation risk per cell division. Various cellular mechanisms such as telomere attrition or apoptosis contribute to cancer suppression, but they can also incur costs for the organism itself. For instance, while a high apoptosis response can remove mutated cells from the tissue more efficiently, killing too many cells could impede tissue maintenance. Interspecific variation in these traits suggests that they might be adapted to the life history of the organism. Here we ask: how do multicellular organisms optimize their cell-level defence strategies in relation to their organismal life history traits? We present a model where we study division and differentiation processes at the tissue-level and investigate optimal cell-level strategies with respect to apoptosis rules, telomere length and tissue structure. Our ultimate aim is to relate these insights to the level of the organism, creating predictions for species differing greatly in body size and lifespan.

Keywords: cancer; life history; ageing; cooperation

Cultural Selection Shapes Network Structure

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Abstract

Cultural evolution relies on the social transmission of cultural traits across a population, along the ties of an underlying social network that emerges from non-random interactions among individuals. Research indicates that the structure of those interaction networks aects information spread, and thus a population's ability for cumulative culture. However, how network structure itself is driven by population-culture co-evolution remains largely unclear. We use a simple but realistic model of complex dynamic social networks to investigate how populations negotiate the trade-o between acquiring new skills and getting better at existing skills, and how this trade-o, in turn, shapes the social structure of the population. Our results reveal unexpected eco-evolutionary feedback from culture onto social network structure and vice versa. We show that selecting for generalists (favouring a broad repertoire of skills) results in sparsely connected networks with highly diverse skill sets, whereas selecting for specialists (favouring skill proficiency) results in densely connected networks and a population that specializes on the same few skills on which everyone is an expert. Surprisingly, cultural selection for specialisation can act as an "ecological trap" where it can take a long time for a specialist population to adapt to a generalist world. Our model advances our understanding of the complex feedbacks in cultural evolution and demonstrates how individual-level behaviour can lead to the emergence of population-level structure.

Distinguishing between recent balancing selection and incompletesweep using deep learning

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Abstract

Balancing selection refers to a variety of mechanisms in which the variation is maintained within populations. In contrast to directional selection and genetic drift, which erode polymorphism by eliminating alleles, balancing selection enhances genetic diversity in populations. Previously reported targets of balancing selection in human genome include genes related to immune response, pathogen defense, reproductive fitness and environmental stressors. Although a growing body of evidence indicates the importance of balancing selection in current phenotypic diversity, our understanding of its prevalence and targets in the human genome remain limited due to challenges associated with its detection. Commonly used methods have been mostly designed to target long term balancing selection and they are sensitive to confounding effects. Specifically, signatures of recent balancing selection are qualitatively similar to those of recent positive selection, such as incomplete sweep. Here, we developed a deep learning framework to detect the signatures of balancing selection and separate them from those of incomplete sweep. The evaluation of the basic model using simulated test data revealed ~95% accuracy in the detection of selection and ~80% accuracy in distinguishing between balancing selection and incomplete sweep. While these results can be improved with an optimized model and larger sample size, our overall results demonstrate the potential of deep learning algorithms for population genetic inferences.

Studying polyploidy with “right” genomes and “right” approaches

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Abstract

All flowering plants are descended from a polyploid ancestor. With only a few exceptions, all of them experienced at least one another round of whole genome duplication (WGD). This repeated cycles of polyploidy have left the traces of only the most recent ones in the plant genomes. Therefore, dating ancient WGDs has been challenging. Here, we investigated the history of the ancient *gamma* hexaploidy found in all core eudicots, using the exceptional genome of grape free from recent WGDs. As an outgroup for a synteny-based comparison, we used the recently published columbine genome from basal eudicots, previously reported to have undergone a lineage-specific tetraploidization. Our novel analyses indicate that the genomes of grape and columbine were shuffled similarly by diploidization, a process under which deletions and rearrangements of various sizes scramble the genetic material, leading to a repacking of the polyploid genome and eventual return to diploidy. This result parsimoniously suggests that these two distantly related taxa have inherited the genome structure of a common tetraploid ancestor. So, columbine tetraploidy is a remnant of a WGD at the base of all eudicots and far more ancient than previously thought. Our result also illuminates the nature of the *gamma* hexaploidy. The triplicate genome structure of core eudicots must be a product of a two- step process: first tetraploidy in the ancestry of all eudicots, then hexaploidy in the ancestry of core eudicots. We further argue that the latter involved allopolyploidization, and that core eudicots thus have a hybrid origin. These findings highlight the value of basal eudicots as an outgroup to the core eudicots and will hopefully encourage larger scale analyses to understand what hybridization has meant for core eudicots — a group which comprises more than 70% of all living flowering plants!

Rigorous Model Ranking and Exhaustive topology Exploration Improve the Functionality of qpGraph

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Abstract

Archaeogenetics, the study of ancient DNA, is growing rapidly, and genome-wide data for hundreds of ancient human individuals are produced every year. Answering questions about history requires testing complex demographic models, i.e. admixture graphs including population splits and pulse- like admixture events. Various graph-fitting methods exist, and qpGraph is a widely used tool relying on *f*-statistics. It produces population graphs with fitted admixture proportions and edge lengths scaled in units of relative genetic drift and can process any type of biallelic genotype data including data generated by targeted capture. Even low-coverage ancient individuals can be included into the model-building process, which is critical for many use cases. qpGraph is also very fast as compared to Bayesian methods relying on site frequency spectra (momi2, rarecoal, fastsimcoal), thus topologies can be explored exhaustively for crucial sub-graphs. Resulting topologies (the order of populations splits or the sources of gene flow) are often compared according to their worst-fitting *f4*-statistics (Z- scores). We show that this approach is far from optimal since it ignores the whole “landscape” of poorly fitting *f4*-statistics and thus often favors sub-optimal models. To overcome this problem, we developed a new rigorous approach that ranks competing models (having the same number of parameters, populations and SNP set) by likelihood and considers likelihood ratios >20 as significant. A group of best models found in this way can be narrowed down even further by counting the number of 0-edges corresponding to trifurcations that are expected to be much less frequent in realistic topologies compared to sub-optimal graph topologies. We also propose a likelihood threshold for comparing models with an added admixture event and present a pipeline for exhaustive non-greedy exploration of ancestry sources in admixed groups. We have applied this graph-based approach for addressing key questions on the prehistory of East Eurasia and America.

Keywords: ancient DNA, qpGraph, complex demographic models, *f4*-statistics

Empirically Tractable Antibiotics Time Machines

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Abstract

Suppose we have a population of bacteria and for each bacterium of a given genotype, an antibiotic alters it to another type with some probability. Mira et al., [PLOS ONE 10 (2015), e0122283] asked if it is possible to apply a set of antibiotics (K in number) with a specified precedence (in N steps) so as to maximize the fraction of bacteria (with d number of distinct genotypes) becoming again the wild type. A straightforward approach would be to explicitly enumerate all the permutations with repetitions, and then compute the probability of returning to the wild type. This procedure examines a total number of KN alternatives, in each of which we need to multiply d-by- d matrices with d-vectors N many times. Such an explicit enumeration algorithm is prohibitively time-consuming, even for moderate size problem instances. Subsequent work by Tran and Yang [Notices of the AMS 64 (2017), 1136] proved that such a treatment plan (referred to as antibiotic time machine) is NP-hard to compute. We, however, have transformed the time machine problem to an empirically tractable optimization problem in two steps. In Step 1, we formulate the problem as a Mixed Integer Linear Program (MILP) involving O(K×N×d) many decision variables and constraints. In Step 2, we attack the resulting “compact-size” MILP (total number of variables and constraints are polynomial in the size of the input) by a well-designed implicit enumeration algorithm called “branch-and-bound,” which also takes advantage of additional features called cutting planes, heuristics and pre-processing. We generated instances to test the efficiency of our approach. Our computational results are quite encouraging. With d=30 genotypes, K=10 antibiotics over N=90 time periods, our approach only requires, on the average, the examination of less than 2000 branch-and-bound nodes within the optimality tolerance of 0.001 units.

Keywords: Antibiotic resistance, genotype, bacterial population, fitness landscape, optimization

The effect of salt concentrations on genome-wide mutation rate on halophilic archeon *Halobacterium salinarum*

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Abstract

As the ultimate source of genetic variation, mutations have a central place in biology and thus, understanding the mutation rate is critical in determining rates of molecular evolution, estimating effective population sizes, understanding the impact of mutations on organismal fitness, and evaluating the power of drift, selection, and recombination in shaping genomes. Today, by applying high-throughput sequencing technology to mutation-accumulation experiments, it is possible to generate the most direct and unbiased estimate of the genome-wide spontaneous mutation rate and spectrum of an organism, which thus allows us to distinguish the intrinsic and extrinsic forces driving the mutation process. Previously, genome-wide spontaneous mutation rates have been estimated for a variety of prokaryotes and eukaryotes. However, in order to understand how environmental (extrinsic) and cellular (intrinsic) factors cooperate and ultimately determine the genome-wide mutation rate and spectrum, it is necessary to expand these experimental assays. In this study, we design a study to determine a genome-wide view of the spontaneous mutations in the halophilic archeon *Halobacterium salinarum* by using the most direct and unbiased method, combining mutation-accumulation experiments and whole-genome sequencing under different salt concentrations. As the same strain of *H. salinarum* has been the subject of our prior work, all new results can be directly comparable to those previously obtained. And we will evaluate the effect of salt stress on spontaneous mutation rate and spectrum in halophilic archaea, while also discussing the underlying genetic and/or biochemical mechanisms of mutation in an organism. This study will contribute to providing a comprehensive insight into mutations and revealing what factors of molecular and genomic architecture affect the mutational process in diverse organisms.

Keywords: Salt stress, Mutation accumulation, Whole genome sequencing, Halophile, Mutation rate, Mutation spectrum

Assessment of Using Three-Way Interactions Between Plants, Microbes and Arthropods in Pest Management: A Case Study of the Three-Way Interaction Between Potato Plant, Mycorrhizal Fungi and Colorado Potato Beetle

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Abstract

The Colorado potato beetle (CPB), *Leptinotarsa decemlineata* (Say) (Coleoptera: Chrysomelidae) is one of the most important insect pests of potatoes. Until now, none of the control techniques developed against this pest including using pesticide has provided the long- term solution and there is a dire need in utilizing alternative approaches. Nowadays, enhancing plant growth and resistance and biological control are considered the key strategies. Various soil-borne microorganism groups have positive effects on plant growth, health and resistance through direct and plant-mediated mechanisms. Symbiotic arbuscular mycorrhizal fungi (AMF) form a key component of the microbial populations by improving rooting and plant establishment, enhancing uptake of low mobile ions, improving nutrient cycling and enhancing plant tolerance to biotic and abiotic stress factors. The overall objective of this research was to determine if AMF increases potato tolerance to CPB. The study was carried out in the climate room providing 24±2°C temperature, 60±10 % RH, and a photoperiod of 14:10 (L:D) h. Biological data obtained were analyzed according to the age-stage, two-sex life table theory to calculate population parameters and simulate the population growth of CPB. The results indicated that the use of AMF affects the growth of potato plants, the mineral content of potato leaves, and the consumption rate and population performance of the CPB. The longer developmental time, lower fecundity and lower foliage consumption of CPB on potato plants treated by AMF resulted in reduced fitness of the pest.

Keywords: *Leptinotarsa decemlineata*, potato, mycorrhizal fungi, population growth

The role of gene flow and hybridization in shaping genetic diversity structure of Populus nigra populations in Turkey

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Abstract

Populus nigra is one of the most economically and ecologically important riparian trees in Turkey. Due to overexploitation, loss of natural distribution area and threat of hybridization and introgression, it is one of the most threatened tree species in Turkey. To detect the genetic diversity structure of Populus nigra species in its natural distribution area three natural poplar populations were screened by nine nuclear microsatellite DNA markers. 10 P. deltoides reference samples were also studied to evaluate the occurrence of hybridization and introgression. Genetic diversity of all populations has been found generally in moderate level. Due to low level of gene flow, three populations were differed significantly from each other. The results of hybrid analysis indicated that four trees in Göksu and one tree in Melet river populations were determined as F2 hybrids with high probability and diagnostic and informative alleles. Göksu population undergone a recent bottleneck event that caused the less amount of allelic diversity and excess of heterozygosity. With help of the obtained information, conservation and breeding studies for later generations of the species would be performed to preserve the desired level of genetic diversity and adaptability to different ecological environments.

Keywords: Diversity, gene flow, hybridization, bottleneck, heterozygosity

Establishing National Early Warning and Monitoring System for Available and Potential Non-native Freshwater Fish Species in Turkey

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Abstract

The damage caused by non-native and invasive species to the local fauna, flora, ecosystem and socio-economic structure has been well known for many years and the studies conducted on this subject have increased significantly in recent years. In this sense, it is essential to identify potential non-native species that may pose a threat, to continuously monitor, to carry out risk analyses and to keep them under control.The aim of the study is to determine native, non-native and invasive fish species located in Turkey's inland waters using traditional and molecular tools, assess their risks and develop a real-time web-based database and monitoring map to maintain proper control and management of these species. For this purpose, water samples were taken from 54 different points of 10 rivers using peristaltic pump and disposable sterile filters with a pore size of 0.22/0.45 µm. The PCR amplifications of the eDNA extracted from the filters were performed with tagged MiFish-U F/R (12S rRNA) primers, indexed via adaptor ligation and aligned with reference sequences from NCBI GenBank and European Freshwater Fish Local Database using the processed pair-ended reads obtained from 500K read per sample high throughput sequencing. The risk analysis of the identified species was performed with the AS-ISK (Aquatic Species Invasiveness Species Risk) software. As a result, a total of 232 species detected in this study to determine invasiveness levels of non-native and invasive species were successfully analysed using AS-ISK program for Turkey inland waters. eDNA metabarcoding of the species, especially the ones that has not been reported before using traditional sampling is one of the most important outcomes of this project. In this regard, it is necessary to create and implement emergency management plans for some species which are not reported previously.

Keywords: AS-ISK, Environmental DNA, Freshwater Fish, Invasive Species

Impact of Deep Sea Mining on Seafloor Ecosystems: A Baseline Study on Clarion-Clipperton Zone (Expedition SO268)

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The demand on metals and rare-earth elements is subject to an increasing trend globally, and economic interest on these materials expected to be increased in future. This trend triggers a pursuit of new, profitable sources. Polymetallic nodules on the deep sea floor are important examples of such potential sources. Abundance of mineral deposits on seafloor and constrains on profitable land sources make deep sea mining a valuable option. Several seafloor exploration licenses have been filed at International Seabed Authority, and deep-sea mining activities are expected to start in near future. However, the possible impact of deep-sea mining on seafloor ecosystems has not been investigated comprehensively yet. A “gold rush” without estimating and considering possible impacts might jeopardize the integrity of seafloor ecosystem with unknown fallout on biodiversity, food web and elements cycles. In spring 2019 a comprehensive interdisciplinary expedition has been conducted at German and Belgian license areas in the Clarion-Clipperton Fracture Zone (central north Pacific Ocean) in order to obtain baseline characteristics of ecosystems in the manganese nodule fields. The two investigated areas show differences in ocean surface primary productivity, bathymetry, and in distribution and size of the nodules. Those differences give the opportunity to study spatial variability of environmental settings and biological assemblages. Specifically variation in microbial community structure, abundance and activities are investigated and will be interpreted together with the data of organic carbon availability, community respiration rates and distribution of benthic fauna. In addition to those baseline surveys, a dredge experiment was performed to simulate the effect of mining, including: i) removal of nodules and the top 10 cm of sediments, ii) sediment resuspension and resettling. Overall outcomes of this study will be to discriminate between natural variability and ecological effects of mining activities and to assess consequences of mining impacts on deep-sea benthic ecosystem functioning.

Keywords: Deep-sea mining, Seafloor Ecosystem, Manganese Nodules, Microbial Ecology, Anthropogenic Impact

Structural Evaluation of DHFR Resistance Conferring Mutations Reveal Distinct Resistance Mechanisms at the Molecular Level

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Abstract

We utilize molecular dynamics (MD) simulations to study the structural changes associated with the experimentally observed trimethoprim resistance conferring mutations in dihydrofolate reductase (DHFR). We have monitored the wild-type (WT) and all 11 single mutant sets of MD trajectories corresponding to those that appear in the morbidostat, a continuous culture device developed to quantitatively study evolution of antibiotic resistance (Toprak *et al.*, Nature Genetics, 2011), to decipher the molecular mechanisms that lead to trimethoprim resistance. While these mutations are observed with various frequencies in the morbidostat trajectories, only nine of them appeared as the first coding region mutation in *folA* gene. Amongst these, D27E, L28R, and W30R are three most frequently observed mutations in the morbidostat and interestingly, these are also the only cases where significant structural changes were identified in the dynamical trajectories (Tamer *et al.*, Molecular Biology and Evolution, 2019). Thus, although antibiotic resistance via target modifications is typically attributed to reduced drug and substrate affinities due to mutations, we identify distinct resistance mechanisms for each of these mutants. Furthermore, we demonstrate the context dependence of the observed dynamics by focusing on four specific examples involving double mutations. We illustrate how epistatic coupling at the atomistic level can give rise to complex fitness landscapes and suggest strategies for exploiting the distinct structural changes for developing mutant specific inhibitors. In particular, the L28R mutation has a distinct mechanism that increases its relative preference for the substrate over the drug molecules (Abdizadeh *et al.*, PhysChemChemPhys, 2017). Thus, it might be possible to design L28R- specific DHFR inhibitors that will mimic DHF without losing its specificity against bacterial DHFR. Since L28R mutation is observed in nearly 80% of all morbidostat trajectories and is synergistically interacting with several mutations, an L28R specific inhibitor will substantially impede evolution of trimethoprim resistance.

Keywords: fitness landscapes, trimethoprim resistance of DHFR, epistasis, biochemical characterication

Determination of Culturable Free-Living Amoebae in the Biofilm in Formation Process

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Abtract

Free-living amoebae (FLA) are protozoa which can be found in various environmental and man-made water systems. They are considered as an important part of the microbial community of biofilm because of their interaction with the bacteria in the same environment as well as their pathogenic properties. Biofilm formation is one of the most important problems frequently encountered in man-made water systems such as cooling tower, which is an indispensable part of industrial plants. The aim of this study was to determine the culturable FLA simultaneously from water and biofilm samples from a model cooling tower system. For this purpose, galvanized steel coupons, which are the cooling tower material, were placed in the system where water was continuously circulated like a cooling tower, and biofilm formation was allowed on the surfaces for 1 month. At certain time intervals (0.5, 1, 2, 4, 8, 24, 48, 72, 96, 168, 336, 504 and 672 hours), isolations were carried out both from the system's water and biofilm. The samples were inoculated on Escherichia coli seeded non- nutrient agar and Petri dishes were incubated at 30°C for 14 days. FLA were identified by morphological criteria according to Page (1988). FLA were detected in all water samples excluding the first sampling time, on the other hand, they were detected in all biofilm samples after 72 hours. Morphological characterization of the isolated FLA strains using the currently available identification key from Page frequently yielded the identification of the genus Vermamoeba from water and biofilm samples. The presence of FLA in both water and biofilm samples in man-made water systems emphasizes the urgent need of implementing effective preventive measures, since they are potentially pathogenic for humans.

Keywords: Free-living amoebae, biofilm, cooling tower, Vermamoeba

POSTERS

Phylogeographic resolution of Botrylloides leachii (Savigny, 1816) from the North-eastern Mediterranean Sea

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Sea squirts (Tunicata) are the closest invertebrate relatives to the vertebrates. Botryllus and Botrylloides are two genera of botryllid ascidians which is the only chordate group having the ability of whole-body regeneration. In this study, we targeted to determine phylogeographic resolution of Botrylloides leachii in the North-eastern Mediterranean Sea by using mitochondrial and nuclear DNA markers (COI and H3). In total 232 samples collected from 8 spatial stations from West to East as Kemer-Side-Alanya-Tershane (Antalya), Tisan-Kız Kalesi-Mezitli (Mersin) and Konacık (Iskenderun). Present study sequences also compared with the sequences that mined from databases, to construct network and phylogenetic trees. Furthermore, living individuals were investigated under light and stereo microscopes to identify their life cycles. Molecular analyses resulted low resolution for the COI gene region among the North-Eastern Mediterranean's B. leachii samples, so far only 2 COI haplotypes were recorded, and on the other hand H3 displayed 9 haplotypes. The results indicate the necessity of an alternative barcode region, beside of COI gene nuclear H3 region can be used to increase the resolution of the species.

Altitudinal effects on innate immune response of Turkish blind mole-rats

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Abstract

Immune defense is costly to maintain and deploy, and the optimal investment into immune defense should depend on risk of infection. Altitude is a natural environmental factor predicted to affect parasite abundance, with lower parasite abundance predicted at higher altitudes because of harsher environmental conditions that reduce parasite transmission such as low temperature, high UV radiation, and low host density.
Using high and low altitude populations of the Turkish blind mole-rat (TBMR) *Nannospalax xanthodon* (cytotype 2n = 58), we tested the effect of altitude on constitutive innate immune defense. Field studies were performed with 34 wild animals in 2017 and 2018 from two low and one high altitude localities in the Central Taurus Mountains, at respective altitudes of 1010 m, 1115 m and 2900 m above sea level. We first compared innate standing immune defense as measured by bacteria killing ability of blood serum. We then measured corticosterone stress hormone levels because stressful conditions may affect immune response. Finally, we compared prevalence and intensity of gastrointestinal parasites of field-captured TBMR. We found that bacteria killing ability of serum is greater in the mole-rat samples from high altitude. There was no significant difference in stress (corticosterone) levels between altitude categories. Parasite prevalence was significantly higher in 2017 samples but there was no significant difference in abundance or intensity between altitudes nor sexes. Small sample sizes may have reduced our power to detect true differences, nevertheless, this study provides preliminary support that greater standing innate immunity in high altitude animals may reflect greater investment into constitutive defense.

Primary Abundance Estimation of the Black Sea Cetaceans in the Adjacent Waters of Zonguldak, Turkey

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Abstract

Vessel surveys is a widely used method to estimate the abundance and density of cetacean populations. In April of 2019 we completed a line transect survey of the local populations of three species of the Black Sea cetaceans in the coastal waters between Ereğli and Türkali (SW Black Sea coast, Zonguldak, Turkey). To quantify the cetaceans density distribution and their abundance up to 6 nautical miles from the coastline, standard principles of vessel line transect surveys design were used; the study was conducted over the area of ~ 630 square kilometers with 11% coverage, and the total transect length of 78,2 km. All Black Sea cetacean species - the bottlenose dolphin (Tursiops truncatus), the short-beaked common dolphin (Delphinus delphis) and the harbour porpoise (Phocoena phocoena), were present. The common dolphin was the most abundant species (estimated N = 4076 individuals, CV = 47%) and had the highest density among the three (6,5 ind/km2). The bottlenose dolphins and the harbour porpoises were less abundant (estimated N=946, CV = 63%; and N=933l, CV = 38%, respectively), with densities 1,5 ind/km2. The harbour porpoises were mostly detected close to the coastline, while the common dolphins were observed at least 4-6 nautical miles from the coast. This study is the first line transect survey in the south-western part of the Black Sea and we report higher density from this area compared to similar studies in Ukraine in 2016-17.

Keywords: Black Sea, line transect survey, cetaceans

Intersexual resource competition and the evolution of sex-biased dispersal

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Abstract

Resource competition is a major driver of dispersal: an emigrating individual leaves more resources to its kin. Existing models of sex-biased dispersal rarely consider intersexual competition for resources. Instead, male reproductive success is often solely assumed to depend on female availability, implying a tacit assumption that male presence never depletes resources, such as food, that are of interest to female kin. In reality, both male and female offspring typically consume resources on their natal site before departing to consume resources elsewhere, and sexually dimorphic body sizes imply that the resource needs can differ. The goal of our study is to investigate how intersexual competition for resources can affect the evolution of sex-specific dispersal, via competition between kin of the same sex or different sexes and the subsequent success elsewhere. Our individual-based simulation model allows not only the dispersal probability but also its timing to evolve. We also highlight the role of sex-specific income/capital breeding strategies, which is understudied in both empirical and theoretical literature of sex-specific dispersal. We show that sex biases in dispersal probability and timing are sensitive to the presence of intersexual competition, sexual differences in capital vs. income breeding strategies, and sexual dimorphism in the quantity of resources consumed. Males may evolve to disperse earlier if they also consume more food, as a result of selection to reduce intersexual kin competition. Alternatively, males may evolve to disperse less as well as later than females, if male fitness depends more on resource accumulation whereas female fitness depends more on reliable income, even if both sexes are equally competitive in consuming resources. Although the more dispersive sex is often the earlier departing sex, we also find cases where the only clear dimorphism is found in dispersal timing. We thus encourage more studies on the timing aspect of sex-biased dispersal.

Keywords: capital/income breeding, dispersal, resource competition, kin selection, sexual dimorphism

Parental Effects in Predictable and Unpredictable Temperatures in Drosophila melanogaster

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Abstract

Organisms tent to adapt environmental changes to ensure their fitness. Besides individual experience, one potential source of adaptation to changing environments is non-genetic inheritance based on parental experience of temperature, called adaptive paternal effects. Although theoretical work has shown that such parental effects can play an important role in evolutionary dynamics by influencing offspring fitness, their adaptive value is still lacking empirical support. To understand adaptive significance of parental effects, we conducted an experimental evolution study by manipulating temperature correlations between parental and offspring generations in Drosophila melanogaster. To quantify the effects of both parental and offspring temperature on offspring fitness, we used a fully factorial split-brood design where parents lived under either cold or hot temperatures and their offspring were split over both treatments. We then observed fitness-related traits such as survival, developmental time and fecundity in offspring groups which have either matched and unmatched temperatures with their parental generations. For the starting population, we observed that both parental and offspring temperature affect fecundity and developmental time of offspring but not survival. Furthermore, we observed that there is an advantage of being in a matched temperature as parental generation for only developmental time of offspring which experienced hot temperature. We also observed the disadvantage of matched temperature on fecundity of the same offspring group. Therefore, we conclude that both parental and offspring temperature shape offspring traits in a complex way. Notably, however, there is a significant change in offspring survival when comparing the group ,which evolved in hot temperature, against the starting population. We argue that the difference in survival can effect influence of parental temperature on other traits. We think that our results may helpful to understand the contribution of parental effects on offspring life time strategy in changing temperatures.

Keywords: Adaptive parental effects, Drosophila melanogaster, Experimental evolution, predictability of temperature, temperature adaptation

The plastic intruder: playback experiments with 3D models in Great Tits (*Parus major*)

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Abstract

Songbirds are an excellent model system to study evolution of communication, partly because they are well suited for experimental research in the field. The conventional method is to use a sound stimulus (e.g. the song of the birds recorded previously) and measure the responses of the subject. This methodology, though in wide use for at least 60 years, is somewhat unnatural in the sense that the responding bird is looking for a "paradoxial intruder": present and loud but invisible. An improvement would be to use a taxidermic mount along with song playback but this requires access to at least one dead bird and a skilled taxidermist. With recent advances in 3D printing, an alternative is to create a 3D digital model and print a model of the bird which can then be painted. In the present experiment we tested the effectiveness of a 3D printed model of a great tit (*Parus major*), perhaps the most widely studied songbird on earth. We tested male great tits once with a 3D model and song playback and once with only song playback. Our response measures were song rate, flight rate and the time spent within 1 meter, and whether or not the bird attacked the 3D model. Three out of 19 subjects attacked the model suggesting that it was a realistic stimulus. There were no significant differences between the 3D model and no model conditions in any of the response variables. Additionally, we found that song rate during the trial correlated negatively with the strength of aggressive response and that birds living in urban habitats were more aggressive than birds living in forest habitats. We discuss these results in the context of both implications for playback methodology and the effect of urbanization on social traits.

Lakeshore Modification and Aquatic Ecosystem Response

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Abstract

Lakeshores are important habitats contributing to ecological functioning of both terrestrial and aquatic environments and socio-economic values of people. These habitats that are vulnerable and fragile to anthropogenic stressors are under pressure because of intense human activities. However, there is no sound and consistent understanding about how to evaluate the ecological status, classification, protection and management of lakeshores in a sustainable way. Here, we aim to develop a framework for assessing the degree of lakeshore zone modifications based on reference conditions, which could provide supportive information to gain an understanding of type-specific (i.e. lake typology) pressure-response relationships and effective management ways across global scale. To do so, we analyse data of 991 lakes under Globolakes project. Furthermore, we compiled catchment and lake basin data for 364 lakes from the USA, Russia, Turkey and Europe. Our preliminary results confirm that shoreline and shore zone delineation depend on basin shape and water level fluctuations. Therefore, we use surrounding topography derived from high-resolution digital elevation model (i.e. 1-arcsecond (30-m) SRTM) to augment the Globolakes dataset. Next stage is to combine seasonal and longer-term dynamics in catchments and shore zones using land cover data from the European Space Agency. This study will enable to identify system change drivers and will link catchment and lakeshore zone modifications to ecological response evident in ecological indicators obtained from satellites (e.g. temperature, productivity (chlorophyll), transparency, blue-green algae) using artificial intelligence (AI) supported Boosted Regression Trees (BRT).

Keywords: Lakeshore modifications, Reference conditions, Typology, Ecosystem Response

Phylogeography of Turkish Honeybees (*Apis mellifera L.*) Based on mtDNA Sequences

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Abstract

There are 26 recognized subspecies of honeybees throughout the world and 5 of them are distributed in Turkey. Due to the migratory beekeepers and queen trade practices in addition to other anthropogenic factors, population structure of these 5 subspecies are under threat and require further research followed by immediate establishment of conservation strategies. In this study, we aimed to determine the phylogeography and biodiversity of Turkish Honeybees.

In order to assess genetic variability and population structure of Turkish Honeybees, we have identified 500 localities considering geographic and climatic factors, and sampled from over 350 stationary beehives throughout the Anatolia. We have isolated DNA from one individual worker bee from each locality. In order to obtain genetic structure, we depended on 3 mitochondrial DNA markers: (i) Cytochrome oxidase B (CytB), (ii) NADH dehydrogenase subunit 2 (ND2), (iii) partial sequences and the intergenic spacer between the Cytochrome oxidase I and II (COXI-COXII). We have completed PCR for every sample and each locus. The next step of the project will consist of sequencing, bioinformatic analysis of these sequences and further assessment of the population structure observed with regard to geographic and climatic restraints in Anatolia.

Keywords: honeybees, phylogeography, Anatolia, mtDNA

Species Level Identification of Marine Fishes and Crustaceans using Ancient DNA Gathered from Underwater Excavations

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Abstract

Throughout the ages Mediterranean and Aegean Sea have been important for coastal settlement strip. Especially, "Liman Tepe and Çeşme -Bağlararası" are one of the most significant areas to examine the cultural and commercial progress dating back to middle of the 5th Millennium BC through the Classical Age.

DNA extraction from ancient samples provide degraded and low-quality DNA. Besides, one of the most important challenge is presence of modern contamination. Especially, modern human DNA matching occurs frequently in ancient DNA samples while doing species level identification. In our study we tried to eliminate this problem by using different concentration of bleach. Ancient fish bones were kept at different time periods and bleach concentrations in sterile water to find the best method to prevent surface contamination. Protocols from different DNA extraction kits were tested and modified with prior incubations to eliminate modern contamination. 25 different primer pairs specific to 5 different gene of fishes were used for this study. According to our results we succeed to eliminate human and microorganism contamination from surface with an optimized incubation of ancient bones for 30 minutes at %3 bleach concentration. BLAST results are showing that the 12S rRNA results with universal fish primers are able to make genus/species level identifications. Identifications were belonging to both freshwater and marine fish species. Since the samples were obtained from underwater excavations and it was known that there was no freshwater fish hunting in these coastal settlements, we evaluated the possible contamination and misidentification results belonging to freshwater fish species from our dataset.

Our results showed that by optimizing our extraction protocol for avoiding contamination, increasing the yield and quality of DNA, together with using primers more specific to target taxa and targeting short fragments species level identification from ancient DNA for marine fish and crustaceans is possible.

Keywords: Ancient DNA, Marine Fish, Crustaceans, Molecular Identification, Archaeology

Prevalence and Diversity of Influenza A Viruses in Sediment Samples in Gediz Delta

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Abstract

Influenza A viruses (IAVs) have caused four pandemics in the last century that killed more than 50 million people worldwide. IAVs are naturally carried by wild aquatic birds and cause asymptomatic gastrointestinal disease in their natural host. Wild aquatic birds are infected orally and they shed the virus through their feces into the environmental sources such as water and sediment. Gediz Delta is one of the hotspot where thousand of waterfowls visit each year. The Delta is located at the center of Mediterranean/Black Sea Flyway. Also, delta hosts many mammalian species that are in the host range of IAV. The persistance of such viruses in water and sediment can cause other birds and mammals to get infected. This would eventually increase the transmission events between birds and mammals. In this study, we aimed to investigate the prevelance and diversity of IAVs in sediment samples. For this purpose, we isolated the viral RNA's from 200 sediment samples that were collected from salty and fresh water bodies at Gediz Delta in 2018. We detected 9 positive samples based on the amplification of hemagglutinin (HA) gene by RT-PCR. We are currently working on the isolation of the viruses in embryonated chicken eggs. After propagation, we will continue with the detailed genomic analysis.

Keywords: influenza A virus, abiotic sources, sediment, waterfowl, environmental stability

Benchmarking tools that estimate relatedness from next generation sequencing data

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Abstract

Next generation sequencing data has been widely used to estimate relatednes from both ancient and modern human samples. There are a variety of tools in the literature that accomplish this task. However there has not yet been a study that investigates the effect of inbreeding and choice of background population on the performance of these software. Here we benchhmark READ, lcmlkin, ngsRelate, KING and Plink and determine the minimum number of SNPs required for each of them by sampling from the CEPH 1463 family data. We also simulate an inbred pedigree from the 1000 Genomes dataset and test the effect of inbreeding on these software. Finally, we test the effect of choice of background population by utilizing closely related and distantly related populations as background.

Demographic and Genetic Structure of Sedentary and Migratory Bears (*Ursus arctos*) within Eastern Anatolia from Genome Wide Genetic Markers

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Abstract

Large carnivores are known for altering life history strategies in response to environmental change. One such shift was recently discovered in Eurasian brown bears (*Ursus arctos*) within eastern Turkey where availability of city dumps as food sources have led to the evolution of two distinct life strategists: sedentary bears that use city dumps as primary food source and wild bears that never use dumps and migrate in search of food. Understanding the demographic and genetic processes that have led to the establishment of these life history strategies is vital for predicting which life history strategy will dominate in the future and the overall impact of anthropogenic pressures on wild carnivores forced to live in human dominated landscapes. Adaptive and genomic processes responsible for the two life-history strategies will be determined using genotype data from over 1,400 bear scat samples collected between 2013 – 2015 and 40 blood samples collected from captured bears inserted with radio collars. Radio collared bears have been tracked continuously for 1 year therefore provide absolute information on migratory behavior. These 40 samples with known migratory behavior will be used in a high-resolution genome-wide association study (GWAS) to characterize genomic regions associated with migratory behavior and random forest analysis to come with a high accuracy SNP set that can discriminate between these two strategies. Collected scat samples will be separated into individuals using multi-locus genotyping (MLG) assigned to behavioral classes using the SNP set discovered and familial relationships between discovered individuals will be estimated using blood and scat samples. Results of the project will help us in understanding the polygenic basis of a complex life history trait and how fast new life history strategies can be established in wild carnivore populations in response to anthropogenic factors such as the availability of new food sources. This information will also be vital for implementing new and more effective conservation strategies aiming to protect wild Eurasian bears and other large carnivores that might be under selective disadvantage due to increased urbanization pressure.

Keywords: Genome-wide association study, SNP , Multi-locus genotyping, brown bears, conservation biology

Preliminary results of faunistic studies on the family Meloidae (Coleoptera) in Ankara Province

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Abstract

The family Meloidae (Coleoptera), commonly known as blister beetles, is almost a cosmopolitan family (except New Zealand, Antarctica and most Polynesian islands). It is also important because of their distinctive biology as well as being used in applied sciences. It has approximately 3000 species belonging to 120 genera. Turkey is also important country about Meloidae fauna an it has 177 species. Main purpose of this study is determine Meloidae fauna of Ankara province for conservation its biodiversity. In this study, a total of 2199 sample were collected by field study (33 days) between May and October 2018. The collection and species determinations of samples and field studies will continue in 2019 as well. Most of collected samples were determined. The remaining samples are still being determined. As a preliminary results, 2 subfamilies, 13 genera, 25 species and subspecies are detected. The most samples were collected from the herbaceous vegetation in July. Distributions of species between counties of Ankara were compared and evaluated. Comprasion was made based on similarity analysis. Similarity analyzes between faunas were done with MVSP 3.21 software using Baroni Urbani & Büser index of similarity.
This study is a part master thesis titled as “Systematic Researches on the family Meloidae (Insecta: Coleoptera) of Ankara Province” and supported by Hacettepe University Scientific Research Project Coordination Unit with a project (Project number: FBA–2018–16318).

Keywords: Meloidae, Ankara, Fauna, Preliminary results

Point Mutations Leading to Ligand Switching in PDZ Domains Explained by A Simple Network Analysis

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Abstract

Point mutations occasionally change protein structure and/or function. Accompanying these changes are important alterations in ligand specificity that may have significant consequences such as the occurrence of antibiotic resistance. Here we study the third PDZ domains which have important roles in mammal neural cell signaling; they construct PSD95 complex by binding CRIPT (ligand I) and T-2F (ligand II) ligands. Previously, its specific mutations have been demonstrated to have preferred ligand specificity: Wild-type (WT) protein has higher binding affinity to ligand I and G330T mutation binds to both ligands I/II while the H372A mutation and the G330T-H372A double-mutation (DM) tend to bind only to ligand II. To scrutinize the response of residues against mutational perturbations, we utilized the Apo-WT protein structure and performed an alanine mutation scan. Then, we conducted network analysis on each structure and calculated the network measures with a focus on average path length (L) and betweenness centrality (BC), as the former characterizes the overall accessibility of each node and the latter demonstrates the central nodes which control the information flow in a residue network. Furthermore, 400 ns-long molecular dynamics simulations of all PDZ structures were investigated. We monitored changes in shortest paths (L) and neighbor counts (k) throughout the trajectories and investigated the differences between ligand I and II bound protein structures to shed light on ligand switching behavior through the lens of thermodynamics. The analyses of H372A and DM cases revealed that the E401 and adjacent residues, mainly at the N-terminus, decrease their accessibility significantly by binding ligand II. We roughly associate k and L measures with enthalpic and entropic variables that contribute to binding. We explain how the changes of the residue centralities by perturbations introduced in the form of mutations lead to the ligand switching behavior in the PDZ domain.

Keywords: PDZ domains, allostery, alanine mutation scan, network analysis, molecular dynamics simulations.

Monitoring Predators in METU Campus : The Case of Wolf Spiders (Araneae: Lycosidae) and Eurasian Scops Owl Otus scops (Linnaeus, 1758)

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Abstract

Wolf spiders (Araneae: Lycosidae) are medium to large sized arachnids, often existing in high population densities in terrestrial communities. Their populations are characterized with stenochrony in seasonal environments, defined as shifts in stage structure and abundances between seasons. Even though such population dynamics can be associated with phenology, depletion effects through predation by higher trophic levels might represent another reason to account for, which remains untested. Eurasian Scops Owl (Otus scops) is a predator of medium to large sized terrestrial arthropods, including wolf spiders, and may significantly influence their abundances.

With the aim of documenting the potential impact of Eurasian Scops Owl on wolf spiders, we measured spider activity density (as a proxy for abundance) inside occupied Scops Owl territories in METU campus (Ankara) during summer 2018. Owl territories were identified with reference to occupied nest-boxes placed on pine trees in the forest, as part of another ornithological study. Control counts were made in parts of the same forest known to have no nesting owls. Spiders were sampled by point counts systematically located at 10 meter intervals along a line transect, forming a distance gradient starting at 10 meters and continuing up to 100 meters from the nest box.

Wolf spiders occurred as a guild dominated by three species (Hogna radiata, Lycosa praegrandis and Alopecosa albofasciata). Results indicate a significant decline on wolf spider abundance inside the owls’ territories, whereas the effect disappears as the distances from nest boxes reached supposed territory limits (80 to 100 meters away). The magnitude of these effects varied among studied territories, indicating a degree of individuality between owls in choice of hunting grounds. Our findings may constitute a rare example of a cascading effect that involves an avian predator and its arachnid prey.

Keywords: Arachnology, Avian Predation, Population Dynamics, Community Ecology

Assessment of Daphnia Diversity on the Alpine Lakes of Turkey by Using DNA Barcoding

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Abstract

Alpine lakes are quite resistant to anthropogenic influences and thus provide a suitable environment for the taxonomical, ecological and evolutionary studies of zooplanktonic organisms. Taxonomy and nomenclature of Daphnia species are problematic because of the lack of detailed diagnosis, phenotypic plasticity, hybridization capabilities, etc. We investigated the mitochondrial COI gene region to determine distribution and diversity of Daphnia species found across permanent alpine lakes on Aladağlar (Taurus Mountain Regions) and Kaçkar Mountain Regions. Seven lakes were studied and a total of four populations were found, one from Kaçkar and three from Aladağlar. Daphnia gr. pulex was identified according to morphological characters. 15 haplotypes from Turkey and 25 individuals from GenBank and Barcode of Life Database were analyzed together. As a result of our study showed us, both Kaçkar and Aladağlar's populations consist of Daphnia cf. pulicaria and Daphnia tenebrosa. Population fixation rate (Fst) was calculated among the Aladağlar and Kaçkar populations and found to be 0.799.

Keywords: Water flea, alpine lakes, Turkey, DNA barcoding, COI

Determining Potential Niche Competition Regions Between Kazdagi Fir (*Abies nordmanniana* subsp. *equi-trojani*) & Anatolian Black Pine (*Pinus nigra* subsp. *pallasiana*) and Conservation Priority Areas Under Climate Change by Using MAXENT Algorithm

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Abstract

Kazdagi fir *(Abies nordmanniana subsp. equi-trojani)* is an endemic, coniferus tree subspecies in Turkey. The species has a narrow distribution and its conservation status defined as EN (Endangered) by IUCN (International Union for Conservation of Nature), due to its decreasing population size. Several wildfires in the past and current anthropogenic activities (gold mining, infrastructure, inapropriate forestation works, etc.) caused severe fragmentation of populations of the species. Besides the human activities unfavoring the species viability, it also suffers from a severe competition with another species which has overlapping distribution with Kazdagi fir; Anatolian black pine *(Pinus nigra subsp. pallasiana).*

The study presented here, aimed to detect conservation priority areas for Kazdagi fir. In order to achieve this, species distribution modeling approach by using MAXENT algorithm was used to model both Kazdagi fir and Anatolian black pine's potential distributions in 2050 by considering the possible effects of global climate change in near future. Then, a series of overlay analyses were made to be able to detect the areas which are better habitats (have greater habitat suitability coefficient based on the model results) for Kazdagi fir than Anatolian black pine.

The results of the study revealed several regions. Yet, considering the current distribution of the species and its dispersal limits, this study proposes two conservation priority areas for Kazdagi fir; Uludag and Kazdagi (Mt. Ida) and this results indicates the urgency of change in forestation methods in both areas towards favoring Kazdagi fir instead of Anatolian black pine.

Keywords: Abies nordmannianna subsp. equi-trojani, Climate Change, Maxent, Conservation, Species Distribution Models

Microplastic Removal Efficiency of Wastewater Treatment Pants: A case study from Yozgat, Turkey

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Abstract

Plastic production has gradually increased since 1950s with a total annual production of 348 million tons in 2017. Because of the low production cost and durability, plastics are found in many substances that we use intensively in everyday life, such as food packs, clothing and cosmetic products (toothpaste, face wash gels). The rapid increase of plastic production resulted in gradual plastic accumulation in different ecosystems, which in turn led to plastic- based environmental problems. Microplastic pollution in aquatic ecosystems has started to attract attention only in last decades and today recognized as an emerging threat. Microplastic pollution was observed even in sub alpine lake and Antarctica where the human effect is the least. Although different definitions have been made for microplastic, plastics with a size less than 5 mm are generally defined as microplastics. Microplastics can be carried to very long distances with different factors such as wind, water flow, air and biological carriers, which make it difficult to determine the microplastic pollution level. Water treatment plants are important in terms of microplastic pollution because they are facilities, where domestic and industrial wastewater containing microplastic particles are collected and treated. However, the wastewater treatment plants used today are not designed considering microplastic pollution. In this study we aimed to investigate microplastic removal rate of Wastewater Treatment Plant (WWTP) in Yozgat. Water samples from inlet (10 L) and outlet (200 L) were filtered through stacked stainless steel sieves (500µ, 328µ and 61µ mesh size). After wet-peroxide oxidation and settlement processes, plastic particles were counted (colour, shape, size) under stereo microscope (40X). According to our preliminary results WWTP removed % 94.7 of the microplastic particles came from influent.

Key words: Microplastic, emerging contaminants, wastewater treatment plant

Improvement of the information theoretic approach for the DNA size and the protein length relation

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Abstract

We previously utilized the information communication theory to relate the encoding DNA and encoded protein lengths as the number of residues of the respective macromolecules, through modifying the equation in the theory. The approach was suggested to be inherently related to the presence of introns in the eukaryotic DNA. The method is actually resulting in the establishment of an allometric relation in the information contents of the encoding DNA and encoded protein molecules. The boosted length of the encoding DNA in eukaryotes is related to that of the proteins by including an exponential rather than a constant as the multiplier of the protein information content. Here we try to improve the model as follows. Modeling such a relation can be done by assuming a basis of relation and testing that basis as the hypothesis, through comparing the model with the experimental values or the literature data. Alternatively, the latter can be used to derive the constants and/or exponents in the suggested model. In this study, both approaches are utilized in an attempt to reinforce one another. It is observed at the first glance that medium or median length values did not appear to be the most appropriate values to be utilized in this approach.

Keywords: Information communication theory, polymeric macromolecule length, allometric relation

Evolutionary Conservation of Gene Expression Changes in Mammalian Brain Ageing

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Abstract

Ageing is a stochastic process that involves physiological changes at different levels, including the accumulation of genetic and epigenetic damage, altered proteostasis, abnormal signalling, cellular dysfunction, and stem cell depletion. Because these processes appear universal across mammals, one may hypothesise that ageing-related gene expression patterns should be conserved across mammalian species. Alternatively, such patterns could be highly divergent among species. This could occur if ageing is contributed by deleterious variants that fix through genetic drift, or if ageing-related gene expression patterns reflect species-specific adaptations (such as efficient responses that curb damage accumulation). Under the latter scenario, we may expect ageing-related expression patterns to be less conserved than those in development, but to be correlated with longevity. Studying conserved versus divergent development- and ageing-related changes in mRNA levels across species with different lifespans could thereby help reveal the mechanisms behind the evolution of ageing. Here we investigate the extent of conservation in ageing-related gene expression change in the human, macaque and mouse brain, in comparison with postnatal development-related changes. We use a time-series RNA-seq data set of the mouse cerebral cortex we had earlier generated, which spans both development and ageing periods. We further use a publicly available transcriptome time-series of human and macaque prefrontal cortex tissues. We thereby compare development- and ageing-related shared expression changes among species to test the hypotheses that development is evolutionarily more conserved than ageing, and also that divergent expression patterns are correlated with longevity.

Keywords: gene expression, brain, ageing, development, evolution, conservation

Host Genetics of Unexpectedly Rich Mycobiome Diversity of *Drosophila melanogaster*

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Abstract

The collection of all prokaryotic and eukaryotic microorganisms that are in a symbiotic relationship with the host constitutes the microbiota of an organism. The microbiota can have profound effects on the health, survival, and reproductive fitness of their host. Most of the microbiota research has focused on the prokaryotic (bacterial) organisms, neglecting the important fungal (eukaryotic) microbiota called as the mycobiome. The mycobiome of the model organism *Drosophila melanogaster* and the genetic factors affecting the mycobiome diversity is largely unknown. In this study, we firstly aimed to uncover the mycobiome of D. melanogaster by next generation sequencing of the ITS region of the eukaryotic microorganisms isolated from the guts of Drosophila Genetic Reference Panel (DGRP) flies. Secondly, we aimed to discover the host genetic factors that affect the abundance of the most common fungal microorganisms identified based on ITS sequencing via whole genome wide association approach. We discovered an unexpectedly rich mycobiome diversity consisting of a total of 126 taxa from Ascomycota, Basidiomycota, Zygomycota, and Chytridiomycota phyla based on ITS2 region sequencing and annotation. Shannon, Simpson, and Chao index ranges were 0.22-1.91, 0.04-0.64, 98.7-120.0, respectively, indicating a large between individual variation. Host genetic association results will be presented. We conclude that *D. melanogaster* can be a model system for studying mycobiome diversity, and host – mycobiome interactions.

Preliminary results of faunistic studies on the family Coccinellidae (Coleoptera) in Ankara Province

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Abstract

The family Coccinellidae is called as “ladybirds” or “ladybugs” and a member of the superfamily Cucujoidea, which belongs to the series Cucujiformia within the suborder Polyphaga of the beetles (Coleoptera). Their relatives within the Cucujoidea are the Endomychidae and Corylophidae. There are almost 6,000 species of ladybirds in worlwide. Main purpose of this study is determine Coccinellidae fauna of Ankara Province. In 2018, this research has been started on the family Coccinellidae. In the scope of research, there are two field study seasons (May to October 2018 and April to October 2019). In the scope of research, field studies were carried out in 270 localities between May and October 2018 (33 days). 4050 specimens were collected. Most of collected samples (3348 specimens) were examined. As a preliminary results, 10 species belonging to 10 genera and 3 subfamily were determined. The remaining samples are still being examined. The most number of specimens were collected from *Coccinella septempunctata* Linnaeus, 1758 (1845 specimens) species and *Hipodamia variegata* Goeze, 1777 (800 specimens) species. In 2019, field studies will be carried out in 36 days and more specimens will be collected from counties of Ankara in different time period from field study periods of 2018. Species identifications of specimens is continuing. The distribution of the species according to the altitude, months and counties are analyzed with MVSP 3.21 software using Baroni-Urbani & Büser index of similarity. This study is part of the M.Sc. thesis titled as “Systematic Researches on the Family Coccinellidae (Insecta: Coleoptera) of Ankara Province” and supported by Hacettepe University Scientific Research Project Coordination Unit with a project (project number: FBA- 2018-16318).

Keywords: Coccinellidae, Ankara, Fauna, Preliminary results

First record of non-indigenous *Botrylloides anceps* (Herdman, 1891) species along the Turkish Levantine Coasts, Confirmed by DNA Barcoding

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Abstract

There are nearly 3000 Ascidian species identified and they are all found in seas. However, the studies on tunicates on Turkish coasts are limited; thus, not much known about the ascidian fauna of Turkish Seas. In this study, presence of the *Botrylloides anceps* (Herdman, 1891) species along the Mediterranean coast of Turkey has been proven by application of DNA barcoding tool for the first time. Sampling was performed in coastal area of the Hatay-Konacık region on 26 September 2018. Mitochondrial Cytochrome Oxidase I (COI) and nuclear H3 genes were used for identification.

Although *B. anceps* were observed in Israel, Australia, India, Brazil and Japan, only Israel and Australia provided gene sequences to the database. In the present study, one *B. anceps* (Israel) species haplotype data was obtained from the Genebank to compare with the present study sample. Phylogeographic resolution of these 2 haplotypes was investigated by using NETWORK software. Five mutation steps differences were observed between present study and previously studied (in Israel) *B.anceps* sample for COI gene and four for H3 gene.

This study is a very first record in terms of using DNA barcoding tool on the *B. anceps* identification for the sample that was collected in Turkish Seas. It is being planned to do whole genome sequencing of the species as a next project.

Key words: *Botrylloides anceps*, Eastern Mediterranean, DNA Barcoding, COI, H3

An Alternative Reference Library for European Freshwater Fish Species

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Abstract

Environmental DNA (eDNA) as a novel genetic tool for assessing and monitoring freshwater fish diversity from water samples. DNA barcode data for the European freshwater fish fauna was already compiled in order to have an overview about the current availability regarding public reference libraries for this taxa. It is highlighted that, while the reference library for European freshwater fishes is almost complete concerning standard DNA barcodes (COI), there is only very limited 12S sequence published data that could be used to taxonomically annotate eDNA derived OTUs. Accordingly, a joint activity within the DNAqua-Net framework was initiated with the objective to create new 12S sequence data and therefore to build the most complete reference library covering the MiFish region for as many European freshwater fish species as possible. The new European freshwater fish 12S database was created based basically on the voucher, tissue and DNA collection mainly built during the Leibniz SAW project FREDIE stored at ZFMK Zoological Research Museum Alexander Koenig in Germany, but also complemented with sequences from the NCBI public resources and the FRESHING project private barcodes already obtained from freshwater fish species occurring in the Douro River Basin, Iberian Peninsula.

From the estimated ~630 European freshwater fish species, our database covers ~400 of these species (240 from BOLD, 160 from Genbank and 20 from FRESHING), which represents a coverage of around the 64%. 1579 12S sequences are compiled in it (30% from BOLD, 68% from GenBank and 2% from FRESHING). In order to improve and increment this coverage, more data will be included after future work. The results shows efficancy of MiFish primers in terms of detection success and must be considered as a potential marker in (e)DNA (meta)barcoding studies that could be implemented into molecular ecology studies targeting bio-monitoring of aquatic ecosystems.

Keywords: European Freshwater Fish, Reference Library, 12S rRNA, DNA Barcoding

Genetic Variability Of Gene COI Of Proterorhinus Marmoratus (Pallas, 1814) In Belarus And Neighboring Countries

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Abstract

Ponto-Caspian species of Gobiidae, including tubenose goby, spread from their natural range to Central Europe via main European invasion corridors. Belarusian watercourses are a substantial part of the Central European invasion corridor. Detailed study of alien species is required, especially at the molecular-genetic level. It is important to learn genetic variability and know the pathways of gobies spread. These data will allow us to study the microevolutionary processes that occur when species established in the new areas. In Belarus, such studies haven't been conducted, therefore the purpose of this study was to conduct a study of genetic variability of gene COI of tubenose goby. The mitochondrial COI gene of 18 specimens of tubenose goby from different locations of Belarusian and Ukrainian rivers was sequenced. The 658-bp barcode region of COI gene was analyzed. Original sequences and sequences obtained from BOLD (55 sequences in total) were used for analysis. Ten haplotypes of tubenose goby were found. Belarusian specimens belong to the three haplotypes. Some Belarusian specimens belong to haplotype 1 as well as Ukrainian specimens, some belong to haplotype 2 with individuals from Germany, Austria and the Czech Republic, and the third part of Belarusian specimens belong to haplotype 3 as individuals from the Ukraine, the USA and Canada. The total number of variable sites was 12. The levels of the average number of nucleotide substitutions (k = 2,7) and nucleotide diversity (π = 0,004) are not high, but the level of haplotypes diversity is quite high and equal to 0,8. The obtained data on haplotypes confirm the data on the pathways of gobies spread available in the literature. The nucleotide variability data of the COI show a large number of closely related haplotypes, which are associated with high haplotypes diversity, and a small historical depth, due to low nucleotide diversity.

Keywords: Gobiidae, alien species, tubenose goby, Proterorhinus marmoratus

Population Genetic Analysis Of *Monilinia* Pathogens Based On First Data Results From Simple Sequence Repeat Loci

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Abstract

A major problem on stone fruits, mainly on peach in Turkey, has been known as brown rot disease caused by *Monilinia* species. Population genetic analysis based on analysis of simple sequence repeats loci provides information about genetic diversities, recent genetic changes in populations and population differentiations. In this study, six 'Sequence Tagged Microsatellite Sites (STMS)' markers were applied to thirty-seven pathogen isolates from peach in Çanakkale, İzmir and Bursa, up to the present. According to the data obtained so far, haploid diversities, private alleles in each population, analysis of molecular variance among the populations were determined. One of the markers was found as monomorphic. Polymorphism differed among the other five markers. Total eighteen numbers of alleles were detected. Total haploid diversity was found as 0.242 and the lowest diversity was observed in samples from Izmir. Eight different multilocus genotypes were found and clone sizes differed. Each sampling group from different cities has at least one private allele. Analyses of molecular variance (AMOVA) showed that majority of diversity occurred within populations. Moreover, the same markers were applied to fifteen isolates of *Monilinia* pathogens from U.S.A. and AMOVA resulted significant variance between samples from Turkey and US.A. based on both a stepwise mutation model and an infinite alleles model. Current results will be discussed in view of presenting and comparing genetic structures of the populations and importance of this data view of disease management.

Acknowledgment: This study was supported by Canakkale Onsekiz Mart University Scientific Research Projects Coordination Unit (Project Number: FYL-2018-2587).

Keywords: *Monilinia*, simple sequence repeats, population genetic analysis

Infaunal Macroinvertebrates in Istanbul Strait in Relation to Season and Varying Levels of Sediment Contamination

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Abstract

One of today's largest scientific challenges is to understand how natural and anthropogenic disturbances affect the structure and functioning of marine ecosystems. Important anthropogenic stressors to marine environments include organic enrichment and inputs of contaminants such as heavy metals and polycyclic aromatic hydrocarbons (PAHs), which accumulate in marine sediments. Benthic macroinvertebrates living in, and feeding on these sediments are commonly used to provide a biologically meaningful measure of ecosystem health. This work forms the basis for a larger *in situ* experimental study to determine species responses to contaminated marine sediments with the primary aim to inform benthic indices. Here we present preliminary results characterizing the seasonal changes in community structure (species composition, diversity, and abundance), and sediment properties at two contrasting harbor locations in Istanbul Strait affected by different levels/types of anthropogenic contaminants. Macrofaunal and sediment samples were collected from Garipçe and Poyrazköy in spring (May), summer (July) and fall (September) of 2019 by divers using hand-held corers (6.4-cm diameter, 10-cm deep). The average concentrations of heavy metals and PAHs varied considerably between the two locations, whereas, sedimentary organic carbon, nitrogen and grain size were similar. Concentrations of most sediment contaminants were relatively higher at Poyrazköy. Polychaetes made-up the largest proportion of the infauna at both locations. The community at Poyrazköy was dominated by Capitellidae spp. Cumaceans, the Spionid polychaete *Spio decoratus*, as well as an unidentified Paraonid polychaete (individuals were often associated with sexually dimorphic ectoparasitic copepods), were also numerically abundant at Poyrazköy. Three syllid polychaetes including *Micronephthys longicornis* and two unidentified morphospecies were numerically dominant at Garipçe. More detailed results regarding spatial and seasonal community patterns in relation to sediment contaminants will be presented using both univariate and multivariate analyses.

Keywords: Turkey, macrofauna, polychaetes, heavy metals, PAHs

DETERMINATION OF INTRONS WITHIN Mt-GENOMES OF DIFFERENT PHYTOPATHOGENIC FUNGAL SPECIES

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Intragenic, intergenic and mobile introns have important roles in structure, genome size and mitochondrial-genome (mt-genome) dynamics of organisms. In some fungal taxa, intron size differences could be used in species level discrimination. On the other hand, mt-genomes do not include any intron in some organisms. Thus, introns in mitochondrial genome are highly important to cause differences within and between fungal species. In this study, the mt-genomes of four economically significant phytopathogenic fungi *Monilinia fructicola* (MK163638), *Sclerotinia sclerotiorum* (NC_035155.1), *Zymoseptoria tritici* (NC_010222.1) and *Fusarium oxysporum* (NC_017930.1) were annotated and mapped. Locations and sizes of the introns were determined. The autoctalytic Group I and Group II introns were determined. While only Group I class intron was found in *F. oxysporum* and *S. Sclerotiorum*, both Group I and Group II class introns were found in *M. fructicola*. No intron was found in mt-genome of *Z. tritici*. Mostly, introns were detected within *cox*, *cob* and *nad* genes. Intron sizes and locations differed among the species and *M. fructicola* has the highest number of introns. Moreover, copy number of genes differed among the species. Besides, genetic distance based on mitochondrial genomes of these fungal species was depicted by using Neighbour-Joining tree. Importance of introns will be discusssed in view of their structural, functional and evolutionary importance for fungal phytopathogens.

Keywords: fungi, self-splicing introns, mitochondrial genome

nvestigation of Microbial Diversity in Lake Tuz by Metabarcoding Approach

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Abstract

Although conventional microbial methods based on the microscopy and culture techniques are very valuable, sometimes they appear to be inadequate to identify a large diversity of microbial species that are present in environmental samples. In the last twenty years, remarkable molecular techniques have been developed and genomic approaches are used to provide more comprehensive and quantitative description of the spectrum and distribution of microorganisms. In this study, a metabarcoding survey of the prokaryotic and eukaryotic communities present in Lake Tuz has been performed. The samples positive by 16S/18S rDNA targeted sequencing contained average of 29 Archaea, 23 Bacteria and 61 Eukarya species and prokaryotes represent 65.3%. In all samples, most frequent Archaea species was *Haloquadratum walsbyi* which belongs to Euryarchaeota phylum, and Bacteria dominant species were the members of *Salinibacter* genus (Bacteriodetes phylum). According to the 18S rDNA sequencing results, the most abundant eukaryote was detected as *Dunaliella salina.* In addition to determining many uncultured prokaryotes and eukaryotes, this study found that one OTU shares identity lower than 97% (≤ 92%) with the 16S rDNA databases. In sum, our knowledge about the microbial community structure and composition in Lake Tuz will be enhanced by this work.

Keywords: Biodiversity, Lake Tuz, Halophile, 16S rDNA, 18S rDNA, Microorganism

Preliminary results of faunistic studies on the family Buprestidae (Coleoptera) in Ankara Province

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Abstract

Research on the family Buprestidae has been started in 2018. In the scope of research, field studies composed of two seasons (May to October 2018 and April to October 2019). 682 specimens belonging to 15 genera and 5 subfamilies were collected by field studies (33 days) in 2018. Field and laboratory studies will continue in 2019 (36 days). After first determination period 30 taxa (species of 15 of them were determined) were diagnosed by examinig collected specimens. According to the subfamilies, the taxa distribution was determined as Julodinae (1 taxon), Polycestinae (7 taxa), Chrysochroinae (9 taxa), Buprestinae (9 taxa), Agrilinae (4 taxa). The most number of specimens were collected from *Coraebus elatus* Fabricius, 1787 (66 specimens) species and *Trachypteris picta decostigma* Fabricius, 1787 (56 specimens) subspecies. Baroni-Urbani & Büser similarity index with MVSP 3.21 software was used to compare faunistic similarities and differences between counties of Ankara in terms of Buprestidae fauna. Distributions of determined taxa due to genera, collecting months and counties of Ankara are shown on graphs and tables. Preliminary results of this study could reveal that this Buprestidae fauna of the Ankara province in detail. This study is supported with a project (project number: FBA-2018-16318 number) by Hacettepe Scientific Research Projects Coordination Unit. This study is also a part of the master of science thesis titled as "Systematic researches on the family Buprestidae (Insecta: Coleoptera) of Ankara Province".

Keywords: Buprestidae, Ankara, Fauna, Preliminary results

Building Reference Library for Marine Fish Species of Azores Archipelago and Bio-monitoring via DNA Metabarcoding

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Abstract

Azores archipelago is an essential habitat for species in coastal areas and shallow seamounts, its biodiversity is well recorded, but difficult to monitoring due to the vast area of Exclusive Economic Zone (EEZ) of Portugal. There are few genetics studies about marine species of Azores archipelago, and even less using eDNA.The aim of this study is to compose a DNA barcode and eDNA metabarcode library for marine fishes of Azores, and assessment of spatial and temporal patterns of the commercial fish, and community assembly around Graciosa Island using eDNA.The barcoded species are mainly commercial fish available on the local market, and some reef species of the island. DNA extractions and purifications from reference fish tissues were made with commercial kits using minor modifications. The selected regions were Cytochrome Oxidase subunit I (COI) for DNA barcoding, using Fish F1R1, Fish F2R2 primers, and 12S gene region of mtDNA for eDNA metabarcoding using MiFish-U F/R primers. For the eDNA samples 2 L of water were filtered with a 0.45 µm membrane, making triplicates with a negative control in each station. The target region of 12S was amplified using a single-step high fidelity PCR with primers with different tags and adaptor ligation protocol and sequenced on a High-Throughput Sequencing platform with 500K read/sample resolution.The preliminary results in community profiling by an eDNA-based approach are changes of trophic levels in different stations, between coastal and oceanic samples, in the different seasons winter and summer.This is explained by biotic factors, like species feeding habits, breeding, biomass and migration, as also abiotic factors like the DNA concentrations that are beneath the detection threshold or due to rapidDNA transportation, degradation and dilution in the environment.Using this new tool, it's possible to take a snapshot of the community structure, that can be used to complement the visual surveys, identify rare species, or new invasive species, as well as support decision for the local fisheries management.

Keywords: eDNA Metabarcoding, Marine Fish, Azores Archipelago, DNA Barcoding, High Throughput Sequencing

Structure Of Ancestral And Modern Populations In Bisexual And Parthenogenetic Lizards Of Genus *Darevskia* In East Anatolia And Caucasus

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Abstract

Daresvkia is a lizard genus distributed through Eastern Turkey, Georgia, Armenia and Azerbaijan. Hybridization among four bisexual species included this genus resulted in seven parthenogenetic (reproducing clonally) species. Although these parthenogenetic populations reproduce clonally, they can maintain their genetic diversity. In this study, we want to elucidate how they are able to conserve the diversity and want to explain their evolutionary history in more detail compared to previous studies. We used a Bayesian clustering program STRUCTURE to infer the ancestry of both bisexual and parthenogenetic populations of *Darevskia* and calculated proportions of shared alleles between the parthenogenetic daughter populations and their parental species using the microsatellite data. According to these results, we found clear separation of bisexual species into three ancestral population clusters (K=3) (as a non-admixture model). The first two clusters represent the maternal, and the third cluster represents the paternal ancestry component, respectively, in the parthenogenetic populations. The proportions of parental ancestry ranged from approximately 1/2 to 1/3 in different populations, indicating a complex pattern of hybridizaiton and subsequent evolution in the clonal lineages. In addition, we found that the proportion of shared alleles between daughter species and their maternal species correlated with geographic proximity, but there was no such correlation with the paternal bisexual species.

Keywords: Reticulate speciation, parthenogenesis, *Darevskia*, microsatellite

Bio-monitoring Hypersaline Lake Environments for Different Taxa

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Abstract

Hypersaline environments like lakes almost saturated in terms of salt level are mainly dominated by prokaryotic communities and diatoms. There are studies comparing the microbiota among different hypersaline environments, there are no studies monitoring other inhabitants somehow related to those ecosystems. In this study we aim to understand detectability and relationship of different taxa detected using eDNA metabarcoding through a set of hypersaline lakes located close to each other.
Five salt lakes around Konya area in Turkey (Tersakan, Uyuz, Tuz, Gök and Düden lakes) were sampled during the field study. Around 2-5 water sample replicates per lake were taken and pooled together before filtering using sterivex filters (0.22 and 0.45 µm pore size). DNA from 18 filters was extracted using the optimised protocol and single-round PCR amplifications were performed using tagged primers targeting different gene fragments for fish, invertebrates, birds, microorganisms and mammals. PCR yields were indexed via adapter ligation protocol for a pair ended 500K read per sample high throughput sequencing. All targeted taxa were resulted with a >97 matching to a species from NCBI GenBank. While most of the species were previously reported, some potentially new species were also identified and need further study in order the confirm if the species or a translocated DNA has been detected. Preliminary results are showing that eDNA metabarcoding methodology could be used for bio-monitoring of different taxa inhabiting or related to hypersaline environments.

Keywords: Hypersaline Lake, Environmental DNA, Metabarcoding, Bio-monitoring, High Throughput Sequencing

Growth Responses of Pinus sylvestris L. to Climate from Its Southeastern Distribution, Turkey: Preliminary Results

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Abstract

Dendroclimatology is an important tool for analyzing past climate and the growth response of trees to local environmental variations. Understanding the effects of climate on different tree species is possible with dendroclimatological methodology. Pinus sylvestris L. has a wide distribution, starting from north of Spain, Scotland, almost throughout Russia, Norway, Sweden, Mongolia, north of Turkey and the Caucasus. Turkey is significantly important as southeastern limit in the Northern Hemisphere. P. sylvestris is a commonly used species in dendroclimatological studies due to its ability to live long and to grow under marginal conditions, therefore being a sensitive indicator. Based on lack of the study for its southeastern distribution, we analyzed the growth responses of P. sylvestris to temperature, precipitation and Palmer Drought Severity Index (PDSI) throughout this region. In previous studies, sampled trees were selected from the limiting environmental conditions. On the contrary, we preferred to take samples from the trees which are in optimum environmental conditions instead of extreme sites to reveal how climate affects the Scots pine. Tree-ring cores were taken from six different regions and each region were grouped into 18 site among themselves according to their proximity to the geographical area. All cores are sampled from pure stands at different elevations and geographical landscape conditions. After measuring tree-ring widths, standard dendrochronological methods are used to build site chronologies. Correlation coefficients between tree-ring widths and temperature, precipitation and PDSI were calculated. Here, we present preliminary results for three site chronologies from Aladağlar which is one of the six regions. Our results showed that both higher temperatures from January to April and higher precipitation in May tend to produce larger annual rings in the region. Tree-ring chronologies and PDSI correlations show that drought from May to August has greater effect in low- elevation and mid-elevation sites than high-elevation sites.

Keywords: Dendroclimatology, Scots pine, PDSI, temperature, precipitation.

Species Richness Patterns of Turkey's Breeding Birds

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Abstract

Three of the world's 35 biodiversity hotspots overlap in Anatolia, creating a unique pattern of species richness across 12 ecoregions. Here, we analysed the geographic variation within- and among-regional richness in avian fauna using data collected during Turkey's Breeding Bird Atlas Survey in 2014-2018. We first estimated three commonly used community indices for each of the 1-by-1 km grids. These were the Margalef index for richness, the Shannon–Weaver index for diversity and the Simpson index for dominance. Next, we investigated the geographical, environmental, climatic and anthropogenic factors underlying the observed patterns in bird species richness, diversity, and dominance. Southern Anatolian montane coniferous-deciduous forest and Eastern Anatolian deciduous forest ecoregions had higher Margalef richness indices. Elevation had a positive effect on species richness; within the vegetation groups the broad leaved forest vegetation type also had a higher index value. There were also negative interactions between elevation and natural grasslands. Northern Anatolian coniferous and deciduous forest and Anatolian conifer and deciduous mixed forest ecoregions had higher Shannon-Weaver diversity indices, whereas Eastern Mediterranean conifer and sclerophyllous broadleaf forests and Eastern Anatolian montane steppe ecoregions had higher Simpson dominance indices. Precipitation during the cold period of the year and annual precipitation increase where the temperature seasonality decreases. This climatic variable had a positive interaction with ecoregions for both Shannon-Weaver and Simpson indices. Furthermore, ecoregions had significant interactions with elevation, latitude and longitude for the Simpson index. Our study demonstrates that breeding bird community patterns show substantial geographic variation among ecoregions in Turkey and explains the underlying geographical, environmental and climatic factors.

Keywords: breeding birds, community ecology, Shannon-Weaver index, Margalef index, Simpson index, Turkey.

The effect of temperature on genome-wide mutational profile in *Haloferax volcanii*

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Abstract

One of the most common environmental variables faced by all organisms is temperature. As all cellular processes are temperature dependent, and DNA stability is no exception, it is critical to evaluate the way in which mutation responds to changes in the thermal environment. To address this question, we use the most direct and unbiased method, combining mutation-accumulation experiments and whole-genome sequencing strategy to clarify the ways in which the rate and molecular spectrum of mutations is altered in response to. Temperature change. We have expanded our previous work with H.Volcanii to include the lowest and highes possible growth temperatures (25 – 47 C). As the same strain of H.volcanii has been the subject of our prior work, all new results can be directly comparable to those previously obtained.And we will evaluate the effect of temperature on spontaneous mutation rate and spectrum in halophilic Archaea, also discuss the underlying genetic and/or biochemical mechanisms of mutation in an organism. This study will provide a comprehensive insight into mutations and reveal what factors of molecular and genomic architecture affect the mutational process in diverse organisms.

Keywords: Mutation accumulation, Whole genome sequencing, Halophile, Mutation rate, Mutation spectrum

Molecular Characterization and Isolation of Avian Influenza A Viruses from Wild Aquatic Birds in Gediz Delta

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Abstract

Influenza A Viruses (IAVs) threaten both public and veterinary health as they infect wide range of species. Although their natural hosts are wild aquatic birds, IAVs are able to transmit to mammals. Izmir possess a great significance for ecology of IAV with Gediz Delta which is located in the center of Mediterranean/Black Sea Flyway that intersects with several other flyways. Therefore, the delta is visited by many different avian species as well as it hosts various mammalian species. This biological diversity of delta fauna provides an excellent opportunity for IAV to cross species barrier, undergo mutations that affect host preference, antigenicity, transmissibility, and pathogenicity of the virus. Our research focuses on the detection and molecular characterization of IAVs circulating in wild aquatic birds residing in Gediz Delta, Izmir. To pursue our goal, so far we collected 644 fecal samples from shorebirds and waterfowls. Among those, 232 samples were already tested for the presence of IAV via RT- PCR. We detected 28 positive samples based on hemagglutinin (HA) gene amplification and 57 positive samples based on Matrix (M) gene amplification. Around, 30 of these fecal samples were inoculated into embryonated chicken eggs for virus isolation. So far, we isolated one virus with hemagglutination titer (HA titer) of 64 and determined its subtype (H6N2) via sequencing HA and NA genes. We are now in the process of screening more fecal samples as well as propagating viruses from RT-PCR positive samples.

Keywords: influenza A, low pathogenic, aquatic birds, virus evolution