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Ekoloji ve Evrimsel Biyoloji Derneği

4th Ecology and Evolutionary Biology Symposium, Turkey

July 11th-13th, 2017

**Symposium Programme
&
Abstract Book**

ITU Ayazağa Campus
Istanbul, 2017

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Symposium Programme

July 11th, 2017

- 8:30 – 9:30 **Registration**
- 9:30 – 10:00 **Opening ceremony**
- 10:00 – 11:00 *Keynote Speaker*
Meryem Beklioğlu
- 11:00 – 11:30 **Coffee /tea break**
- 11:30 – 11:50 **Arpat Özgül** - “ Coupled Dynamics of populations and phenotypic traits in changing environments”
- 11:50 – 12:10 **Begüm Uzun** - “Population genetic structure of harbor porpoises (*Phocoena phocoena*) in the turkish waters”
- 12:10 – 12:30 **Kaan Kerman** - “Effects of Social Context on Risk-taking Behavior in Adult Zebra Finches [*Taeniopygia guttata*]”
- 12:30 – 14:00 **Lunch**
- 14:00 – 14:20 **Erol Akcay** - ” Evolution of Cooperation on Dynamic Networks”
- 14:20 – 14:40 **Tutku Aykanat** - “Towards disentangling global genetic modulators of life history variation in Atlantic salmon”
- 14:40 – 15:00 **Yann Czorlich** - “Evidence for evolution of age at maturity in Atlantic salmon In a 40-year time series from the Teno river”
- 15:00 – 15:20 **Melis Akman** - “Climatic gradients shape intraspecific divergence in plasticity for functional traits and gene expression in a South African Protea”
- 15:30 – 16:00 **Coffee /tea break**
- 16:00 – 16:20 **Brock Kinsey** - “Evolution of color and pattern as Influenced by ecological breadth”
- 16:20 – 16:40 **Can Elverici** - “Phylogeography of Rock Nuthatches - an Integrating Approach”
- 16:40 - 17:00 **İsmail K. Sağlam** - “Concatenation methods in phylogenomics can lead to severe overestimates of evolutionary parameters”
- 17:00 – 17:20 **Aslı Şalcıoğlu** - “A phylogeographic investigation of the Picarel (*Spicara Spp.*) around the Turkish coastal waters with comparisons to the Mediterranean Sea and Atlantic”
- 17:30 – 18:30 **Dinner**

July 12th, 2017

9:30 – 10:30 *Keynote Speaker*

Claus Wedekind

10:30 – 11:00 **Coffee /tea break**

11:00 – 11:20 **Andres Aravena** - “Assigning taxonomy without a reference sequence”

11:20 – 11:40 **Ferhat Kaya** - “Mammal Paleobiogeography and Paleoecology of”
Anatolia during the Neogene

11:40 – 12:00 **Billur Bektaş** - “Simulating Late Quaternary Vegetation with a Dynamic
Vegetation Model”

12:00 – 12:20 Ünal Akkemik

12:30 – 13:30 **Lunch**

13:30 – 13:50 **Gül Deniz Salalı** - “Marital ties, cooperative childcare and the sharing of
medicinal plant knowledge in Mbendjele Pygmy hunter-gatherers”

13:50 – 14:10 **Gulsah Merve Kilinc** - “Investigation of the Néolithisation in Anatolia
and the Aegean by using ancient DNA”

14:10 – 14:30 **Nefize Ezgi Altınışik** - “A New Model for Peopling of the American
Arctic”

14:30 – 14:50 **Recep Ozgur Taskent** - “Archaic hominin introgression in Africa”
contributes to functional salivary MUC7 genetic variation

15:00 – 17:00 **Poster Session**

17:00 – 19:00 **General Assembly of EKOEVO**

July 13th, 2017

9:30 – 10:30 *Keynote speaker*

Philipp Khaitovich

10:30 – 11:00 *Coffee /tea break*

11:00 – 11:20 **İsmail Bekar** - “Cold-related germination in plants of Central Anatolian steppes: the role of biogeographical origin”

11:20 – 11:40 **Çağatay Tavşanoğlu** - “Resprouting ability encapsulates the most functional variability in the Mediterranean Basin flora”

11:40 – 12:00 **Korhan Özkan** - “Forest bird community response to a decade of forestry activities in Istranca Forests”

12:00 – 12:20 **Selin Küçükavşar** - “Exploring Marine Microbial Community Structure Using 16S rRNA Amplicon Sequencing: First Results to Understand Their Role in the Oligotrophic Marine Ecosystem”

12:30 – 14:00 *Lunch*

14:00 – 15:00 **Poster Session**

15:00 – 15:20 **Evrin Karacetin** - “Organic vs. Conventional? How do butterfly communities respond to farming type and agricultural practices in olive groves in Ayvacik, Çanakkale, Turkey?”

15:20 – 15:40 **Mert Elverici** - “Let’s Sample It Later Again (or Not?): An Empirical Assessment on Repeatability of Invertebrate Surveys”

15:40 – 16:00 **Anıl Soyumert** - “Monitoring wildlife populations using camera-traps: Large mammals in a wildlife reserve in north-western Anatolia”

16:00 – 16:30 *Coffee /tea break*

16:30 – 16:50 **Mustafa Yücel** - “State of a deep-sea chemosynthetic ecosystem 12 years after a volcanic eruption: In situ chemical sensor and submersible-based observations from April 2017 R/V Atlantis - Alvin expedition”

16:50 – 17:10 **İbrahim Kaan Özgencil** - “Elucidating the Patterns in Mid-Winter Waterfowl Surveys by Using Macrophyte Records and Lake Water Level Fluctuations”

17:10 – 18:00 **Closing ceremony**

ORAL PRESENTATIONS

Coupled dynamics and phenotypic traits in changing environments

Arpat Ozgöl¹

(1) University of Zurich

A major goal in population ecology is to predict how populations will respond to environmental change. Recent studies have highlighted rapid phenotypic changes accompanying and often preceding demographic regime shifts, indicating that a trait-based demographic approach can improve our ability to predict a population's response to environmental change. Furthermore, these studies show that some species can adapt to environmental change more easily than others through a range of evolutionary and ecological mechanisms; understanding these differences is crucial for identifying species that are more susceptible. In this talk, I will present the links between the abiotic environment, population density, individual traits (such as body size) and demography using long-term data from several empirical and experimental systems and address the following question: "How do populations respond demographically and phenotypically to environmental perturbations

Population Genetic Structure of Harbour Porpoises (*Phocoena phocoena*) in the Turkish Waters

Begüm Uzun^{1,2}, Arda M. Tonay¹², Ayhan Dede¹², Ayaka A. Öztürk¹², Bayram Öztürk^{1,2} Raşit Bilgin³

(1) Istanbul University, Faculty of Fisheries, Ordu Cad. No:200 Laleli, Istanbul, Turkey

(2) Turkish Marine Research Foundation (TUDAV), P.O. Box: 10 Beykoz, Istanbul, Turkey

(3) Boğaziçi University, Institute of Environment Sciences, Hisar Campus, Bebek, Istanbul, Turkey

In the Mediterranean basin, the harbour porpoise lives mainly in the Black Sea, and it is less common in the Turkish Straits System and Aegean Sea. The Black Sea population is recognized as the subspecies *Phocoena phocoena relicta* distinct from the Atlantic subspecies both morphologically and genetically, and has been listed as endangered (EN) in the IUCN Red List since 2008. A good understanding of the genetic structure of Black Sea porpoises is crucial for their conservation management, since they are threatened by many factors including bycatch, overfishing, habitat loss, and pollution. The general pattern that emerges from previous studies based on mtDNA control region is that Black and Aegean Sea haplotypes form a cluster together, which is different from the Atlantic and Pacific clusters. The results also suggest that Black Sea could be the source for the Aegean porpoises. Moreover, the findings of a unique haplotype in the Marmara Sea, which genetically differentiates the TSS population from the Black Sea populations, based on haplotype frequencies, point out to a potential isolated population in the TSS. More samples will be sequenced with the same mtDNA marker, as well as with RAD-sequencing in the context of an ongoing project, CetaGen to help guide efforts for its conservation

Effects of Social Context on Risk-taking Behavior in Adult Zebra Finches

[*Taeniopygia guttata*]

Kaan Kerman¹ & Kendra Sewall²

(1) Department of Biological Sciences

(2) Virginia Polytechnic and State University

Persistent individual differences in behavior have been described as 'personality' traits in animals. One personality measure, 'boldness', can be quantified as individuals' latency to access resources when facing a potential danger. Although social interactions influence risk-taking behavior in many species, personality measures including boldness are usually tested in social isolation. The objective of this study was to characterize the impact of social context on repeated measures of boldness in adult zebra finches. We measured latency to approach a novel object in 5 different contexts: (1) social isolation, (2) adjacent to a novel flock, (3) adjacent to a familiar flock, (4) within a novel flock, (5) within a familiar flock. We found that social context significantly impacted estimates of boldness. On average, zebra finches were bolder when housed individually in a cage, regardless of the presence or absence of a stimulus flock nearby. We found slight albeit insignificant trend where bolder individuals tended to belong to housing flocks with higher average boldness scores. Finally, neither sex nor dominance rank of focal individuals influenced boldness phenotype. Our results have shown the importance of considering social factors for understanding the ecological and evolutionary role of boldness, as focusing on traditional solitary tests alone may not represent the dynamic nature risk-taking behavior in socially complex populations.

Evolution of Cooperation on Dynamic Networks

Erol Akçay¹

(1) University of Pennsylvania

The dynamic social structure of animal societies has myriad effects on ecological and evolutionary processes, including social behavior, disease transmission, and resource exploitation. Here, we present a model for the evolution of social traits on dynamically coevolving social networks. In our model, social behaviors such as cooperation determine individuals' fitnesses (i.e. birth or death rates), while social connectivity traits determine their connections in the social network. We find that while certain types of networks promote cooperative behaviors, cooperative behaviors, when established in the population, tend to disfavor such networks. In this way, cooperation is revealed to be self-limiting. We discuss mechanisms that can break this self-limiting feedback

Towards disentangling global genetic modulators of life history variation in Atlantic salmon

Tutku Aykanat¹, Jaakko Erkinaro², Craig R. Primmer¹³

(1) University of Turku, Department of Biology, Turku, Finland

(2) Natural Resources Institute Finland, Utsjoki, Finland

(3) University of Helsinki, Department of Biology, Helsinki, Finland

Life history theory, a major field in evolutionary biology, explains variation in the life cycle of organisms (e.g. life span, age of sexual maturity, fecundity, survival and reproductive behaviour) in relation environmental variation, and fitness. Despite a well-grounded theoretical quantitative genetic framework, models linking life history variation to functional genetic variation are rare, due to the polygenic nature of fitness traits resulting in rapid depletion of statistical power of analysis.

With a genome-wide association study across 57 wild Atlantic salmon populations, we identified a single locus explaining 39% of the total variation in sea age-at- maturity, a fitness trait that is tightly linked with individual size, and highly variable within and among populations.

The *Vgll3* gene, an adiposity regulator, also exhibited sex dependent dominance, promoting earlier and later maturation in males and females, respectively, thus minimizing sexual conflict for expression of the optimal trait values for the sexes. Recent analyses suggest that the region, along with another region on chromosome 9, have large-scale association to other reproductive strategies in salmon. The discovery of large effect loci modulating life history variation opens up the opportunity to causally link cellular and molecular mechanisms to population and ecosystem level functions, within an evolutionary framework.

Evidence for evolution of age at maturity in Atlantic salmon In a 40-year time series from the Teno river

Czorlich Y^{1,2}, Aykanat T¹, Erkinaro J², Niemela E², Orell P², Primmer CR^{1,3}

- (1) Department of Biology, University of Turku
- (2) Natural Resources Institute Finland (Luke)
- (3) Dept. of Biosciences | Biotechnology Institute, Helsinki

The time Atlantic salmon spend at sea before maturation is an important life-history trait as it can influence both individual survival and reproductive success. However, global declines in large, late maturing, individuals have been observed over the last decades,

This trait is heritable and is strongly associated with a single genome region near the *vgll3* gene. We assessed whether rapid temporal variation in the mean age at maturity of two Teno river (far north Finland) salmon populations over the last 40 years may be caused by natural selection, by genotyping around 2000 individuals at 197 SNP loci, including loci near *vgll3*. The observed temporal decline in frequency of the *vgll3* allele associated with late maturation was the highest among all 197 loci. This suggests that the evolution of age at maturity in Teno river populations is likely to be driven by natural selection, with earlier maturing individuals having higher fitness in the main Teno river population recently. Time varying selection and influence of changes in fishing management strategies and environmental conditions (e.g, sea temperature) will be explored using a Wright-Fisher model,

Climatic gradients shape intraspecific divergence in plasticity for functional traits and gene expression in a South African *Protea*

Melis Akman¹, Jane E. Carlson², Andrew M. Latimer³

- (1) UC Berkeley
- (2) National Park Service
- (3) UC Davis

Under rapidly changing climates, species' ability to persist will initially depend on the capacity to physiologically adjust via plasticity. Like many phenotypic characters, plasticity is subject to selection, creating a landscape of plasticity differentiation across environmental conditions. Populations of an evergreen shrub from the Cape Floristic Region of South Africa, *Protea repens*, show ample variation in growth patterns and leaf morphologies, which is associated with the climatic gradients along the species' distribution range indicating local adaptation. In addition to population differentiation in trait means, this variation in climate might also lead to differentiation in plasticity. Accordingly, we experimentally tested if plasticity differentiation among populations are associated with climate and if lower plasticity can be linked to lower performance. Five-months old plants grown in a greenhouse from seeds collected at 8 climatically-distinct sites were subjected to 12 days of drought. We measured stomatal conductance, functional leaf traits, growth, and carbohydrate storage after 6 and 12 days into the treatment, and we also analyzed plasticity in gene expression by sequencing whole transcriptomes. We found that plasticity in plant

growth and in three co-expressed gene networks declined with increasing altitude of the seed source population sites. These gene networks were related to heat shock proteins, photorespiration, stress response and carbohydrate metabolism. We also showed that populations with lower plasticity show higher mortality when drought is followed by increased temperatures. Together, these results suggest that *P. repens* populations in relatively cold sites are characterized by low plasticity for drought, which may leave them particularly threatened by climate change with projected increasing temperatures in the region

Evolution of color and pattern as Influenced by ecological breadth

Brock Kinsey¹

(1) University of California, Merced

The evolution of color and pattern is strongly influenced by the ecological breadth a species inhabits. Here we use phylogenetic comparative methods to investigate the co-evolution of sexual dichromatism and niche breadth in a widespread Australian lizard family, the Agamidae, that vary immensely in degree of dichromatism and ecological niche breadth. The evolution of greater sexual dichromatism is also thought to relate to rates of speciation.

Phylogeography of Rock Nuthatches - an Integrating Approach

Can Elverici¹, Hakan Gür², Banu Şebnem Önder¹, Utku Perktas^{1,3}

(1) Department of Biology (Biogeography Research Lab.), Faculty of Science, Hacettepe University, 06800, Beytepe - Ankara, Turkey

(2) Department of Biology, Faculty of Arts and Sciences, Ahi Evran University, Bağbaşı, 40100 Kırşehir, Turkey

(3) Department of Ornithology, American Museum of Natural History, Central Park West 79th Street, New York, 10024, NY, USA

There are 32 species belonging to Sittidae (Nuthatches) family of passerines distributed across Nearctic, Oriental and Palearctic Regions. Most of the species of this group prefer forests, woodlands, parks and gardens but only two of them prefers rocky areas and cliffs. This study focused on these two species preferring rocky habitats; the Eastern Rock Nuthatch (*Sitta neumayer*) and the Western Rock Nuthatch (*Sitta tephronota*). The difference between these species in terms of ecological and morphological aspects had been well studied because they are representing the classical case of character displacement. However, these two taxa had not been studied in terms of geographic variation of genetic diversity within each species. By integrating phylogeographical and ecological niche modeling approaches, this study evaluated the pattern of genetic diversity and the range shifts of Eastern and Western Rock Nuthatches during the Quaternary climatic fluctuations, especially during the last 130 000 years before present. This study itself is a well example of comparative phylogeography.

Concatenation methods in phylogenomics can lead to severe overestimates of evolutionary parameters

İsmail K. Sağlam¹

(1) Hacettepe University

Next-generation sequencing has greatly impacted phylogenetic and phylogeographic studies. Today studies are based on large number of loci spanning the genome which enable even complex evolutionary histories to be modeled. However most studies are based on concatenation methods which infer phylogenies by combining multiple loci into a single supermatrix with the assumption that the tree obtained is an accurate estimate of the species tree. Given that most gene trees have similar topologies to the species tree, concatenated data sets are often reliable estimates of species relationships (i.e. tree topology). However little attention has been given to estimation of branch lengths in concatenated data sets which will always be erroneous because coalescence of genes predates species divergence. Here we quantify the errors associated with branch lengths obtained from concatenated multi-locus data sets using examples from closely related Turkish mountain crickets and highly endangered desert fish species. We show that concatenation methods can lead to severe overestimation of species divergence times and mutation rates, a problem which increases proportionally with effective population sizes and time since speciation. We also show that concatenation methods are unreliable estimators of systematic relationships when the data set contains multiple closely related populations and species.

We conclude that the vast amount of loci provided by NGS methods do not guarantee reliable results under concatenation and propose that phylogenetic and phylogeographic studies should be based on the multispecies coalescent which can account both for topological and temporal variance when estimating evolutionary history of species.

**State of a deep-sea chemosynthetic ecosystem 12 years after a volcanic eruption:
In situ chemical sensor and submersible-based observations from April 2017 R/V
Atlantis - Alvin expedition**

Mustafa Yücel¹, Batuhan Cagri Yapan¹, Julia Guimond², Peter Chace³, Allysya Findlay⁴, Emily Estes², Don Nuzzio⁵, George W Luther²

- (1) Middle East Technical University, Institute of Marine Sciences, Turkey
- (2) University of Delaware, College of Earth, Ocean and Environment, USA
- (3) Oregon State University, College of Earth, Ocean and Atmospheric Sciences, USA
- (4) Aarhus University, Geomicrobiology Center, Denmark
- (5) Analytical Instrument Systems, Inc. IUSA

Seafloor hydrothermal vents along mid-ocean ridges (MOR) emit high temperature, metal and sulfide-laden fluids to the ocean. Upon mixing with cold, oxic ocean waters, the vents host redox gradients, enabling microbial chemosynthetic lifestyles. The MOR segment at East Pacific Rise (EPR), has been observed by the scientific community since 1990s. Here, a full cycle of macrofaunal succession has been documented between two eruptions that occurred in 1991 and 2005. In April 2017, 12 years from the latest eruption, we have conducted research at the site using submersible Alvin. Tubeworms have been extensively observed around Tica and Biovent sites, however the temperatures and sulfide concentrations around these invertebrates were lower than the earlier phase of the volcanic cycle. Mussels started to invade tubeworm habitats, confirming the cooling pattern. In contrast, away from the classic tubeworm habitats new diffuse flow sources are emerging, excluding tubeworms and mussel assemblages, only inhabited by high-T tolerant species such as sulfur-oxidizing microbial mats and *Alvinella pompejana*. In situ voltammetric chemical sensor measurements indicate that the new diffuse sources are much higher in dissolved metal content, leading to low sulfide/temperature ratios which may explain the differences between the habitats

Assigning taxonomy without a reference sequence

Emrah Kirdok, **Andres Aravena**¹

(1) Istanbul University

Environmental studies must deal with the taxonomic classification of DNA fragments from organisms that have not been isolated or sequenced. In these cases, the fragments cannot be aligned and it is hard to identify the taxonomy in a robust way. The alternative is to use alignment-free methods, which rely on the statistical composition of the DNA sequence. Most of these methods characterize each organism by the relative frequency of all k-mers (i.e. DNA subsequences of fixed length k). Each DNA fragment gets a putative taxonomy according to a score that depends on the frequency of its k-mers and on the underlying model. The challenge is to determine the confidence level for this putative taxonomic assignment. In this work, we study the properties of the scores used for putative taxonomic assignment. We study how much the k-mer characterization is conserved through taxonomy and thus how much can we trust it as an index of phylogenetic distance. We also study the statistical distribution of some of the published k-mer score functions and how can we determine p-values and confidence intervals for them. Finally, we propose a strategy to assign an "average" putative taxonomic identity to DNA fragments that lack a good reference.

Mammal Paleobiogeography and Paleoecology of Anatolia during the Neogene

Ferhat Kaya¹

(1) University of Helsinki

Reconstructing the paleobiogeographic development of Anatolian Neogene mammal faunas has been a complex task mainly due to incompleteness of the fossil records. However, accumulations of chronologically and taxonomically revised data sets and advancements in methodologies during the last decade have provided better tools and broader perspectives for investigating the faunal development of the Old World Neogene mammals both in continental and regional scales. Here, genus-level faunal resemblance index and mean hypsodonty analyses were used to assess the paleobiogeographic and paleoenvironmental development of faunas and faunal provinciality, with a particular interest in understanding the paleobiogeographic history of Anatolian late Miocene mammal faunas. The combined results of these analyses illustrate that Anatolian Neogene mammals were profoundly influenced by Neogene climate trends. In the first stage, the pre-Neogene global tropical humid forest type ecosystem continued until the middle Miocene and patchy protosavanna- type habitats appeared towards end of the middle Miocene. Increasing aridity heralded the appearance of savanna type environments and fauna during the late Miocene. This extensive late Miocene savanna paleobiome eventually fragmented into Eurasian and African branches. The third stage was characterized by the initial development of current biogeographical realms with increased faunal provinciality.

Simulating Late Quaternary Vegetation with a Dynamic Vegetation Model

Billur Bektaş¹, Dilşad Dağtekin¹, İstem Fer², H. Nüzhet Dalfes¹

(1) Istanbul Technical University, Istanbul, Turkey

(2) Boston University, Boston, MA, USA

Anatolia's vegetation history is an amalgam of natural processes and impacts from human occupation related pressures on forest resources. Here we used a dynamic vegetation model (DVM) (LPJ-GUESS incorporated to a modeling framework, PEcAn) and force it with climate information for the mid-Holocene and the LGM coming from NCEP-NCAR dataset and climate simulations with MIROC. We focused on four pollen record sites: Beyşehir, İznik, Karamik and Söğüt. It is observed that DVM outputs for the periods considered (in terms of leaf area index percentages for the plant functional types) include C3 grasses along with boreal and temperate woody PFTs. For the LGM, at all sites, boreal PFTs are dominant. Comparing DVM output with pollen records is challenging because i) local signals recorded in pollen data may not be captured by area-wise model predictions, and ii) pollen counts resolve usually at the genus-level. As a first attempt, we binned taxa information of the pollen profiles into PFTs that are comparable to model outputs. However, we observed discrepancies between model predictions and pollen records. Thus, we will use a biomization method to further reconcile pollen records with model outputs. Impacts of human occupation will also be investigated as a potential source of discrepancy.

Marital ties, cooperative childcare and the sharing of medicinal plant knowledge in Mbendjele Pygmy hunter-gatherers

Gül Deniz Salalı¹, Nikhil Chaudhary¹, James Thompson¹, Olwen Megan Grace², Xander M. van der Burgt², Mark Dyble¹, Abigail E. Page¹, Daniel Smith¹, Jerome Lewis¹, Ruth Mace¹, Lucio Vinicius¹ and Andrea Bamberg Migliano¹

(1) Department of Anthropology, University College London, London WC1H 0BW, United Kingdom

(2) Royal Botanic Gardens, Kew, Surrey, TW9 3AB, United Kingdom

Human evolution is marked by long-term pair bonds between men and women, exogamy (marriage outside one's own group), and our unique ability to recognize both maternal and paternal kin. The importance of marital ties (i.e. affinal kin) in allowing peaceful interactions between groups has long been acknowledged in anthropological literature. However, their role in cultural transmission has been neglected. Given that marital ties are the key links connecting distant families in hunter-gatherers, their importance in transmission and accumulation of knowledge should be substantial and requires further investigation. Marital ties also play a crucial role in childrearing, because individuals connected through marriage often have shared reproductive interests. Interactions through childcare provide not only fitness benefits, but also a medium for knowledge and skill exchange that is necessary for survival. Here, I investigate the role of marital ties and cooperative childcare in the transmission of plant knowledge in Mbendjele BaYaka Pygmies of Congo-Brazzaville.

Investigation of the Néolithisation in Anatolia and the Aegean by using ancient DNA

Dilek Koptekin^{1,2}, Gülşah Merve Kılınç^{2,3}, Çiğdem Atakuman⁴, Arev Pelin Sümer⁵, Reyhan Yaka⁵, Cemal Can Bilgin⁵, Ali Metin Büyükkarakaya⁶, Douglas Baird⁷, Anders Götherström³, İnci Togan⁵, Mehmet Somel⁵

- (1) Department of Health Informatics, Middle East Technical University, 06800, Ankara, Turkey
- (2) Department of Biological Sciences, Middle East Technical University, 06800, Ankara, Turkey
- (3) Department of Archaeology and Classical Studies, Stockholm University, Lilla Frescativaegen 7, 114 18, Stockholm, Sweden
- (4) Department of Settlement Archaeology, Middle East Technical University, 06800, Ankara, Turkey
- (5) Department of Biological Sciences, Middle East Technical University, 06800, Ankara, Turkey
- (6) Department of Anthropology, Hacettepe University, Beytepe, 06800, Ankara, Turkey
- (7) Department of Archaeology, Classics, and Egyptology, Liverpool University, Liverpool L69 7WZ, United Kingdom

In recent years, archaeogenomics studies revealed that early Neolithic farmers in Europe were genetically distinct from the European Mesolithic hunter-gatherers. Based on this result and the archaeological data showing the rapid appearance of Neolithic communities in the Aegean, it has been suggested that the westward spread of farming 7,000 cal BC was mainly the outcome of population migrations, originating from Anatolia or the Levant. In this context, we further evaluated the finer- scale population relationships within west Eurasia, by compiling published genome sequence data of a total of 99 ancient humans from west Eurasia from a time period extending from Paleolithic to Neolithic. We performed population genetics analysis to dissect the relationships between a set of ancient Eurasian populations. Our findings raise the possibility that pre-Neolithic inter-regional gene flow, before 7,000 cal BC, had already created a diverse and distinct gene pool in the Aegean.

A New Model for Peopling of the American Arctic

Pavel Flegontov¹, **N. Ezgi Altinişik**, Piya Changmai¹, Pontus Skoglund^{2,3}, M. Geoffrey Hayes⁴, Dennis O'Rourke⁵, Ron Pinhasi^{6,7}, Robert Sattler⁸, Edward J. Vajda⁹, Johannes Krause¹⁰, David Reich^{2,3}, Stephan Schiffels¹⁰

- (1) Life Science Research Center, University of Ostrava, Czech Republic
- (2) Department of Genetics, Harvard Medical School, Boston, Massachusetts 02115, USA
- (3) Broad Institute of MIT and Harvard, Cambridge, Massachusetts 02142, USA
- (4) Division of Endocrinology, Metabolism, & Molecular Medicine, Department of Medicine, Northwestern University Feinberg School of Medicine, Chicago, Illinois
- (5) Department of Anthropology, University of Kansas, Lawrence, KS 66045
- (6) School of Archaeology and Earth Institute, Belfield, University College Dublin, Dublin 4, Ireland
- (7) Department of Anthropology, University of Vienna, Althanstrasse 14, 1090 Vienna, Austria
- (8) Tanana Chiefs Conference
- (9) Department of Modern and Classical Languages, Western Washington University, Bellingham, WA, USA
- (10) Department of Archaeogenetics, Max Planck Institute for the Science of Human History, Kahlaische Str. 10, 07745 Jena, Germany

Paleo-Eskimos, coming from Chukotka around 5000 BP, were the first people who settled broadly in the American Arctic, stretching between northern Alaska and Greenland. After dominating this region for four thousand years, they were replaced by other archaeological cultures, continuous with the present-day ethnic groups speaking Eskimo-Aleut languages (Inuit, Yupik, and others). Genetic connections between Paleo-Eskimos and present-day populations of the region remain controversial despite extensive studies of modern and ancient genomes.

In this project, we generated targeted enrichment and shotgun sequencing data for 16 ancient samples (Aleuts, Athabaskans, and Inuit) and for dozens of present-day individuals. Using an array of high-resolution methods relying on rare variants, autosomal haplotypes or allele frequencies, we have updated the established three-wave model for the settlement of North America. We show that all present-day and ancient human populations of the continent are derived from two, not three, migration streams: First Americans and Paleo-Eskimos. Eskimo-Aleuts, which were thought to represent an independent migration into America, are all derived from admixture between Paleo-Eskimos and First Americans, and Na-Dene Native Americans show lower proportions of Paleo-Eskimo ancestry. Our results provide indirect evidence in favour of the Dene-Yeniseian language macro-family hypothesis, which suggests the Na-Dene languages in America and Yeniseian languages in Siberia are related.

Archaic hominin introgression in Africa contributes to functional salivary MUC7 genetic variation

Recep Ozgur Taskent¹, Duo Xu¹, Pavlos Pavlidis², Nikolaos Alachiotis³, Colin Flanagan¹, Ran Blekhman⁴, Stefan Ruhl^{5*}, Omer Gokcumen^{1*}

(1) Department of Biological Sciences, State University of New York at Buffalo, New York 14260, USA

(2) Institute of Molecular Biology and biotechnology (IMBB), Foundation for Research and Technology-Hellas, Heraklion, Crete, Greece

(3) Institute of Computer Science (ICS), Foundation for Research and Technology-Hellas, Heraklion, Crete, Greece 70013

(4) Department of Genetics, Cell Biology, and Development, University of Minnesota, Twin Cities, Minnesota 55455, USA

(5) Department of Oral Biology, School of Dental Medicine, State University of New York at Buffalo, New York 14214, USA

MUC7 gene, which encodes for one the most abundant proteins in human saliva, mucin-7, carries copy number variable subexonic repeats (PTS- repeats). These PTS-repeats primarily affect the glycosylation potential of the protein. We previously demonstrated that the MUC7 copy number variation evolves under selective pressures among primates. However, no study to the date investigated MUC7 evolution in humans. Our results indicate that MUC7 PTS-repeat copy number variants have been evolving recurrently in human lineage, generating distinct haplotypes harboring either 5 or 6 PTS-repeat copy number alleles. One MUC7 haplotype with 5 PTS-repeats shows extensive divergence to all other haplotypes. Based on multiple simulations, we conclude that the highly divergent MUC7 haplotype originated in an unknown African hominin population and introgressed into ancestors of modern Africans. We also found that MUC7 haplotypic variation is significantly associated with the oral microbiome, indicating the crucial roles of MUC7 in oral immunity.

Cold-related germination in plants of Central Anatolian steppes: the role of biogeographical origin

İsmail Bekar¹, Cansu Ülgen², Eftalya Güneş², Ş. Serter Çatav³, Gökhan Ergan², Barış Özüdoğru², Çağatay Tavşanoğlu²

(1) Hacettepe University, current affiliation: ETH Zürich

(2) Hacettepe University

(3) Muğla Sıtkı Koçman University

The pronounced cold period observed in Central Anatolian steppes (CAS) is expected to have a significant impact on the germination properties of plants in the region. We hypothesized that seeds of CAS plants experiencing a cold period should be more prone to germinate than the ones that are not exposed to any cold period. To test this hypothesis, seeds of 61 species in CAS were stratified at 4 °C for 1 to 3 months, and then were incubated at 20 °C to follow their germination. The final germination percentages of treatment groups were compared to the control using a generalized linear model assuming the binomial distribution. Germination

patterns of various plant functional groups were further analyzed using linear mixed models, considering the exposure period, distribution range and phytogeographic origin as fixed factors, and family and genus as random factors. One-third of species positively responded to at least one of the cold stratification treatments, whereas another one-third showed negative response. The species of Irano-Turanian origin and the ones with limited distribution (Anatolian species) had significantly higher germination after cold exposure than cosmopolitan species. Our results suggest that biogeography can play an important role in seed germination in response to environmental cues.

Resprouting ability encapsulates the most functional variability in the Mediterranean Basin flora

Çağatay Tavşanoğlu¹, Juli G. Pausas²

(1) Hacettepe University

(2) Centro de Investigaciones sobre Desertificación

Growth form is considered among the most important traits in plants. We hypothesized that in Mediterranean ecosystems; the ability to resprout is as important or even more than growth form in explaining the functional variation of plants. We evaluated this hypothesis using the BROTE database of functional traits for the Mediterranean Basin flora and considering three general growth form classifications: (1) herb, woody; (2) annual herb, perennial herb, woody; and, (3) annual herb, perennial herb, scrub, shrub, tree. For each of these classifications, we compared the variability of nine functional traits (seed mass, seed germination, height, leaf size, specific leaf area, mass-based leaf nitrogen content, root depth, shoot:root ratio, and stem density) before and after considering the resprouting ability of the woody species. The results showed that for most traits, resprouting ability accounts for a significant variability after considering growth form. For all Mediterranean plants, resprouting explains more functional variability than woodiness (herb/woody); and for woody plants, resprouting had more explanatory power than growth form (scrub/shrub/tree). Overall the results suggest that despite resprouting is a simple binary trait, it is a key trait in the Mediterranean flora and encapsulates a very large portion of plant functional variability.

Forest bird community response to a decade of forestry activities in Istranca Forests

Korhan Özkan¹

(1) Institute of Marine Sciences, Middle East Technical University, Erdemli, Mersin

Forests in temperate regions have been extensively managed for timber production. Consequently, forestry activities has modified large forest areas with cascading effects on various organism groups. Turkish forestry practices generally aim at creating homogeneous forest stands and have ten-year production cycles. The impact of these activities on forest bird communities has not been quantified in Turkey. I aimed at understanding the effect of timing and intensity of forestry activities on bird communities of Istranca Forests. These forests cover north west Thrace, consist of a large diversity of habitats and thus subject to varying intensity of forest activities. A breeding bird atlas survey has been conducted across 12000 km² forests at 443 locations in 2009. Breeding bird abundance, diversity and forest habitat characteristics have been recorded at each location. Furthermore, forestry activities across the Istranca forest has been compiled and digitized from official forestry registry forms covering the entire production cycle before the survey (1999-2009). The date of forestry activity and the amount of timber production have been calculated for all forest stands. The bird community abundance, diversity and composition were analyzed in relation to current habitat characteristics as well as timing and intensity of the forestry activities.

Exploring Marine Microbial Community Structure Using 16S rRNA Amplicon Sequencing: First Results to Understand Their Role in the Oligotrophic Marine Ecosystem

Selin Küçükavşar, Arzu Karahan, Şadi Sinan Arkin

(1) Middle East Technical University, Institute of Marine Sciences

Biogeochemical cycle, biotechnology or basic researches done by standard methods (culturing) provide biased and limited information. Next Generation Sequencing (NGS) platforms are the best tool that uses culture-independent approaches and thus provides data related to the microbial genetic diversity, while the organic matter produced by marine plants (photosynthesis) sinks to the bottom of the sea, some are exposed to decomposition by bacteria that produce the inorganic nutrients necessary for marine plants. This recycling/decomposition performed by bacteria makes them a central component of the marine biogeochemical cycles, which in turn signifies their importance in some of the most important environmental problems facing the world, including climate change and eutrophication. Despite the many important roles they play, bacteria are one of the least known components of the marine biogeochemical cycles and their representation in the marine biogeochemical models is highly limited. Here we will present the first culture independent 16S rRNA amplicon sequencing study results in the northeastern

Mediterranean Sea. Seawater sample collected from the surface in the 200 meters' station of the Erdemli Time Series stations and sequenced by next generation sequencing platform to explore community composition and to understand their functional diversity. The number of OTUs assigned is 143 and 96% of it was classified as Bacteria, 1% as Archaea and 3% unclassified. It is the first data to develop a gene-centric model to determine the rates of the reactions that the bacteria perform.

Organic vs. Conventional? How do butterfly communities respond to farming type and agricultural practices in olive groves in Ayvacik, Çanakkale, Turkey

Karacetin E.¹, Balkiz O.², Bilgin, C. C.³, Elverici M.^{3,4}, Guclu H.⁵, Karabacak P.¹, Turak A.², Demirbas-Caglayan S.², Vural M.⁵, Bekyurek Y.⁶

- (1) Environmental Engineering Department, Faculty of Engineering, Erciyes University, Kayseri, Turkey
- (2) Nature Conservation Centre (DKM), Ankara, Turkey
- (3) Department of Biological Sciences, Faculty of Arts and Sciences, Middle East Technical University (ODTU), Ankara, Turkey
- (4) Department of Biology, Faculty of Arts and Sciences, Erzincan University, Erzincan, Turkey.
- (5) Department of Biology, Faculty of Arts and Sciences, Gazi University, Ankara, Turkey.
- (6) Directorate of Provincial Food Agriculture and Livestock, Kayseri, Turkey.

Organic farming is mostly acknowledged as environmentally and biodiversity friendly, yet many studies have contradictory results and conclude the effects differ between organism groups and landscapes. In this study we concentrated on olive groves in Ayvacık, Çanakkale, Turkey. We selected 15 organic and conventional olive groves and 3 natural habitats (> 6 ha each) by GIS methods to randomize the sampling units and minimize the influence of topography, anthropogenic elements (roads, buildings, etc.), climate, and vegetation and we established a standardized sampling scheme. We placed transects and measured butterfly diversity, abundance and behavior from 2015 to 2017. Soil management types resulted to have meaningful impacts on both abundance and habitat use of butterflies. According to the preliminary results, herbicide application in conventional sites and deep plowing in organic sites had significant influence on vegetation cover compared to hay cutting and surface plowing. Pesticide use was nearly minimal in both types of farming methods. We conclude that individual farming methods should be well defined when aiming for biodiversity friendly farming and when establishing support schemes at the national scale. This study was funded by TÜBİTAK under the project TOVAG 213 O 147.

Let's Sample It Later Again (or Not?): An Empirical Assessment on Repeatability of Invertebrate Surveys

Mert Elverici^{1,2}, Evrim Karaçetin³, C. Can Bilgin¹

(1) Middle East Technical University

(2) Erzincan University

(3) Erciyes University

Field based inventories or community level surveys of terrestrial invertebrates can be very useful for addressing various problems from land use decision giving or conservation, to testing scientific questions in ecology or biogeography. However, their implementation is rare due to difficulties associated with studying with invertebrates. One major challenge is about time, as both sampling (or collection) and taxon identification procedures are quite labor intensive and time consuming. Therefore, scientists may need to use replicates or sampling units collected at different time intervals, even from different years, despite the fact that temporal fluctuations are known in invertebrate populations. It remains untested if such fluctuations also exist at the community level; if so, repeatability should be questioned. We tested this on spider (Araneae) communities in typical Mediterranean habitats at 14 locations from Ayvacık, Çanakkale. Same sampling method was repeated for three times at each locale: two consecutive sampling events in 2015 at May and June, and one in 2016 at June. UPGMA clustering, ordination and permutational analyses were generally able to assign replicates to their respective locations. Community composition remained stable and thus was repeatable for spiders at May-June period, even between consecutive years (2015/2016). This study was partly funded by YÖK and TÜBİTAK (TOVAG213O147).

Monitoring wildlife populations using camera-traps: Large mammals in a wildlife reserve in north-western Anatolia

Anıl Soyumert¹, Alper Ertürk^{1,2}, Çağatay Tavşanoğlu²

(1) Kastamonu University

(2) Hacettepe University

Camera-traps are being widely used to collect data about large mammals. But the data should be based on a long-term monitoring and a systematic survey to permit a concrete evaluation for the target population. In Kartdağ Wildlife Reserve (Kastamonu, Turkey) camera-trapping surveys were conducted in two distinct periods, 2009-2010 and 2015-2016; with 6,128 and 3,604 camera-trap days, respectively. During both periods, 12 large mammal species were detected including brown bear (*Ursus arctos*), gray wolf (*Canis lupus*), golden jackal (*Canis aureus*), wild cat (*Felis silvestris*), red fox (*Vulpes vulpes*), red deer (*Cervus elaphus*), wild boar (*Sus scrofa*) and roe deer (*Capreolus capreolus*). A permutation test was performed to compare relative abundance indices values of two periods for each species. Although the Reserve was registered as a conservation area for red deer in 2005, the number of camera-trap records belonging to the target species was lower in the second survey period, but this difference was not statistically significant ($p > 0.05$). On the other hand, significant increases in relative abundance

indices of brown bear ($p = 0.001$) and wild boar ($p < 0.0001$) were detected. Our study supports that cameratrapping is a useful tool for long-term monitoring of large mammal populations

A phylogeographic investigation of the Picarel (*Spicara* Spp.) around the Turkish coastal waters with comparisons to the Mediterranean Sea and Atlantic

Aslı Şalcıoğlu¹, Grigorous Krey², Deniz İnnal³, Derya Güroy⁴, Serdar Sakınan⁵, Raşit Bilgin¹

(1) Institute of Environmental Sciences, Boğaziçi University, Bebek-İstanbul, Turkey.

(2) Hellenic Ministry of Rural Development and Food Hellenic Agricultural Organization Demeter, Fisheries Research Institute, Kavala- Greece.

(3) Mehmet Akif Ersoy University, Natural Sciences Faculty, Hydrobiology Department, Burdur, Turkey

(4) Department of Aquaculture, Armutlu Vocational College, University of Yalova, Turkey.

(5) Middle East Technical University, Institute of the Marine Sciences, Erdemli, Mersin, Turkey.

In this study, the effect of the Turkish Straits System (TSS), on the evolutionary history, phylogeography and intraspecific gene flow of the picarels (*Spicara maena*, *S. flexuosa* and *S. smaris*) a demersal fish species, were investigated. Considering *Spicara* genus, we see that phylogenetic relationships and morphologic discrimination of *Spicara maena* and *Spicara flexuosa* are not clear in the Mediterranean as well as Turkish coastal waters. Specifically *S. maena* is considered to be the dominant species found along the Turkish coasts, rather than *S. flexuosa*. In this perspective, another aim of the study is to investigate whether *S. maena*, or *S. flexuosa* is the common species in the Turkish coastal waters using a molecular approach. The results of the study indicated that the distinction of the three taxa under *Spicara* was made with the help of three different mtDNA markers, e.g. (16S, CO1, cyt-b) and one nuclear gene (IRBP). In addition, some morphometric measurements were also made for the identification of the three species of *Spicara*. The results from morphological PCA indicated that 94.4 % of the examined species were correctly identified. Of all the samples analyzed in this study, a total of 192 out of the 194 samples (% 98.9) were identified as *S. flexuosa*, and only two samples were determined as *S. maena* in the Turkish coastal waters, showing that *S. flexuosa* is by far much more dominant than *S. maena* in the Turkish coasts. On the other hand, an absence of genetic structure between subpopulations indicate the connectivity of the *Spicara flexuosa* populations from Turkey, suggesting that the TSS is a corridor, rather than a barrier to gene flow, for this species.

Long Interspersed Nuclear Elements (LINEs) may promote gene duplication in human and mouse genomes

Alexey Yanchukov¹, Vaclav Janousek^{2,3}, Christina M. Laukaitis⁴, and Robert C. Karn⁴

(1) Department of Biology, Faculty of Arts and Sciences, Bülent Ecevit University, Zonguldak, Turkey

(2) Department of Zoology, Faculty of Science, Charles University in Prague, Prague, Czech Republic

(3) Institute of Vertebrate Biology, ASCR, Brno, Czech Republic

(4) Department of Medicine, College of Medicine, University of Arizona

Retrotransposons impose major structural and regulatory changes in mammalian genomes. LINEs, in particular, may serve as breakpoints during Non-Allelic Homologous Recombination (NAHR), resulting in misaligning of homologous sequences during meiosis and subsequent duplications (deletions) of large gene clusters. This mechanism might explain association between LINE density and the size of gene families in human and mouse, as well as apparent enrichment of LINEs at the edges of segmental duplications. Because LINEs themselves can be part of segmental duplications, they may serve as new breakpoints for subsequent NAHR events, potentially resulting in a runaway duplication process. We propose a simple theoretical model where such stochastic runaway expansion is offset by steady deterioration of sequence similarity between LINEs, so that the probability of a NAHR between two LINEs decreases with time since their divergence. Simulation results outline the range of population genetic parameters that make a rapid gene expansion or contraction possible. Importantly, the process becomes more volatile with increasing gene family size: we thus predict that in the absence of selection, the runaway process can lead to large differences in paralog family size even among closely related taxa.

POSTER PRESENTATIONS

Phenome-Environment Interaction and Explanation In Biology: A Philosophical Analysis

Özlem Yılmaz¹

(1) Istanbul Technical University, Faculty of Arts and Sciences, Department of Humanities and Social Sciences, Maslak Istanbul

For explaining a specific phenotypic trait, scientists design experiments: they measure/observe subject phenotypic trait of a specific organism, at a specific time point, in a specific environment. The measured phenome is caused by interaction between that specific organism (the whole phenome) and its environment. The encounter with an environmental factor causes changes in the processes of a living system. These changes begin in the sensory processes, continue in the signal transduction and are spread through ramified reaction cascades resulting changes in gene expressions. These happen very dynamically in a multilevel complexity. Because of this complexity, in the occurrence of phenome, there are many interrelated causes and we usually investigate them through one of the subareas of biology. If we want to give more comprehensive explanations, then we should collaborate with other biologists. In any case, our explanation depends on our specific experiment context and the current state of society and the scientific community.

Genomic organization and standing structural variation of the Major Histocompatibility Complex of the three-spined stickleback

Sengupta M.¹, Panchal M., Samonte I.E., Chain F., Eizaguirre C., Feulner P.G.D., Kalbe M., Bornberg-Bauer E., Reusch T.B.H., Milinski M & Lenz T.

(1) Max-Planck-Institut für Evolutionsbiologie

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. Previous work revealed local adaptation of locus-specific MHC allele pools to distinct parasite communities. However, little is known about the evolutionary factors that drive its structural variation. In this project, we unravel the genomic organization of the MHC class II region in the three-spined stickleback (*Gasterosteus aculeatus*), for which we found a candidate region at one end of Chromosome VII. We used state-of-the-art genomic tools, including BAC library construction and next generation sequencing. Several distinct CNV haplotypes of the MHC region were assembled and annotated, creating a reference map for the characterization of the haplotypic diversity found in natural populations. This work will shed light on the effect of host- parasite coevolution on the structural organization of complex genomic regions, and thus illuminate the importance of CNVs in ecological speciation.

Population genomics of Behcet disease susceptibility

Goncagul ARPAZ¹, Efe SEZGIN¹

(1) Laboratory of Nutrigenomics and Epidemiology, Department of Food Engineering, Izmir Institute of Technology, Urla, Izmir, Turkey

Behcet disease (BD) is a polygenic complex disease with high prevalence in populations along the silk road. We aimed to characterize the allelic nature, evolutionary history, and infer possible selective forces acting on BD associated variants. Populations are grouped according to the prevalence of Behcet's disease. Population genome sequence data from 1000 genomes project, Behcet disease related candidate gene and GWAS data from published studies are analyzed. Ancestral and derived allelic states of disease related genes are examined. Individual genes, gene groups, and their biological pathways are identified. Population differentiation and historical selection is assessed by geographical genetics and principal component analyses. Results suggest high genetic differentiation with respect to BD associated variants, and possible historical immune response based selection on genes identified along the cytokine related biological pathways. We conclude that population genomic analysis and statistical modelling of genomic data from different populations within a disease pathogenesis framework can identify evolutionary histories and selective forces maintaining complex disease risk genetic variants.

Metatranscriptomic analyses of honey bee colonies

C. Özge Tozkar¹, Meral Kence², Qiang Huang³, Jay D. Evans³

(1) Yüzüncü Yıl University, Faculty of Agriculture, Department of Agricultural Biotechnology, Van, Turkey

(2) Ecological Genetics Laboratory, Middle East Technical University, Department of Biological Sciences, Ankara, Turkey

(3) USDA-ARS Bee Research Laboratory, Beltsville, Maryland, USA

Honey bees face numerous biotic threats from viruses to bacteria, fungi, protists, and mites. Here we use deep ILLUMINA-based RNA sequencing to describe a thorough analysis of microbes harbored by worker honey bees collected from field colonies in geographically distinct regions of Turkey. Turkey is one of the World's most important centers of apiculture, harboring 5 subspecies of *Apis mellifera* L., approximately 20% of the honey bee subspecies in the world. Levels of key honey bee pathogens were confirmed using quantitative PCR screens. We contrast microbial matches across different sites in Turkey, showing new country recordings of Lake Sinai virus, two *Spiroplasma* bacterium species, symbionts *Candidatus Schmidhempelia bombi*, *Frischella perrara*, *Snodgrassella alvi*, *Gilliamella apicola*, *Lactobacillus* spp.), neogregarines, and a trypanosome species. By using metagenomic analysis, this study also reveals deep molecular evidence for the presence of bacterial pathogens (*Melissococcus plutonius*, *Paenibacillus* larvae), *Varroa destructor*-1 virus, Sacbrood virus, *Apis* filamentous virus and fungi. Despite this effort we did not detect KBV, SBPV, Tobacco ringspot virus, VdMLV (*Varroa Macula* like virus), *Acarapis*

spp., *Tropilaeleps* spp. and *Apocephalus* (phorid fly). We discuss possible impacts of management practices and honey bee subspecies on microbial retinues.

Enhanced seed germination by heat shock in Mediterranean Fabaceae

Gökhan Ergan¹, Cansu Ülgen¹, Çağatay Tavşanoğlu¹

(1) Hacettepe University

Members of Fabaceae family are important components of post-fire plant communities in the Mediterranean Basin. However, there is a lack of comprehensive information on the seed germination after fire in this family, especially in annual species. To understand fire-related germination in Mediterranean Fabaceae, seeds of 29 plant taxa from this family were exposed to heat shocks at different intensities (60, 80, 100, 120, and 140 °C for 5 min.) and also to mechanical scarification, and their germination was observed. A generalized linear model assuming binomial distribution was used to test if significant differences in germination exist between treatments and the control. Germination enhanced with heat shocks in 14 taxa, and with mechanical scarification in 18 taxa, while germination in remaining taxa was not significantly different from the control. The most efficient heat-shock treatments to improve germination were 120 and 100 °C. Germination of all three woody species and the half of annuals in the study enhanced after heat-shock application. The data obtained in the experiments prove that fire temperatures are necessary for germination in many taxa in Fabaceae family. The results have implications for sustaining biodiversity and for a better postfire management in Mediterranean habitats.

Ecology in Backyard: METU Erdemli Ecological Campus Project

Batuhan Çağrı Yapan¹, Gizem Akkuş¹, Saba Başkır¹, Emrah Çoraman², Fatıma Nur Oğul¹, Korhan Özkan¹, Begüm Ece Tohumcu³, Deniz Yalçınkaya⁴ and METU Ecological Campus Project Team*

- (1) Middle East Technical University Institute of Marine Sciences
- (2) Institute of Environmental Sciences, Boğaziçi University
- (3) Middle East Technical University Department of Biological Sciences
- (4) Toros University Department of Medical Laboratory Techniques,

Middle East Technical University Erdemli Campus is located on the South East Mediterranean Coasts of Anatolia within Mersin city center. It covers 660000 m² area with c. 1.5 Km of coastline. It is one of the last less-intensive human settlements on Mersin coastline and serves as an important natural area. In spite of its small size, the campus hosts native coastal sand dunes as well as a great diversity of habitats. Ecological Campus Project started in spring of 2016 to understand the biodiversity and ecology of METU Erdemli Campus and provide strategies for better management of the campus to enhance its ecological functions. The first phase of the project aims at understanding the diversity and spatiotemporal patterns of organism groups in the campus area: plants, arthropods, fish, reptiles and amphibians, birds and mammals. All surveys have been conducted by using standardized ecological field methods that enables

inter-group and inter-annual comparisons. The abundance and occupancy patterns in species and diversity is used to understand their interaction with their habitats and the extent of the anthropogenic effects. In this poster, we will present the first results of the field surveys and the project

Somatic copy number variant detection using single-cell genome sequencing data

Mehmet Somel^{1*}, İdil Yet¹, Poorya Parvizi¹, Ulaş Işıldak¹, Zeliha Gözde Turan¹

(1) Biological Sciences, Middle East Technical University, Ankara, Turkey 06800

While germ-line mutations are a source of evolutionary diversity, somatic mutations also contribute to diversity within the body and can have important consequences. Understanding the mechanisms generating variability among somatic cells, such as central nervous system neurons, remains a basic challenge. For instance, mutations causing structural variation in the human genome could be a particularly important driver of neuronal diversity and brain disease. Indeed, chromosomal copy number variation (CHROM-CNV) that arises due to loss or gain of whole chromosomes or fragments thereof have been described both in the normal and diseased adult human brain, such as in schizophrenia and Alzheimer's disease (AD) patients, but the prevalence of somatic CHROM-CNV's is debated. In addition, whether somatic CHROM-CNV hotspots correspond with germ-line CHROM-CNV hotspots identified in population genomic data remains contentious. Today, single cell genomics technology provides a means to systematically assess CHROM-CNV in the normal and diseased tissues, with respect to its overall frequency, regional distribution and type of chromosome complement involved. To this end, here we analyzed four published datasets [1-4] to detect aneuploidy in single cells among different tissues. We analysed over 2000 single cell genomes and compared different methods developed for estimating CHROM-CNV's in low coverage single cell data [5,6]. We confirmed reported cases of aneuploidy in these datasets, and additionally detected putative patterns of partial aneuploidy in some cells' genomes. We are currently studying the overlap between the identified somatic CHROM-CNV's and published germ-line CHROM-CNV's. The work will illuminate shared or divergent copy number mutation mechanisms in somatic and in germ-line cells.

Seed-borne Metaorganism Evolution of Wheat

Ezgi Özkurt¹, Eva Stukenbrock^{1,2}

(1) Christian-Albrechts University of Kiel

(2) Max Planck Institute for Evolutionary Biology

Previous studies show that environmental factors alone cannot explain the composition of microbial species inhabiting plants. Furthermore, there is evidence that bacterial populations are able to re-establish on the phyllosphere in the similar patterns seen in previous generations. These findings suggest that microbes can be acquired both from the environment and the internal reservoir, which is the vertical transmission from seeds to seedlings. Here, we examine wheat

seeds as a conceivable way of early introduction of endophytes into seedlings when competition among endophytes is weak. We aim to identify a core community of seed-associated microbes migrating to seedlings and reveal the dynamics of community composition across generations. To do this, we work with wild and domesticated wheat seeds derived from Southeast Turkey, located in the center of origin of wheat. We germinate seeds under sterile conditions and characterize microbes migrating from seeds to seedlings. Preliminary sequencing has identified different microbes in wheat seeds including the fungus *Alternaria infectoria*, the oomycete *Phythyium oopapillum*, and the bacteria *Pantoea agglomerans*. Ultimately, we aim to characterize microbial species tightly associated with wheat seed.

Fixation Bias for Extended Homopolymers in Primate Genomes

Elif ozlak¹, Yetkin Alici², Evrim Fer¹, Melike Donertaş³, Rasmus Nielsen⁴, Mehmet Somel²

- (1) Middle East Technical University, Informatics Institute, Department of Bioinformatics, Ankara, Turkey
- (2) Middle East Technical University, Department of Biology, Ankara, Turkey
- (3) European Bioinformatics Institute EMBLEBI, Cambridge, UK
- (4) University of California Berkeley, Department of Integrative Biology, Berkeley, California, USA

Previously we showed that, in the human genome, mutations that extend same base sequences (e.g. AGCGG → AGGGG) are fixed more rapidly in comparison to mutations that disrupt such sequences (e.g. AGGGG → AGCGG). This putative homopolymer fixation bias is observed genome-wide and could be an example of a directional neutral process shaping genome composition. Such processes may be important to incorporate into models of genome evolution in order to increase accuracy. Here, we check whether the mentioned fixation bias is also present among other primate species. Here we use published genome-wide single nucleotide polymorphism data from chimpanzee, bonobo, orang-utan and gorilla populations, together with between species comparative genome data. Frequencies of mutations that remain polymorphic and that are fixed throughout genome are compared in a McDonald-Kreitman framework, to determine the prevalence of the homopolymer fixation bias in primate genomes.

Continuous monitoring of *Chelonia mydas* and *Caretta caretta* Hatchling Emergence Using In-situ Camera System

F tim Nur Oğul^{1*}, Franziska Huber^{12*}, Sinem Cihan¹, Kumsal Düzgün³, Ahmet Erkan Kideş¹, Korhan Özkan¹

- (1) Institute of Marine Sciences, Middle East Technical University, Erdemli, Mersin, Turkey
- (2) Paris Lodron University of Salzburg, Faculty of Natural Sciences, Salzburg, Austria
- (3) Faculty of Veterinary Medicine, Ankara University, Altındağ, Ankara, Turkey

Understanding sea turtle hatchling emergence behaviour and duration is very important for better coastal management. Therefore, development of novel monitoring methods is very important for more efficient monitoring. We used, for the first time, infra-red (IR) cameras for continuous recording during 2014 and 2015 hatching emergence period for one green turtle (*Chelonia mydas*) and four loggerhead turtle (*Caretta caretta*) nests in the north-east

Mediterranean, Turkey. Results showed that hatchlings emerged from the nests asynchronously in varying numbers of groups and different group sizes. Most of the hatchlings (98.6%) emerged during night with a peak activity between 21:00 and 00:00. No relationship between hatchling emergences and moon phase has been detected. Total emergence activity continued after the egg deposition for 60-65 days. Therefore, we recommend that these durations should be considered for nest excavations and beach management for further studies. Our study provided exhaustive insights on sea turtle hatchling behavior with more reliability than conventional beach monitoring on daily pattern, emergence synchrony, emergence period and group emergences of sea turtle hatchlings. We believe, IR camera monitoring is a promising tool, which is more time saving and less labor intensive method for sea turtle conservation in protected study sites.

The Effect of Human Beach Use on the Abundance and Distribution of Ghost Crabs in East Mediterranean

Melisa Bal^{1,2}, Batuhan Çağrı Yapan², Korhan Özkan²

(1) Faculty of Atatürk Education, Marmara University, Istanbul, Turkey

(2) Institute of Marine Sciences, Middle East Technical University, Mersin, Turkey

Ghost crabs (*Ocypode cursor*) are one of the important elements of the coastal and marine ecosystems. They are exposed to increasing anthropogenic pressures and experience local and regional population declines. Therefore, we investigated ghost crab populations at four beaches in Mersin, Turkey with contrasting anthropogenic pressures and habitat characteristics in 2016 summer. Understanding the factors affecting ghost crab populations is instrumental for efficient coastal zone planning. We surveyed abundance, distribution and behavior of ghost crabs using quantified methodologies. A total of 12 transects, which are located in METU beaches as a protected area with limited human use and a total of 13 transects, which are located in neighboring public beaches as an unprotected area with intense human use have been surveyed. Our results showed that burrow composition, density and distribution significantly differed in response to human use. Protected sites hosted more ghost crab burrows and more diverse age groups than public beaches. The negative impact of human use on ghost crab populations was also observed within the protected sites. Furthermore, this study revealed that the protected areas act as a refuge area for ghost crab populations and support the populations in neighbouring beaches facing higher anthropogenic pressures.

The Effect of Serotonin in Hypoxia Induced Hemoglobin Producing Pathway in Water Fleas (*Daphnia magna*)

Barış Can Mandacı^{1*}, Babür Erdem^{1*}, Meral Kence¹, Meryem Beklioğlu¹

(1) Department of Biology, Middle East Technical University, Ankara, 06800, Turkey

Environmental factors such as increasing population, illumination period and hypoxia affect the phenotype of water fleas (*Daphnia magna*). Increasing hemoglobin amounts in water

fleas' that are subjected to hypoxia result in visible red pigmentation. According to literature, serotonin shows a reducing effect to methyl farnesoate (juvenile hormone) synthesis. In studies on serotonin (5-HT) in different crustaceans, methyl farnesoate provides hemoglobin production by activating the globin 2 (hb2) gene. The hemoglobin ratio in water fleas change according to the oxygen level in the environment. Our hypothesis suggest that serotonin has suppressive effect on hypoxia induced hemoglobin pathway in *Daphnia magna*. Therefore, we demonstrate an experiment to test our hypothesis with using both agonist and antagonist of serotonin receptor (5HT-2) which is probably related with hemoglobin producing pathway on *Daphnia magna*, in different satiety of oxygen concentration as both hypoxic and normal environment.

Fast Species Detection from Ballast Water Using Environmental DNA Approach

Tu e Aygen¹, Sevgi Kaynar, Ozan Çiftçi, Emre Keskin

(1) Evolutionary Genetics Laboratory (eGL), Ankara University Agricultural Faculty Department of Fisheries and Aquaculture

Ballast water is the water with its suspended matter taken on board to control trim, list, draft, stability or stress of the vessel. Ballast water can contain thousands of aquatic or marine microorganisms, plants and animals, which are then carried across the globe. In this study, sea water samples from ballast tanks were filtered through Sterivex filter units by using a peristaltic pump. After the filtration, DNA was extracted from the membrane surface. PCRs were performed with universal primers for specific taxonomic groups (MiFish-u F/R for fish and Euk_1391f/EukBrfor micro-eukaryotes) and PCR products were pooled into libraries with Nextera XT library preparation kit. The fragment sizes of each library were verified and quantified by using Qubit fluorometric system and the libraries were sequenced on Illumina MiSeq platform. Raw FASTQ reads were quality-filtered using FastQC software. Further data processing and taxonomic classification through comparison with databases were performed by using OBITools and Qiime softwares. The results show that water samples are valuable sources to gather information about organisms from ballast tanks and environmental DNA approach can be used as a practical method for preventing introduction of non-native species which may be threatening for the introduced ecosystem.

Plant diversity and the Paleoclimate of the Yatağan Basin (southwestern Turkey) during the middle Miocene inferred from plant macrofossils.

H şeyin Tuncay Güner¹, Johannes Martin Bouchal², Nesibe Köse¹, Thomas Denk²

(1) Istanbul University, Faculty of Forestry, Forest Botany Department, 34473, Turkey

(2) Naturhistoriska riksmuseet, 50007, Stockholm, Sweden

Plant macro fossils from the lignite mines of Eskihisar, Tınaz and Salihpaşalar (Yatağan Basin, southwestern Anatolia) were investigated to establish biogeographic links of the paleoflora and to infer the palaeoenvironment. The age of the Eskihisar lignite seam is well constrained by vertebrate fossils (MN 6), and lithological and palynological correlation strongly suggest that the

lignite seams and overlying marls in the three lignite mines were formed at the same time. After three field seasons it appears that the sample areas are characterized by different sets of taxa and abundance of certain taxa strongly differs among areas. For example, *Fagus* is restricted to Eskihisar, while *Populus* and *Myrica* are locally abundant only in Tınaz. Also, different types of Rosaceae and Fabaceae are found in Tınaz and Eskihisar. Salihpaşalar is characterized by the great abundance of foliage of *Quercus* Group *Ilex*. These results enable us to obtain climate-related knowledge at the macro level, as well as to reveal species differences at the micro level. However aimed to reconstruct past climate of the sampled sites based on dicotile woody Angiospermae using CLAMP (Climate Leaf Analysis Multivare Programme) with 106 described different taxa

The brown bear as a seed disperser: Germination of seeds after passage through the gut

D. Deniz Kazancı¹, Alper Ertürk², Anıl Soyumer², Cihan Ü. Değirmenci¹, Çağatay Tavşanoğlu¹

(1) Hacettepe University

(2) Kastamonu University

We studied the potential of the brown bear (*Ursus arctos*) as a seed disperser by analyzing the germination of seeds after passage through the gut. Fecal samples were collected from a temperate mixed forest in northwestern Anatolia (Turkey). Fresh plant and seed material were collected from the field and identified, to serve as a reference database for seeds in fecal samples. Of the 127 examined fecal samples, we identified seeds of 22 plant taxa at various taxonomic levels, but also 8 unidentified taxa. We compared the germination between fecal samples and the control groups in 6 taxa which had enough seeds from the fresh and fecal material. Seeds of *Malus sylvestris* (European wild apple) and *Pyrus elaeagnifolia* (wild pear) had significantly higher germination in feces than the control, while germination in those of *Vaccinium* spp. and *Lonicera* sp. were lower in fecal samples. There was no significant difference in the germination of *Rubus* spp. and *Rosa canina* (rosehip) between control and feces groups. Our results suggest that the brown bear is an important seed disperser in temperate mixed forests of Anatolia, and the germination of seeds of wild fruit trees enhance after passage through the brown bear gut.

Anatololacerta species complex: Is it GSD or TSD?

Tülin Çetin¹

(1) Bornova Belediyesi Dost Bilim Evi (Mevlana Toplum ve Bilim Merkezi)

Reptiles possess two main sex determination mechanisms. One of them is genotypic sex determination (GSD) where the sex of an individual is determined by sex chromosomes; i.e. male or female heterogamety. The other one is temperature-dependent sex determination (TSD) where sex chromosomes are absent and sex is determined by nongenetic factors like effects of

incubation temperature on developing embryos. All crocodiles and most of the turtles share TSD and unlike the other groups lepidosaurs (tuataras and squamates) which possess variability in sex-determining systems, both TSD and GSD can be found in different species of lineage. However, based on largely cytogenetic data some lineages of squamate reptiles (especially lacertid lizards have $2n = 38$ chromosomes and they have ZZ/ZW sex chromosomes) possess highly evolutionary stable sex chromosomes. Anatololacerta species complex is endemic to western and southern Anatolia and some neighboring Aegean islands in the Anatolian Peninsula. In this study using conventional cytogenetic techniques revealed that species of Anatololacerta genus have $2n = 38$ chromosomes and they have ZZ/ZW sex chromosomes. These data can conclude that species of Anatololacerta genus has GSD. However evolutionary transitions from GSD to TSD have been experimentally induced in a reptile in the laboratory. Testing this hypothesis and further investigation on Anatololacerta genus can expand limited knowledge of genetic content of squamate sex chromosomes and can contribute a reliable reconstruction of evolutionary history of sex determination in this group.

Determining the Factors for Homopolymer Fixation at High Rate in Human Genome

Evrin Fer¹, Yetkin Alici², Elif Bozlak¹, Melike Dönertaş³, Rasmus Nielsen⁴, Mehmet Somel²

(1) Middle East Technical University, Informatics Institute, Department of Bioinformatics, Ankara, Turkey

(2) Middle East Technical University, Department of Biology, Ankara, Turkey

(3) European Bioinformatics Institute EMBL EBI, Cambridge, UK

(4) University of California Berkeley, Department of Integrative Biology, Berkeley, California, USA

Human genome is partially shaped by neutral evolutionary agents, that bear some sort of directionality. For instance, cytosines in CpG context are readily mutated into thymines (a context-dependent mutation bias), while G/C alleles are preferentially fixed over A/T at recombination hotspots (a fixation bias). We showed that, a neighbouring sequence context-dependent fixation bias, in favor of extended G or C homopolymers, also exists in human genome. This fixation bias might have shaped human genome composition in longterm, such that 3mer and 4mer sequences of G or C bases accumulated in human lineage at higher numbers in comparison to sequences formed by mutations disrupting homopolymer pattern. This G/C homopolymer fixation bias is absent in genic and regulatory regions, suggesting that it is not caused by natural selection and is not strong enough to compete with natural selection. We study and discuss possible relations with

mutation rate and recombination rate heterogeneities in non-coding regions of the genome.

Convergent Evolution of Testis Gene Expression at the Cell Autonomous Level Driven by Mating Type Differences

Etka Yapar¹, Ekin Saglican¹, Rori Rohlf², Handan Melike Donertasf, Ezgi Ozkurt⁴, Haiyang Hu⁵, Rafik Neme⁶, Babur Erdem¹, Philipp Khaitovich⁷, Mehmet Somel¹

- (1) Middle East Technical University
- (2) San Fransisco State University
- (3) University of Cambridge
- (4) Max Planck Institute for Evolutionary Biology
- (5) Chinese Academy of Sciences
- (6) Columbia University
- (7) Skolkovo Institute of Science and Technology

Among mammals, taxa such as chimpanzees, macaques or house mice display the “multimale” mating type, where females mate with multiple males during estrus, leading to inter-male sperm competition. In contrast, taxa such as humans or gorillas display the “singlemale” mating type with weak inter-male sperm competition. We recently showed that these mating type differences also significantly shape the testis transcriptome, leading to convergent evolution of expression levels among single- and multi-male species. We had attributed this effect to multi-male species having a higher proportion of germ-line cells in their testes. However, it remained unclear whether convergent expression evolution may be present at the cell autonomous level. Here, we investigate the effect of mating type on cell autonomous gene expression using published RNA-sequencing data from purified pools of spermatocytes and spermatids from human, rhesus macaque and mouse testes. We find that mice cell type-specific transcriptome profiles show higher correlation to those of macaques than to those of humans for both cell types, although phylogenetically, the mouse is expected to be equally distant to both taxa. This provides the first evidence for possible convergent evolution due to mating type differences at the cell autonomous level.

Molecular Explanation for Mammalian Aging

Zeliha Gozde Turan¹, Poorya Parvizi¹, Handan Melike Donertasf², Jenny Tung³, Philipp Khaitovich⁴, Mehmet Somel¹

- (1) Department of Biological Sciences, METU, Ankara, Turkey
- (2) European Molecular Biology Laboratory, European Bioinformatics Institute EMBL- EBI, Wellcome Trust Genome Campus, Hinxton, Cambridge, UK
- (3) Departments of Evolutionary Anthropology and Biology, Duke University, Durham, NC, USA
- (4) CAS-MPG Partner Institute for Computational Biology, Shanghai, PRC

Aging is a complex process that causes decline in an organism’s reproductive capacity and chance of survival. One of the primary evolutionary theories of aging is the mutation accumulation theory, which predicts that genes that are highly expressed later in life should be less conserved

than those expressed early. The theory's predictions have been previously supported using fitness variance within populations. Here we attempt to test the theory combining inter-species molecular conservation data with gene expression datasets. We performed a meta-analysis of 58 transcriptome datasets, including 8 tissues from 4 mammalian species. We studied the protein sequence conservation of genes expressed at different levels during adulthood. In the brain and lung, we found age-related decrease in transcriptome conservation, such that genes with increased expression during aging show low evolutionary conservation, while genes with decreasing expression during aging show high evolutionary conservation. Meanwhile, no such consistent trend was observed in other tissues. We will perform further analysis to find common genes across different tissues that are highly expressed in old age and exhibit low sequence conservation may contribute to the senescence phenotype in mammals, consistent with the mutation accumulation theory. We further discuss our results in the context of the antagonistic pleiotropy theory of aging.

Age-related immune function variation in the bush-cricket *Isophya speciosa* (Frivaldszky, 1868) (Orthoptera)

H s n Sevgili¹, Nilgun Tokgoz¹, Kenneth M. Fedorka²

(1) Ordu University, Faculty of Arts and Sciences, Department of Molecular Biology and Genetic, 52200, Ordu, TURKEY

(2) University of Central Florida, Department of Biology, 4110 Libra Drive, Orlando, FL 32816, USA

Immune function has been noted to decline with advanced age in insects. How immunity varies early in life, however, is an underexplored facet of insect immune function. Here we examine sex-specific, early life immune variation in the bush-cricket, *Isophya speciosa*. To this end, we examined two measures of potential immunity, phenoloxidase and lytic activity, over the first 20 days of adulthood, which represents the first half of their adult lifespan. We found that in the first 10 days, males and females exhibited a 100% increase in phenoloxidase activity. This pattern was reversed over the next 10 days, with individuals exhibiting a symmetrical 50% decline in phenoloxidase activity. No age-related change in lytic activity was noted, nor were sex differences detected. Considering that both male and females become sexually mature around day 10, the sharp decline in phenoloxidase is likely due to a reallocation of resources from immunity towards reproduction. Furthermore, this shift appears to be anticipatory, given that all individuals in this study were virgins. These data suggest that the relationship between age and immunity in *I. speciosa* is non-linear early in life. Variation in when the sexes initiate their allocation away from immunity should have a significant impact on age-specific fitness and life history evolution in this system.

What do Aquilegia genomes tell us about the population structure and genome architecture of a basal eudicot?

G kçe Ak z¹, Daniele Filiault, Magnus Nordborg

(1) Gregor Mendel Institute, Vienna

The Columbine genus *Aquilegia* first attracted the attention of Verne Grant more than 50 years ago. Inspired by his influential studies on the role of floral isolation in plant speciation, several follow-up studies reinforced the idea that *Aquilegia* is an ideal model plant to study speciation. Originating in Eastern Asia, *Aquilegia* colonized both North America and Europe. Whole-genome sequencing of ~50 individuals collected worldwide shows that the split of European *Aquilegia* contradicts a bifurcating speciation model and there exists a great population structure within Europe. Being at a taxonomically key place between core eudicots and monocots further raises *Aquilegia* as a good source for comparative genomics. The core eudicots, sister to the *Aquilegia* bearing lineage, has been previously shown to share a hexaploidization event. *Aquilegia* genome, however, bears the traces of a tetraploidization event: many old gene duplicates show similar levels of divergence and form synteny blocks, consistent with the idea that they were all created at the same time by whole genome duplication. We are now investigating yet another peculiarity of hermaphrodite columbines: a chromosome that resembles sex chromosomes in that it has higher transposable element density, lower gene density and lower gene expression.

Sanger and Next-Generation Sequencing Based Nuclear Genetic Analyses of the Long-Fingered Bat, *Myotis capaccinii* around the Mediterranean Basin

Küpra Karaman¹, Aslı Salcıođlu¹, Kanat Gürün¹, Emrah Çoraman¹, Andrzej Furman¹, Ahmet Karataş², Raşit Bilgin¹-

(1) Boğaziçi University, Institute of Environmental Sciences

(2) Niğde University, Department of Biology

Myotis capaccinii, long-fingered bat, has a wide distribution in the western Palearctic, covering the Mediterranean basin and spreads into North Africa, and reaching Anatolia and Iran to the east. It is considered to be polytypic with a taxonomic break in the former Yugoslavia. A recent mitochondrial DNA analysis with samples from the Mediterranean coasts of Europe, North Africa, Anatolia and Iran showed the presence of two genetic breaks; a deeper one in southeastern Europe, and a more recent one around the Alps, potentially corresponding to species and subspecies level differentiation, respectively. In this study, first, using a nuclear intron marker, we aimed to see whether these mitochondrial DNA breaks were reflected in the nuclear DNA as well. The results indicated no parallel differentiation in nuclear DNA, suggesting conspecificity of all three mitochondrial groups. However, the lack of differentiation could be due to the lack of resolution of the intron marker. Therefore, more detailed analyses with ddRAD-seq which is a higher resolution marker were conducted. The ddRAD structure, spanning over 3000 loci, paralleled the mtDNA differentiation. The ddRAD and mtDNA structure suggests that the three lineages could be considered different species, although further morphological analyses are

necessary for their confirmation.

Comprehensive characterization of long-non coding RNAs (lncRNAs) in Teleost Genomes

V hap Eldem¹, Gokmen Zararsiz², Halil Bilgin², Selcuk Korkmaz³, Dincer Goksuluk⁴

- (1) Department of Biology, Faculty of Science, Istanbul University, Istanbul, Turkey
- (2) Department of Biostatistics, Faculty of Medicine, Erciyes University, Kayseri, Turkey
- (3) Department of Biostatistics, Faculty of Medicine, Trakya University, Edirne, Turkey
- (4) Department of Biostatistics, Faculty of Medicine, Hacettepe University, Ankara, Turkey

Ongoing advances in sequencing technologies and a drastic drop in the cost of sequencing allow us to obtain genome-wide genetic information for virtually all kingdoms of life. Particularly, transcriptome sequencing (RNA-Seq) has uncovered the genomic dark matter and reveals regulatory elements called long non-coding RNAs (lncRNAs) whose functions linked to linked to a number of functions including cell division, embryogenesis, organ development and response to environmental stress sources. In this study, using transcriptome-based sequencing approaches, we have characterized the lncRNAs for 33 teleost species belonging to 27 teleost family. The teleost- lncRNAs were recovered from ~14 terabases sequencing data using genome-guided and de novo transcriptome analysis approaches. After removing protein-coding domains and assessing protein-coding potentials of reconstructed-transcripts, above ~8,500 lncRNAs were obtained, regardless of the species used, which showed sequence conservation in intergenic regions compared to other genomic regions. Evolutionary analysis showed that lncRNA conservations between osteichthyes and chondrichthyes was found to be weak. The contribution of teleost-specific duplication (TSD) on the number of teleost lncRNAs was evaluated and compared the result with protein-coding genes, we found that there is a moderate contribution of TSD on teleost-lncRNA numbers.

Mitochondrial Phylogeography Of The Whiting (*Merlangius Merlangus*) Along The Turkish Coastal Waters With Comparisons To The Atlantic

Aslı Şalcıoğlu¹, Grigorous Krey², Adem Yavuz Sönmez³, Raşit Bilgin¹

- (1) Institute of Environmental Sciences, Boğaziçi University, Bebek-İstanbul, Turkey.
- (2) Hellenic Ministry of Rural Development and Food Hellenic Agricultural Organization Demeter, Fisheries Research Institute, Kavala- Greece
- (3) Kastamonu University. Fisheries Faculty, Merkez, Kastamonu.

In aquatic environments, fish are accepted as one of the most important natural resources and reduction of the genetic diversity of natural fish populations has become an important fisheries management problem. Measuring genetic diversity in natural fish population is essential for interpretation of fish stocks. In this study, the effect of the Turkish Straits System (TSS), comprising a biogeographical boundary that forms the connection between the Mediterranean and the Black Sea, on the evolutionary history, phylogeography and intraspecific gene flow of the whiting (*Merlangius merlangus*) a demersal fish species, was investigated. For

comparisons samples collected from other region, Greece and samples from France, Atlantic obtained from GenBank and Barcode of Life Database were made to help better understand the phylogeographic history of the species at a larger geographic scale. Within this study, high level of genetic differentiation was observed along the Turkish coastal waters based on *cyt-b* gene, suggesting that TSS is a barrier to dispersal. The presence of two different subspecies was also corroborated with the mitochondrial DNA generated in this study, one distributed in Turkish coastal waters and Greece (*M. m. euxinus*), and the other one (*M. m. merlangus*) in the Atlantic, France.

Genetic Diversity and Phylogenetic Analysis of Gray Wolf and Red Fox from Different Geographical Sites in Turkey

İlkay Civelek¹, Nehir Sevim¹, Ayşe Mergenci¹, Çağan H. Şekercioğlu², Mark W. Chynoweth², Raşit Bilgin¹

(1) Boğaziçi University, Institute of Environmental Sciences

(2) University of Utah, Department of Biology

The gray wolf (*Canis lupus lupus*) and the red fox (*Vulpes vulpes*) are extremely mobile carnivores, which have spread globally to find new habitats and mates. These carnivores are the most significant predators within Canidae family, living in the Northern Hemisphere. Turkey is a country with wide ecological and geographical continuity in the middle Asia and the Middle East, at the intersection of three global biodiversity hotspots. Hence, the conservation of gray wolf and red fox populations in Turkey is very important. In our study, we evaluated 53 samples (49 gray wolves and four red foxes) by building neighbor-joining trees. We determined that the maximum diversity for gray wolf was in Northeastern Europe with nine distinct haplotypes. In addition, we observed that the number of haplotypes in Turkey (eight haplotypes in total) was relatively high. At the same time, our samples from Turkey (Kars and Karabük) formed groups with Eastern Asia, Eastern Balkans and Caucasus clades. For red fox samples, we have seen that the haplotypes showed mostly global distributions and we observed the haplotypes from Kars/Turkey clustered with these global haplotypes, without forming any distinctive clades.

Global Review of Phylogenetic Relationships of Brown Bear (*Ursus arctos*)

Ayşe Mergenci¹, Nehir Sevim¹, Çağan Şekercioğlu², Mark Chynoweth², Raşit Bilgin¹

(1) Boğaziçi University, Institute of Environmental Sciences

(2) University of Utah, Department of Biology

The brown bear is the most widely distributed Ursid, which has a broad geographic range in the Holarctic. So far, many studies on phylogeography of brown bear have focused on regional analyses or used limited number of samples from different regions. In this study, we aimed to make a comprehensive analysis and reexamine the phylogenetic and phylogeographic relationships of the global brown bear populations using 348 partial mtDNA control region sequences, from 23 countries, obtained from GenBank. We also used 63 newly generated sequences from two populations from Turkey, Yenice-Karabük and Sarıkamış-Kars, to see where their sequences fell in this global perspective. Maximum likelihood and neighbor-joining trees showed localizations (regional clades), potentially due to female philopatry, and some haplotypes from distant clades were grouped together, which may be explained by male dispersal. Caucasus has the highest number of haplotypes and formed four main clades based on neighbor-joining tree. Haplotypes from Kars and Karabük clustered with the Caucasus clade except one haplotype from Karabük, which clustered with the Balkan clade. One haplotype from Kars was identical with a haplotype from middle-eastern brown bear which was kept captive in a zoo and was identified as *Ursus arctos ocsacus*.

Comparison of Different Sampling Methods in Identification of Ciliated Protozoan Fauna in Lake Tersakan (Konya, TURKEY)

Nergis EMANET¹, Serhat ERTUĞRUL¹, Nazlı Deniz EYİCE ÇAĞATAY¹, Sırma ÇAPAR DİNÇER¹

(1) Hacettepe University, Faculty of Science, Department of Biology, Ankara, TURKEY

Introduction: Aimed to demonstrate difference of sampling methods in ciliate identification, at Lake Tersakan, a salt lake in Konya Closed Basin.

Materials and methods: Samples were collected monthly with direct sampling method, by using a planktonic net by means of artificial substrate. Morphologies were examined alive with DIC attachment light microscope. Photographs and measurements were materialized by Leica Application Suit V3 image analysis system. For the similarities, Sorensen and Jaccard indices were utilized.

Results: Throughout the study, 35 taxa were identified from the stations. In these stations, for the Sorensen index: both net and direct sampling method were similar 0.31, net and artificial substrate 0.36, direct sampling and artificial substrate indicate 0.41. Considering the Jaccard index: net and direct sampling method were similar 0.18, net and artificial substrate 0.22, direct sampling and artificial substrate give 0.26. Conclusion and discussion: The different sampling methods led to reach a different number of taxa, greatest number of taxa were reached with artificial substrate (22 taxa), followed by direct sampling (7 taxa) and net method (6 taxa). In terms of Sorensen and

Jaccard indices, it may be argued that these three methods do not sample fauna elements similar to each other, given that the values were at a range of 0-0.41. These results emphasized the importance of using different sampling methods in identification of ciliated single-cells, having and desiring different habitats in the aquatics.

Characterization of Gene Expression Reversals in Mouse and Its Comparison with Human

Hmit Izgi¹, Mehmet Somel¹

(1) Department of Biological Sciences, Middle East Technical University, 06800, Ankara, Turkey

Ageing, characterized by the progressive loss of functions in an organism, has not been fully understood at the molecular level. In a previous age-series transcriptome study done on human postmortem brain samples (Somel, 2010), it has been shown that majority of gene expression levels in ageing (after 20 years of age) reverse back to postnatal developmental stage's showing a reversal pattern. Furthermore, prevalence of gene expression reversals in human brain has been systematically investigated and confirmed using multiple datasets in a meta-analysis study by a colleague, previously. Now, we ask whether gene expression reversals are also observed in other species, namely in *mus musculus*. We have generated time-series RNA-sequence of 64 mouse samples representing lifespan of the mouse including from 2 days to 905 days, spanning 4 different tissues (cortex, liver, lung and skeletal muscle). We will first investigate the reversal pattern across different tissues in mouse samples. Then, we aim to search for common gene expression reversals between mouse and human.

Genetic variation in the invasive potato pest, *Leptinotarsa decemlineata*, populations based on insecticide resistance-related acetylcholinesterase2 gene

Ayça OZKAN KOCA¹, Burcu LAÇIN², irfan KANDEMİR²

(1) Department of Gastronomy and Culinary Arts, Faculty of Fine Arts, Maltepe University, Istanbul, Turkey

(2) Department of Biology, Faculty of Science, Ankara University, Ankara, Turkey

Potato beetle is the most important pest in potato and in other Solanaceae crops growing regions worldwide. Acetylcholinesterase, encoded by the *AChE* gene, is the molecular target of Organophosphate (OP) insecticides applied to potato beetle as well as to other agricultural pests. Different mutations have been previously identified in *AChE2* gene. Two major mutations (R30K and S291G) in *AChE2* gene have previously been identified in the potato beetle yield different level of OP resistance. To infer the genetic differences based on *AChE2* gene region associated with OP resistance in different beetle populations in Turkey, we analyzed sequences of a large fragment of 1037 bp polymorphically specified *AChE2* region and also combined data with the published sequences of potato beetle haplotypes that are available in the NCBI Genbank Database. Based on preliminary results, different haplotypes were found in Turkish populations. The sequences of *AChE2* region in different populations were aligned with 50 haplotypes from North America and Europe. The haplotypes in the studied populations of the different regions in Turkey were

commonly found across Europe. Our results based on mtDNA COI-COII gen region also demonstrated that the single haplotype found in Turkish populations was also the common haplotype found in European populations.

A natural antibacterial: *Impatiens balsamina* L. from Indonesia

Aioa Nurul Barokah, Humam Ari Wahyudin, Fatih Duman

- (1) Erciyes University
- (2) Gazi University

As a tropical country which is surrounding the equator, Indonesia has high biodiversity especially in plant such as decorative plants like Garden Balsam (*Impatiens Balsamina* L). Garden Balsam, An ornamental annual herb, 30-90 cm high. Leaves up to 15 cm long, lanceolate, acuminate, deeply serrate. Flowers large, axillary, showy, of various colours. Capsules spindle-shaped, tomentose. Flowers contain flavonoid pigments anthocyanins and 2-hydroxy-1,4-naphthoquinone. The antibiotic principle present in the flowers has been identified as 2-methoxy-1,4-naphthoquinone. Garden balsam is one of the plant that can be used for natural antibacterial or pesticide in the agricultural sectors. In this research, ethanol will be taken by extracting substances from flower part of garden balsam and then will be analyze the ability and the activeness using 25%, 50%, 75% 100% concentrate of extract to the plant. In the result, as the higher concentrate will be used, the higher of ability and activeness of antibacterial will be present.

Detecting differences in evolution rate between Human and Chimpanzees

Nursen DuhaAlioglu¹, Ekin Saglican, Etkay Yapar, Mehmet Somel

- (1) Hacettepe University

Protein-coding genes evolve at different rates. Although the main component for evolutionary rate difference is the level of purifying selection, positive selection can also drive differences in rates. Numerous studies have shown that a major factor that influences these rates is the tissue in which a gene is expressed in. Moreover, genes expressed in the same tissue could evolve at different rates even in close-related species, due to lineage-specific shifts in evolutionary pressure. One such example is testis- expressed genes in humans and chimpanzees. Genes expressed in the testis are known to be generally fast-evolving but could also show rate variation among lineages, depending on the mating behaviour. Our study attempts to investigate whether testis specific genes may be evolving under different rates in chimpanzees than in humans, because of the multi-male mode of chimpanzee mating. For this purpose, we use an alignment of all publicly available primate genomes, and use the PAML (phylogenetic analysis using maximum likelihood) software to estimate lineage-specific positive and negative selection levels on each gene. We will then compare testis-specific genes with those specifically- expressed in other tissues, to test two hypotheses: Does testis-specific genes evolve under stronger positive

selection in chimpanzee? Is there evidence for relaxation of constraint in testis-specific genes in the human lineage?

Understanding migration of sheep from its domestication center in Southeast Anatolia to West Anatolia by using of ancient mtDNA: Preliminary results

Onur Özer^[1], Dilşad Dağtaş^[1], Eren Yüncü^[1,11], Füsün Özer^[1], Ayşegül Birand^[1], Can Açıkan^[1], Ali Akbaba^[1,2], Rana Özbal^[3], Gülçin İlgezdi^[4], Can Yumni Gündem^[5], Evangelia Pişkin^[1], Mehmet Somel^[1], Yasin Gökhan Çakan^[6], İnci Togan^[1]

- (1) Middle East Technical University,
- (2) Ankara University,
- (3) Koç University
- (4) Ahi Evran University
- (5) Batman University
- (6) İstanbul University

Sheep domestication started in Southeast Anatolia about 10 000 years before common era (BCE) and spread to from there to other regions by demic diffusion of managed/domesticated sheep, cultural diffusion or both. To contribute to the understanding of the process of sheep domestication and spread within Anatolia, ancient sheep bones were collected from three archaeological sites; Barcın Höyük (Bursa, 6500-2300 BCE), Tepecik Çiftlik Höyük (Niğde, 6850-5800 BCE) and Yeşilova Höyük (İzmir, 6252-5800 BCE). Ancient DNA was extracted from these samples and 144 bp long fragment of mitochondrial DNA control region was sequenced. Genetic continuity between sheep populations from lower levels of Barcın (Barcın1,6500-6100 BCE)- upper levels of Barcın (Barcın2, 3800-2300 BCE), Tepecik Çiftlik - Barcın 1 and Tepecik Çiftlik - Yeşilova Höyük was tested assuming exponential growth, mutation rate range of 10⁻⁸ to 10⁻⁶ and effective population size range between 50 to 1500. Genetic continuity between Barcın 1-2 and Tepecik Çiftlik - Barcın1 could not be rejected. However, continuity was rejected for Tepecik Çiftlik - Yeşilova for low mutations rates and/or low population sizes. Our preliminary results suggest that West-central Anatolian sheep originates from another gene pool than the Central and North-west Anatolian sheep.

Elucidating the Patterns in Mid-Winter Waterfowl Surveys by Using Macrophyte Records and Lake Water Level Fluctuations

İbrahim Kaan Özgencil¹

(1) Middle East Technical University Department of Biology

Many Turkish lakes possess a global and local importance for waterfowl populations wintering in the Northern Hemisphere. Due to its mild climate, geographical location, and diverse ecoregions it has, Turkey hosts a substantial number of waterfowls during winters.

Water levels of freshwater lakes in Turkey fluctuate depending on factors such as their physical location, prevailing climate, and human use. Often, changing water levels lead to other changes in lakes including shifts between eutrophic and clear water states, and varying submerged macrophyte cover. These and other physical and biological changes are expected to affect waterfowl communities which depend on lake ecosystems to survive.

The objective of this study is to use Mid-Winter Waterfowl Surveys (MWS) to examine the effects of changing water levels, macrophyte coverage, and climate on wintering waterfowl communities in four Turkish freshwater lakes, namely, Lake Beyşehir, Lake Marmara, Lake Uluabat, and Lake Mogan. All four lakes are Important Biodiversity and Bird Areas with a total record of 72 wintering waterfowl species. Of these, three are known to be of near-threatened status, three vulnerable, one endangered, and one critically endangered, hence signifying the importance of this study.

To achieve the objective of the study, MWS data, macrophyte coverage data, plant macrofossil records from sediment cores and NAO index for the relevant years is studied. The outcomes of the study can assist scientists and conservationists design more efficient future conservation plans to preserve lakes as improved waterfowl habitats for wintering waterfowl species in Turkey.

The evolution of mental time travel

Alican Basdemir¹

(1) Bilkent University, Molecular Biology and Genetics

Mental time travel (MTT) is the faculty that allows us to mentally project backwards in time to re-live or forward to pre-live the events which is a subdomain of declarative memory (Suddendorf & Corbalis, 2007). The mental projection into the past is usually called 'episodic memory' which is a declarative memory concerning the experiences of events in spatiotemporal manner whereas future-oriented mental time travel is called 'foresight' in our ordinary language. Although there are many cases of false memories by which we lose our memories and insert new ones, we can construct a future imagination of events based the particularities of episodic memories like emotional attachments, the actors and the actions involved in the specific events (Loftus & Ketcham, 1994). Mental time travel has been considered to be uniquely human capacity

but it is still questionable whether other animals (i.e. nonhuman primates and scrub jays) have mental time travel or some sort of future-oriented cognition such as episodic-like memory (Suddendorf & Corballis, 2007) (Malanovski, 2015). To see whether it is unique to human animals or not, we have to identify a behavioral, non-verbal criteria for this capacity (Tomasello et al, 2005). Tulving originally proposed the *www criterion* which is about when, where and what components of an event (Tulving, 1975). Scrub jays are reported to be successful in tests involving this criterion (Clayton et al. 2001) (Dally et a. 2006). Then, he dropped the *www* criterion and adopted a notion called *autoneosis* which is subjective/phenomenological sense of time that is required for mental time travel and episodic memory (Tulving, 2002). Birds, rodents and primates have a capacity of future-oriented cognition and that of mental time travel in the past such as caching behavior and pilferage avoidance. However, none of these animals are reported to reveal a genuine capacity of MTT while they lack a set of subsidiary mechanisms such as high-level folk physics, self-reflective consciousness, recursive thought, representational theory of mind (ToM) although they have working memory, representational capacity of goal constellation (i.e. niche construction) and some sort of self-recognition (Baddeley, 1992) (Corballis, 1991) (Whiten & Suddendorf, 2001) (Povinelli, 2001) (Son & Kornell, 2005) (Hauser et al, 2002).. The current scientific research is not able to find any instances of MTT in other animals - a cognitively-expensive and error-prone capacity but it can be found in the future with more developed state-of-art methods. MTT provides us with highly flexible capacity by which one can imagine the future (i.e. alterations in the environmental regularities) and act accordingly which is evolutionarily advantageous.