

ECOLOGY AND EVOLUTIONARY BIOLOGY SYMPOSIUM TURKEY 2015

Oral Presentations:

August 6, 9:15

Collective action and the collaborative brain

Sergey Gavrilets*

Presenting Author's Affiliation: Department of Ecology & Evolutionary Biology, Department of Mathematics, Associate Director for Scientific Activities, National Institute for Mathematical and Biological Synthesis, University of Tennessee

Humans are unique both in their cognitive abilities and in the extent of cooperation in large groups of unrelated individuals. How our species evolved high intelligence in spite of various costs of having a large brain is perplexing. Equally puzzling is how our ancestors managed to overcome the collective action problem and evolve strong innate preferences for cooperative behaviour. Here, I theoretically study the evolution of social-cognitive competencies as driven by selection emerging from the need to produce public goods in games against nature or in direct competition with other groups. I use collaborative ability in collective actions as a proxy for social-cognitive competencies. My results suggest that collaborative ability is more likely to evolve first by between-group conflicts and then later be utilized and improved in games against nature. If collaborative abilities remain low, the species is predicted to become genetically dimorphic with a small proportion of individuals contributing to public goods and the rest free-riding. Evolution of collaborative ability creates conditions for the subsequent evolution of collaborative communication and cultural learning.

August 6, 10:15

Phylogenomic reconstructions predicts a single unique event leading to the origin of two icons of science Devils' Hole and Devils Hole Pupfish.

İsmail K. Sağlam*, J. Baumsteiger, M. Smith, J. Linares-Casenave, A.L. Nichols, S. O'Rourke and M.R. Miller

Presenting Author's Affiliation: Hacettepe University, Department of Biology

The Devils' Hole pupfish *Cyprinodon diabolis* is considered to be one of the most iconic species alive. It is both the most vulnerable vertebrate species alive is also an evolutionary anomaly having survived for thousands of years in the smallest habitat know to a vertebrate. However molecular studies show that *C. diabolis* is only 400 years old and most probably an artificial population. Since evolutionary dating depends on many assumptions our goal was to come up with a method for accurate estimation of the divergence of *C. diabolis* that would depend on as little assumptions as possible and that could also be predictive. Using RAD sequencing we interrogated 2/3 of the genome and reconstructed multiple independent phylogenomic trees. We then estimated divergence times under multiple scenarios by calibrating a single node and using only this prior information for predictive modeling. Our model has two novel strengths: 1) The reconstructed trees are unbiased estimates of evolutionary history and 2) parameters effecting divergence times are inferred and not fixed a prior. Our results not only capture the known mutation rate of vertebrates but predicts that *C. diabolis* is much older and is the same age as Devil's Hole (60ka). Hence our model predicts that a yet unknown single event led to the origin of both Devils Hole and *C. diabolis*.

August 6, 10:30

Age at maturity in 56 Atlantic salmon populations is controlled by a single large effect locus with sex dependent dominance

Tutku Aykanat*

Presenting Author's Affiliation: University of Turku, Department of Biological Sciences

Sea age at maturity in Atlantic salmon is a life history trait closely linked to fitness, and displays remarkable, temporally stable, variation among populations. By conducting a genome-wide association study (GWAS) using 210k SNPs on 1734 individuals from 58 wild populations from several European Atlantic salmon (*Salmo salar*) lineages, we detected a single major association with age at maturity. The association covered an 83kb region that encompassed two genes, one of which is involved in adipogenesis and has been associated with puberty in humans, and another that is important for sperm motility in mammals. This result is consistent with the prediction where larger effect loci are expected to evolve when demes with differential fitness optima have ongoing gene exchange, an inherent property of salmon populations. The signature of positive selection in this locus varied as a function of populations' sea age prevalence, suggesting ongoing selection for the optimum phenotype to maintain local adaptation. Finally, the genetic architecture of inheritance is consistent with sex dependent dominance which provides a genetic mechanism for buffering fitness conflicts by delaying maturity in females compared to males.

August 6, 11:15

Individual based modeling of future prevalence of Lyme disease vectors in Turkey

Ahmet Tuncer Durak*, H.N. Dalfes

Presenting Author's Affiliation: Istanbul Technical University, Informatics Institute

In recent years, modeling the effects of climate change on the distribution of infectious disease vectors has become a subject of considerable attention. However, due to the focus on population level modeling, and the generalizations required to express them, most of the local effects are absent in current incarnations. Although it is possible to decrease population size and rely on a metapopulation approach to increase granularity, it is more fruitful to follow this approach to its logical conclusion and employ individual based models. Individual based models, while computationally more demanding, are inherently able to incorporate local effects, such as microclimatic variability, and involve stateful individuals, such as disease carriers with altered modus operandi. For this study, we have constructed a framework for developing individual based models running on high performance computing clusters, exploiting parallel processing features, in order to handle higher computational demand. Then, using this framework, we adapted a population level model of Ixodidae ticks, a vector of Lyme disease, as proposed by Ogden et al., as an individual based model. Based on our model, supplied with climate data from Weather Research and Forecasting (WRF) Model, we predict a higher prevalence of Lyme disease in the future, for our pilot area, Thrace region of Turkey.

August 6, 11:30

Population genetics features of an invasive Tunicate time series samples in a central Californian marina

Arzu Karahan*, J. Douek, G. Paz and B. Rinkevich

Presenting Author's Affiliation: Middle East Technical University, Institute of Marine Sciences

Despite their simple appearance, the tunicates (accepted as ancestors group to the Chordata) are marine vertebrate animals. Some tunicates live as solitary individuals, but others replicate by budding and become colonies. Most adult tunicates are sessile and others swim in the pelagic zone. The earliest unequivocal species of tunicate appeared in the fossil records in the early Cambrian period. Over the past few decades, some tunicates have been invading coastal waters in many countries. We introduce here one

of the invasive colonial Tunicates *Botryllus schlosseri*. The *Botryllus schlosseri* population of the Elkhorn Yacht Club (EYC) harbor, CA, USA was repeatedly sampled over a 12-yr period (1996-2008), in addition to a single sampling (2001) of five other USA west-coast populations (from Washington and California). High numbers of unique alleles were identified. The most common microsatellite alleles, whilst being prominent throughout the entire period, fluctuated between the different sampling dates. Three clusters emerged when considering all 12 west-coast sites/samples according to the non-coding region. COI revealed two clades and 13 haplotypes (EYC). These results not only provide valuable insights into the dynamics of *Botryllus* dispersal at the local (EYC area) and USA but also reflect major changes within less than a year in microsatellite allele frequencies.

August 6, 11:45

Ecophysiology of *Reinekea forsetii* – the representative of a highly clonal and opportunistic gammaproteobacterium population recurrently associated with North Sea spring phytoplankton blooms

Burak Avci*, R. Hahnke, M. Chafee, J. Harder, B. Fuchs, R. Amann and H. Teeling
Presenting Author's Affiliation: Max Planck Institute for Marine Microbiology

In 2009 we investigated the response of bacterioplankton to the release of algae-derived organic matter during a spring phytoplankton bloom in the North Sea. We observed a swift succession of distinct bacterioplankton clades with different ecological niches, likely due to changes in substrate availability over time. Within the succession, *Reinekea* spp. rapidly increased to 16% relative abundance and subsequently vanished again. Explanations for this short-lived *Reinekea* bloom remained elusive. We isolated a *Reinekea* strain (*Reinekea forsetii* Hel1_31_D35) during the 2010 spring bloom at the same location. We studied this isolate to shed light on the ecophysiological role of *Reinekea* spp. in the environment using (i) in silico metabolic reconstruction, (ii) dedicated growth experiments, and (iii) reanalysis of metatranscriptome data. The extent of recurrence and the level of clonality of *Reinekea* spp. during the subsequent blooms (2009-2012) were also investigated using metagenome data and 16S rRNA gene tag sequencing. The *Reinekea* population recurred during the subsequent blooms, albeit with decreasing abundances and exhibited a high level of clonality. The representative isolate *Reinekea forsetii* Hel1_31_D35 is an opportunistic bacterium surviving in variable redox conditions and utilizing a broad substrate spectrum with effective phosphorous scavenging. It features free-living and attached life styles and can produce a toxin potentially used as a defence strategy or as a mechanism to actively acquire additional substrates.

August 6, 12:00

Functioning of marine chemosynthetic ecosystems: A biogeochemistry perspective

Mustafa Yücel*, D. Giovannelli, A. Dale, S. Sommer and N. Le Bris
Presenting Author's Affiliation: Middle East Technical University, Institute of Marine Sciences

Chemosynthesis occurs along natural biogeochemical gradients, where entire ecosystems are solely based on microorganisms tapping the energy from these gradients. While contributing to global elemental cycles, these ecosystems also create hotspots of biodiversity and present conservation challenges. Still, the fluxes of material and energy in these systems are poorly understood. We will first present results from the Baltic Sea where H₂S-oxidizing chemosynthetic mats cover extensive seafloor area that is intersected by a pelagic redoxcline. These bacterial 'carpets' mitigate the input of toxic hydrogen sulfide from sediments to bottom waters, with benefits to an already degraded Baltic Sea ecosystem. Secondly, we will focus on seafloor hydrothermal vent ecosystems, where entire communities of exotic invertebrates are based on a symbiosis with sulfide-oxidizing chemosynthetic bacteria. Besides the high chemosynthetic carbon production near vents, we found that the flux of slowly oxidizing nanoparticle iron from vents to the deep-sea is significant and this previously unrecognized iron source could eventually fertilize biologically unproductive open ocean areas. This presentation will conclude with brief remarks on potential

chemosynthetic habitats in the seas surrounding Turkey, with a focus on their biogeochemistry and conservation status.

August 6, 12:15

Impact of climate and nutrient enrichment on ecology of shallow lakes of Turkey using multiple approaches

Meryem Beklioğlu*, A. Çakıroğlu, N. Tavşanoğlu, E. Levi, A. Özen, J. Coppens, S. Brucet Balaman and E. Jeppesen

Presenting Author's Affiliation: Middle East Technical University, Department of Biological Sciences

Mediterranean climate with natural annual and interannual oscillations of wet and dry periods leads to changes in the water balance, which strongly affects the functioning of shallow lakes with implication for major ions and nutrient balances. Over forty shallow lakes spanning over 5 latitudes from the warm temperate north to the semi-arid to arid mid and south of Western Anatolian Plate of Turkey were sampled for physico-chemical, biological variables including fossil proxies in the sediment as well using well-established snap-shot sampling protocol as well as long-term monitoring two of the local lakes. The space for time substitute data showed that there are four relatively distinct groups of lakes according to altitude and latitudinal gradients. The coastal ones were more eutrophic compared to the upland ones, furthermore, southern coastal ones were also saline as well as eutrophic. On the other hand, northern upland ones were in clear water with macrophyte domination and large piscivorous fish. The saline and eutrophic ones were characterized with high net evaporation as well as temperature enhance as well as eutrophication. Long term monitoring data also showed the similar pattern that during the drought periods compared to wet periods salinity and eutrophication increased several-fold. Salinity and availability of phosphorus appeared to be the most important controlling factor for plankton, fish and macrophyte community both in contemporary and paleolimnological fossil data.

August 6, 12:30

Analyzing dynamics of a hybrid zone and testing endosymbiont hypothesis

Kahraman İpekdal*, C. Burban, T. Kaya, L. Saune and C. Kerdelhue

Presenting Author's Affiliation: Ahi Evran University, Department of Biology

We recently showed that ranges of the two species of the pine processionary moth complex, *Thaumetopoea pityocampa* and *T. wilkinsoni*, two dangerous forest pests in the Mediterranean Basin, contact in Turkey and few individuals bearing molecular evidences of a possible hybridization. However, the dynamics of the hybridization remained unsolved. In this study, we asked two questions: 1) What is the nature of the hybridization between the two species? 2) Do the endosymbionts contribute to this hybridization? We analyzed 13 microsatellite loci for 216 individuals from Turkey, Cyprus, Greece, Bulgaria, and Lebanon, in addition to sequences of COI, ITS-1 and photolyase genes. By using the entire data set we aimed to assess directionality and actuality of the hybridization. We also scanned the samples for endosymbiont bacterial flora for further explanation regarding the observed hybridization pattern. We found introgression of mt-genome from *T. pityocampa* and further evidences for hybridization in the nuclear genome. Microsatellite analyses revealed F2 and backcross generations but we could not find any F1 generation. Directionality of the mtDNA introgression and absence of the F1 generation are widely observed especially when an endosymbiont contributes to hybridization. However, we could not find any evidence for the presence of endosymbiont bacteria in the sampled populations. Our next research concern will be phenology and mating behavior of the parental species and the hybrids.

August 6, 13:45

Aggressiveness, reliable signaling and survival in a songbird

Çağlar Akçay*, E. Campbell and M.D. Beecher

Presenting Author's Affiliation: Virginia Tech University, Department of Biological Sciences

The evolution and maintenance of honest or reliable signaling has been a major question in evolutionary biology. The question is especially puzzling for a particular class of signals used in aggressive interactions: threat signals. Here we report a study on song sparrows (*Melospiza melodia*) in which we assayed males with playbacks in their territories to quantify their aggressiveness and aggressive signaling levels and asked whether these affect their survival on territory. We found that the effect on survival of residual signaling (signaling above or below the level predicted by their aggressiveness) depended on aggression levels such that among males with low aggression, those with higher residual signaling scores had higher survival. The residual signaling did not have a strong effect among high aggression males. Aggressiveness by itself did not have an effect on survival. These results present a first step in understanding the fitness consequences of honest signaling in aggressive contexts.

August 6, 14:00

Cytoneuclear discordance in the Marbled Crab, *Pachygrapsus marmoratus* (Fabricius, 1787) along the Mediterranean coasts of Turkey

Cansu Çetin*, A. Furman, R. Bilgin, E. Kalkan

Presenting Author's Affiliation: Boğaziçi University, Institute of Environmental Sciences

The marbled crab, *Pachygrapsus marmoratus* is a commonly found species in the Mediterranean and along the coasts of Turkey. Its distribution extends the north-eastern part of the Atlantic Ocean. Here, using putatively neutral and fast evolving microsatellite markers, we found high levels of genetic differentiation between populations of *P. marmoratus* constrained to the Mediterranean coasts and those distributed all around the Turkish coasts. The use of putatively neutral and fast evolving markers, microsatellites, enabled a clear discrimination of two populations of *Pachygrapsus marmoratus*, throughout the Turkish coasts. Both populations, however, share the same or have very similar mtDNA CO1 haplotypes. Connection between the Black Sea and the Mediterranean, which has been interrupted several times in the past, might have influenced the pattern detected in this study. Two relevant explanations for this observed cytonuclear discordance include retention of ancestral polymorphisms or gene flow after secondary contact. Although both of these processes might have contributed to this discordant pattern, the former is considered to be more likely because no geographical patterns were detected. Mitochondrial markers with faster mutation rates than CO1, in addition to microsatellites, and sampling individuals from the rest of the Mediterranean and from the Atlantic Ocean can be useful in resolving the pattern. Especially, obtaining samples from the African Mediterranean coasts can be crucial because they would shed light into the origin of common population. In addition, RAD sequencing might be effective in resolving the phylogeography of the species.

August 6, 14:15

A screen for the Bateson-Dobzhansky-Muller incompatibility regions in yeast

Gönensin Ozan Bozdağ*, E. Karakoç, D. Rogers, A. Nolte and D. Greig

Presenting Author's Affiliation: Max-Planck Institute for Evolutionary Biology

Biological species are described as reproductively isolated entities. Since mutations causing reproductive isolation (RI) are in various types, different models of RI have been proposed. One of these models, the Bateson-Dobzhansky-Muller (BDM) 'genic incompatibilities', has received great attention since 1930s. However, scarce evidence is mainly limited to *Drosophila*. Thus further extension of evidence to different taxa is needed. Yeast species, *S.cerevisiae* and *S.paradoxus*, are good candidates to test the BDM model.

When diploid hybrids undergo meiosis, only 1% of the offspring survive. By overcoming the anti-crossover problem between two species, we increased hybrid-offspring viability remarkably (up-to ~30%). Next, we genotyped over 300 euploid hybrid-offspring to discover the BDM regions between the two yeast genomes.

August 6, 14:30

Interaction between insulin signaling and exposure to males mediates female lifespan and fitness in *Drosophila melanogaster*

Irem Sepil*, P. Carazo and S. Wigby

Presenting Author's Affiliation: University of Oxford, Department of Zoology

Across taxa, similar factors mediate female lifespan: high levels of mating, reproduction, and insulin signaling all tend to reduce survival. Although lifespan extension in insulin-signaling mutants is typically accompanied by reduced fecundity, we know little about the potential interacting effects of mating rates and lifespan-mediating genetic pathways on survival and fitness. To Affiliation this, we varied male exposure levels in *Drosophila melanogaster* females with ablated insulin-like-peptide producing median-neurosecretory cells (mNSCs). Lifespan declined with exposure to males in both mNSC-ablated and control females, and mNSC-ablated females had increased lifespan, reduced early-life egg laying and increased egg-adult viability across all male exposure treatments. However, mNSC-ablated female lifespan extension was maximized under intermediate exposure to males (i.e. one in every four or eight days), but with no concomitant reduction in mating rate or lifetime reproductive success. In contrast, under high and low exposure to males, mNSC-ablated females had more modest lifespan increases and reduced mating rates and reproductive success. The results indicate interacting effects of insulin signaling and exposure to males on female life history, and suggest that the lifespan extension of mNSC-ablated females under "optimal" mating conditions can occur with little reproductive cost.

August 6, 14:45

Examining the evidence for MHC-dependent mate selection in humans and non-human primates

Jamie Winternitz*, J. Abbate

Presenting Author's Affiliation: Czech Academy of Sciences, Institute of Vertebrate Biology

Compounds of the Major Histocompatibility Complex (MHC) are integral for effective vertebrate adaptive immune response, and are also implicated as cues for sexual selection. The evidence for this is supportive of MHC-based preference for diverse and dissimilar mating partners, in a range of vertebrates from fish to non-human primates. However, the evidence for a similar role of these genes and the evolutionary benefits of their diversity in human mate choice has been more controversial. We review the results of 34 primary studies on MHC-mediated mate choice in humans and non-human primates in an effort to understand what processes may underscore, or belie, such differences. Both human and non-human primate studies show evidence of mate selection for MHC dissimilarity and diversity, with fewer results in support of mate selection for optimal diversity or for specific 'good genes'. In general, stronger support comes from female-choice studies as opposed to male-choice studies (though male preferences and choice are investigated less often). This study suggests that the majority of mate choice results from contemporary human studies is consistent with our evolutionary history, but also reveals that only in humans do we find evidence for preference for mates with similar MHC composition. Overall, we show that contextual nuances, namely population structure, multiple sensory cues that signal different information, and hormonal influences may explain the conflicting results observed for the role of MHC in human sexual preference, and argue for the exploration of such caveats in less well-studied systems to discern between general patterns and qualities unique to humans.

August 6, 15:00

Evolution of gene regulation: Dynamics of transcription factor binding site evolution

Murat Tuğrul*, T. Paixao, G. Tkacik and N. Barton
Presenting Author's Affiliation: IST Austria

Evolution has produced a remarkable diversity of living forms and organizations within and across populations/species on the earth. Evolution of gene regulation can be crucial for our understanding of overall phenotypic evolution and diversity. Sequence specific binding of transcription factors to DNA is an important mechanism determining gene expression levels. We use a biophysical model of directional selection on gene expression to estimate the rates of gain and loss of transcription factor binding sites (TFBS), under both point mutations and short indels. Our results show that rates of gain and loss of a single site are typically slow. Gain of a single TFBS is extremely unlikely under neutral evolution or weak selection: strong selection in a large population is needed for rapid evolution of a site, and even then, the initial sequence must be close to a functional sequence. The stationary distribution of binding sequences is also typically approached very slowly. These results for a single TFBS suggest that evolution of longer sequences (i.e. enhancer and promoter) are important to make TFBS evolution possible over realistic time scales, making the length of the available functional regulatory DNA another important parameter in TF binding evolution. This is confirmed by simulations, which also suggest that both cooperativity and the ghosts of previously functional sites can promote faster TFBS evolution.

August 6, 15:45

Genome wide data from Neolithic Anatolia bring new insights to the spread of farming

Ayça Omrak*, T. Günther, C. Valdiosera, P. Skoglund, H. Kiesewetter, W. Aylward, J. Stora, M. Jakobsson and A. Götherström
Presenting Author's Affiliation: Stockholm University, Department of Archaeology and Classical Studies

Anatolia played a key role in the Eurasian Neolithisation. The expansion from this area was driven west and northwards by migration, but we know little about the actual establishing of Neolithic societies in Anatolia, and what kind of population dynamics affected their gene pool. We present the first ancient genome wide data from a 6700 year old Anatolian excavated from a late Neolithic context in Kumtepe. We show that this individual display genetic similarities to the European Neolithic genepool, which anchors the Neolithic expansion in Europe to Anatolia. Further, the Kumtepe individual does not only contain the genetic element that is frequent in early European farmers, but also a component found mainly in modern-day populations from the Near East and Caucasus, suggesting gene flow into Anatolia in the late Neolithic. The scene presented by Kumtepe is compatible with gene flow into Europe from or through the Neolithic core area in Anatolia. And it is likely that this occurred early, perhaps just after the Neolithic core area had been established in southeastern Anatolia. This area was entangled in a complex web of contacts with other parts of the Near East, and the distribution of genetic variation in early European farmers suggests that the contacts with the European continent also remained and replenished with people's constant movements in and out of Anatolia.

August 6, 16:00

A study on swordfish populations of Turkey's Mediterranean and Aegean Seas, along with ancient samples by using mitochondrial DNA (mtDNA) and microsatellite markers

Eren Yüncü*, F. Özer, F.S. Karakulak, T.Z. Alıçlı, M. Gökoğlu, V. Onar and İ. Togan

Presenting Author's Affiliation: Middle East Technical University, Department of Biological Sciences

Swordfish (*Xiphias gladius*) is a globally and locally important food source. Swordfish populations in Turkish shores are considered as a part of the Mediterranean stock. In this study, genetic structure of the swordfish populations inhabiting in the shores of Turkey are analyzed in order to understand population demography and genetic relationship of these populations with the rest of the Mediterranean Sea. Possible genetic changes in these populations through time are examined by using ancient swordfish samples. Swordfish samples were collected from Turkish shores of Mediterranean/Northern Levantine Sea (n=42), and Aegean Sea (n=26), partial mtDNA control region was sequenced and eight microsatellite loci were employed to determine the genetic structure of these populations. Ancient DNA (aDNA) were extracted from swordfish samples unearthed from Yenikapı excavation (n=6), and same mtDNA region were analyzed in 5 overlapping fragments. mtDNA results evaluated comparatively with the data in literature, it is observed that Aegean and Northern Levantine populations are relatively distant from populations in the western Mediterranean and aDNA samples are genetically different than modern day samples. Additionally, microsatellite data show effective population size decrease for both Aegean and Northern Levantine Sea populations which can be results of overharvesting.

August 6, 16:15

Neanderthal introgression into Western Asian human populations

Recep Özgür Taşkent*, D. Alioğlu, Ö. Gökçümen and M. Somel

Presenting Author's Affiliation: Middle East Technical University, Department of Biological Sciences

An earlier study has shown that present-day non-Africans inherit a small percentage of their genomes (1 to 4%) from Neanderthals. This is consistent with a single pulse of admixture event between modern humans and Neanderthals that occurred 80.000-50.000 years ago when two species co-existed in the Middle East. More recent studies, however, have shown that East Asians share a higher proportion of their genomes with Neanderthals than do Europeans, a finding which is largely incompatible with a single pulse of admixture scenario. With even more studies reaching the same conclusion, the current consensus in the field is that the admixture history between Neanderthals and modern humans was complex, and involved at least two pulses of admixture events: one occurred in the Middle East before Europeans and Asians diverged, another occurred later in Asia. Given this complexity of human-Neanderthal admixture history, mixing in the Western Asia could have lasted for longer periods of time, even after humans spread to remote parts of Eurasia. A straightforward implication of this hypothesis is that present-day Western Asian human populations have a higher proportion of Neanderthal ancestry compared to Europeans. To test this hypothesis, we sequenced the whole-genomes of 10 present-day individuals from four different populations: three individuals with Western Asian ancestry (Druze), four individuals with North-Western European ancestry (Finn and CEPH), and three individuals with African ancestry (Pygmy). We then compared the introgression rates to these populations. Genetic analyses indicate that there is no difference in the amount of shared Neanderthal ancestry between current-day Western Asian and European populations. A direct interpretation of these results is that our initial hypothesis was wrong and interbreeding between Neanderthals and humans did not last in the Middle East for longer periods of time. However, another plausible explanation could be that initially higher rates of Neanderthal introgression in the Middle East have been diluted by subsequent immigrations to the region and emigrations out of the region. To further elucidate these findings, we will use the whole genome sequences of 16 present-day Turkish individuals, which were obtained by a previous study, and compare the introgression rates to Turkish population with modern European populations included in the 1000-genomes project.

August 6, 16:30

Species extinctions: prediction, understanding, prevention

Reşit Akçakaya*

Presenting Author's Affiliation: Department of Ecology and Evolution, Stony Brook University in New York

Research on species extinctions is developing in three directions: predicting species extinction risks; diagnosing the reasons for species endangerment; and optimizing conservation actions to reduce the risk of extinction. Despite much progress in using population dynamic models and rule-based systems such as the IUCN Red List to predict extinction risks, new threats such as global climate change present new challenges for identifying species vulnerable to extinction. A new approach integrating climate, niche and demographic models allows predicting the impact of climate change on species dynamics and testing methods used for identifying threatened species. A long-standing division in conservation biology is the qualitative analysis of the causes of past population declines (the "declining population paradigm") vs. the quantitative projection of future population trajectories (the "small population paradigm"). A new approach based on a Bayesian framework attempts to unify these paradigms, by diagnosing causes of declines quantitatively and integrating causal mechanisms into predictive modeling. These developments will enhance the predictive accuracy of population models and improve systems for identifying effective management and policy solutions, allowing realistic recovery planning that takes into account emerging threats such as climate change and infectious diseases.

August 7, 9:00

The Genetic Basis of Human Physiological Adaptation

Rasmus Nielsen*

Presenting Author's Affiliation: Department of Integrative Biology & Department of Statistics, University of California Berkeley

As the first anatomically modern humans spread around the globe, they had to adapt to a new and diverse set of environments. Today we can find the traces of this evolutionary process in the genomes of modern humans. In this talk, I will give two examples of human physiological adaptation to the local environment. The first example concerns physiological adaptation to the hypoxic environment of the high-altitude plateau of Tibet. Tibetans harbor genetic variants in two genes, EPAS1 and EGLN1, that affect hemoglobin production. Recently, we have shown that the adaptive EPAS1 haplotype was transferred into humans by introgression from Denisovans. I will discuss recent progress on understanding the process of adaptive introgression in humans and its role in altitude adaptation. The second example is adaptation of the indigenous people of Greenland, the Inuit, to life in the Arctic, including low temperatures and a diet based primarily on fish and marine mammals and rich in ω -3 polyunsaturated fatty acids (PUFAs). Studies of Inuit have been used to argue for the benefits of a high dietary intake of ω -3 PUFAs. We recently performed the first scan of Inuit genomes for signatures of adaptation and find extreme signals in several loci, relating to metabolism of fatty acids, particularly PUFAs. Using association mapping, we show that the selected alleles have strong effects on a number health-related phenotypes, and we replicate the findings in Europeans. Our results show that Inuit have unique physiological adaptations to life in the Arctic, in particular a diet rich in ω -3 PUFAs.

August 7, 10:00

Evolution of hunter-gatherers distinctive social structure, equality and cooperation

Andrea Bamberg Migliano*, M. Dyble, G.D. Salali, N. Chaudhary, A. Page, D. Smith, J. Thompson, J. Strodes, R. Mace and L. Vinicius

Presenting Author's Affiliation: University College London Anthropology

The social organization of mobile hunter-gatherers has several derived features, including low within-camp relatedness, fluid meta-groups and high cooperation with unrelated individuals. Here we explore how these distinctive social characteristics emerged, using agent based models to understand norms of coresidence, sharing and cooperation. We compare our results with data collected over 2 years amongst the Agta from the Philippines and the BaYaka from Congo on migration food sharing and cooperation. Our results suggest that pair-bonding and increased sex egalitarianism as well as generalized egalitarianism are central for the evolution of cooperation amongst unrelated individuals and may have had a transformative effect on human social organization.

August 7, 10:15

Sharing of plant knowledge and its implications on resilience in Mbendjele BaYaka hunter-gatherers of the Congo Basin

G. Deniz Salali*, N. Chaudhary, J. Thompson, M. Dyble, A. Page, D. Smith, R. Mace and A.B. Migliano
Presenting Author's Affiliation: University College London Anthropology

Transmitting knowledge of the use of plants is important for health and nutrition in small-scale populations. The wide sharing of adaptive knowledge, which contributes to an individual's chance of survival and reproductive success, may explain the resilience of current day populations who do not have access to modern medicine. Here, we study the use of 33 plant species in 219 Mbendjele BaYaka hunter-gatherers living in the northern rainforests of the Republic of Congo. We examine whether similarity in

sex, age group, camp membership and pairwise relatedness affect the extent of shared plant knowledge. In particular, we ask whether the type of information affects knowledge transmission. To this end, we categorized the types of plant uses into four groups: medicinal, social beliefs, foraging and material-making. We then investigated the knowledge sharing networks for each category among female-female, male-male and female-male dyads. We found that while knowledge of medicinal plant uses were shared more within families, knowledge on plant uses for foraging, social beliefs and making materials were shared regardless of the family membership. Our results indicate that transfer of knowledge in humans is affected by the function of information, which may have implications on the trajectory of cultural evolution, and resilience of human populations.

August 7, 10:30

Partner choice in symbiotic mutualisms: The role of population structure

Erol Akçay*

Presenting Author's Affiliation: University of Pennsylvania, Department of Biology

Mutualisms, where two species provide benefits to each other, are among the most important ecological interactions. Many mutualisms, such as the one between legumes and rhizobia, involve costly investments: traits that are directly costly to their carriers, and beneficial only to the partner species. For such costly investments to evolve, some sort of feedback mechanism must exist that more than recoups the direct costs. Multiple feedback mechanisms are known to operate in mutualisms, yet there is relatively little known about the interaction of these mechanisms with each other. Two feedback mechanisms in particular have long been recognized as important: (i) partner choice, where one mutualist preferentially interacts with, or rewards, more cooperative partners, and (ii) population structure among mutualists, which allows costly investments to evolve through kin- (or group-, depending on one's inclination) selection. Yet, how partner choice operates in structured populations, and how the interaction between the two feedback mechanisms affects the overall course of selection remains understudied. In this talk, I present a model that explores the effects of host partner choice on structured symbiont populations. I model two different interaction scenarios: one in which the host's investment into the symbiont is fixed and one where the host investment increases with the total benefit from the symbiont population, a condition termed partner fidelity feedback. In the former case, I find that population structure (i.e., increased relatedness amongst symbionts) generally reduces the benefit from partner choice to the more cooperative symbiont. This is because population structure reduces the available variation for the host to choose from. On the other hand, partner fidelity feedback works in the opposite direction, allowing returned benefits to go to relatives. The overall effect of partner choice depends on the balance of the two types of host investment. Interestingly, under both scenarios, partner choice and population structure can generate both positive and negative frequency dependence, with implications for the maintenance of variation among symbionts. These results point to the importance of integrating multiple selective mechanisms and suggest new empirical questions to probe the evolution and maintenance of cooperation in mutualisms.

August 7, 11:15

East African vegetation under the influence of tectonic uplift

İstem Fer*, B. Tietjen, F. Jeltsch and M.H. Trauth

Presenting Author's Affiliation: University of Potsdam, Plant Ecology and Nature Conservation

Once covered with mixed tropical forest environments, East Africa has been subjected to a progressive aridification as the region has been uplifted over the last Cenozoic resulting in substantial changes in its vegetation cover. The late Cenozoic vegetation history of East Africa is particularly of interest as it would set the scene for the contemporary events in evolution. For instance, a continuous forest belt in the region as opposed to fragmented forest patches it has today, might have provided migration and dispersal corridors for early hominins. In this study, we simulate the East African paleovegetation by forcing a

dynamic vegetation model with different climatic scenarios to investigate under which conditions a forest belt, preceding and connecting the modern patches, could have existed along the equator. We considered varying environmental factors namely, temperature, precipitation and atmospheric CO₂ concentrations. Our results show that all of these variables play a significant role in supporting the forest biomes and a continuous forest belt could have occurred under certain combinations of our experimental settings. With our current knowledge, it is likely that the region had hosted these conditions during the late Cenozoic and we demonstrate how fluctuating environmental conditions might be recognized on the biosphere level.

August 7, 11:30

Asia Minor: A pleasant refuge during tough times

Eren Ada*, U. Perktaş and H. Gür

Presenting Author's Affiliation: Hacettepe University, Department of Biology

Present-day distribution patterns of many species have been affected by rapid climatic oscillations. The climatic conditions of Late Quaternary have caused range expansion and restrictions for many species. To understand how species have responded to these conditions is important in terms of their biogeographical history. There have been three well-known for Europe so far, which are Iberian, Italian and Balkan peninsulas. These refugia provided suitable climatic conditions to many European species during the Last Glacial Maximum (LGM, 21 000 ya.). However, recent studies have indicated that Anatolia has also been an important refugium for European biota. We also suggest that Anatolia was one of the major refugia for many vertebrate species. In this study, we examined an amphibia species (*Triturus karelinii*) to present the refugia role of Anatolia during Last Glacial Maximum and today. We used advanced independent ecologic and phylogeographic analyses to support our hypothesis. First, ecological niche modelling (ENM) was developed to predict the geographic distribution of these species under reconstructed past (the Last Glacial Maximum) and present. Bayesian based historical demography analyses were used to understand expansion and contraction pattern for both species. At last, ecological niche modelling and phylogeographic results were used together to assess landscape genetic pattern of these species. All independent analyses showed that Anatolia is an important part of European biogeography and it covers a significant place in recolonized European biota.

August 7, 11:45

Plant-herbivore interactions in a forested rangeland

Burak Pekin*, B. Endress and M. Wisdom

Presenting Author's Affiliation: Zoological Society of San Diego

Ungulate herbivores are keystone species in grasslands and forests around the globe. However, much controversy surrounds the impact of ungulate herbivory on vegetation communities particularly in the western United States. We present findings of long term experimental research aimed at assessing the impact of native and non-native herbivores on vegetation dynamics. Responses of the forest understory in terms of plant species composition and diversity to prolonged herbivory at different intensities are discussed. The impact of cattle is compared to that of elk, a native ungulate herbivore of western North America, and interactions between grazing and forest management activities including prescribed fire and logging are explored. Our findings demonstrate that herbivory maintains plant diversity at recently burned and logged forest sites even at low intensities. While cattle and elk have differing impacts on plant guilds, their overall impact on native plant diversity is similar. Our findings suggest that ungulate herbivores have an important role in mitigating competitive species interactions within early seral vegetation communities associated with recent forest management activities, and that cattle or elk can be used to maintain the diversity of certain plant guilds following stand thinning and prescribed burning.

August 7, 12:00

A thorough investigation of the phylogeography and evolutionary history of *Miniopterus schreibersii* (Mammalia: Chiroptera) with new microsatellite data

Kanat Gürün*, J. Juste, S. Puechmaile, P. Hulva, R.K. Lucan, P. Presetnik, D. Hamidovic, C. Ibañez, A. Karataş, B. Allegrini, P. Georgiakakis, D. Scaravelli, M. Uhrin, H. Nicolou, M. Abu-Said, Z.L. Nagy, S. Gazaryan and R. Bilgin

Presenting Author's Affiliation: Boğaziçi University, Institute of Environmental Sciences

Miniopterus schreibersii is a cave-dwelling bat species that has a sub-cosmopolitan distribution and consists of lower taxa, multiples of which have been elevated to species level recently, and is therefore well suited for phylogeographic investigations at large geographic scales. In this study, 396 samples that were collected from 38 populations and 12 different geographic regions that span the entire range of *M. schreibersii* were analyzed using nuclear microsatellite markers, to investigate the taxonomy, evolutionary history and conservation of this species. A previous study that made use of 6 microsatellite markers was expanded with the use of 6 additional markers and eventually, the phylogeography of the species across its whole distribution area was examined in greater detail, thus increasing the body of knowledge regarding its phylogeographic history significantly and providing the necessary validation of the studies that only made use of mitochondrial markers. The examination of these nuclear loci confirmed the findings of previous studies, including the pattern of local differentiations previously detected in mitochondrial DNA, and provided a more complete picture of the species' genetic distribution. Significant differentiations of the nuclear DNA were detected between all geographical regions, including Anatolia, Thrace-Balkans, North Africa, Russia, France, and Iberia.

August 7, 12:15

Intraspecific lineages might respond differently to climate change: Evidence from past and present range expansion of Kuhl's Pipistrelle

Emrah Çoraman*, A. Furman

Presenting Author's Affiliation: Boğaziçi University, Institute of Environmental Sciences

Kuhl's Pipistrelle expanded its distribution range drastically in the last couple of decades. This expansion is mainly in the east, where the populations are attributed to a distinct lineage. In order to evaluate how *Pipistrellus kuhlii* responds to climate change and how this response differs among lineages, we analysed its phylogeographic structure in association to ecological niche models (ENMs). We found that *Pipistrellus kuhlii* is composed of three deeply diverged lineages, which evolved in separate Pleistocene refugia located in Iberia, the North Africa, and the Middle East. These clades differ on mtDNA and microsatellites, but are not reproductively isolated. Comparing both the current and the past predictions of ENMs with the observed genetic diversity patterns indicates that the clades have distinct niche identities, which were conserved for long periods of time. Nevertheless, we show that the future predictions of the 'clade only' models are consistent with the currently observed population expansions rather than the 'species' models. Our findings indicate that incorporating phylogeographic information into ENMs is crucial for predicting species' response to climate change.

August 7, 12:30

Genetic impact of anthropogenic factors on honey bee diversity in Turkey

Mert Kükrer*, M. Kence and A. Kence

Presenting Author's Affiliation: Middle East Technical University, Department of Biological Sciences

Intense admixture of honey bee (*Apis mellifera* L.) populations is mostly attributed to migratory beekeeping practices and replacement of queens or colonies with non-native races or hybrids of different subspecies. These two practices are also heavily carried out in Turkey. Here, we carried out an analysis of population structure of Turkish honeybees sampled from six different regions (n = 250) in order to test the genetic impacts of migratory beekeeping, colony trade and isolated regions. A total of 29 microsatellite markers were used in four multiplex reactions. The genetic impact of migratory beekeeping was demonstrated based on a comparison of assignment probabilities of individuals to their geographic populations where migratory colonies showed less fidelity. The effects of queen and colony trade were revealed by the presence of introgression from the highly commercial Caucasian bees. Comparison between regions that are either open to migratory beekeeping or not let us evaluate the status of isolated regions as centers of limited gene flow and showed the importance of establishing such regions. Despite signs of gene flow, our findings confirm high levels of geographically structured genetic diversity of four subspecies of honey bees in Turkey and emphasize the need to develop policies to maintain this diversity.

August 7, 13:45

Dispersal in a bottle: movement ecology of *Tetrahymena thermophila* ciliates

Nicolas Schtickzelle*, F. Pennekamp

Presenting Author's Affiliation: Université catholique de Louvain, Biodiversity Research Centre

Individual movement is a universal feature of animal life with wide implications for the ecology and evolution of species. Understanding of what drives movement at the level of the individual and how it influences large-scale processes is a long-term goal in ecology. Variation in the movement phenotype of individuals can be influenced both by genetic and environmental sources and disentangling their effects is crucial for understanding the evolution of individual movement and its consequences at the population scale. Experimental studies of microscopic movement and resulting processes at the population level can provide such insights, but are so far rather rare. We experimentally studied movement and dispersal using 44 genotypes of the actively dispersing unicellular, aquatic model organism *Tetrahymena thermophila*. We found substantial genetic variation in the movement behavior among but also within genotypes. By using individual-based movement simulations we show that movement and dispersal are indeed tightly linked and strongly driven by genetic differences. However, environmental differences considerably improved model predictions resulting in the full movement model accounting for more than 50% of variation in observed dispersal. We finish by interpreting the genetic and environmental sources in the context of the movement ecology paradigm.

August 7, 14:00

Transcriptome sequencing reveals population differentiation in gene expression linked to functional traits and environmental gradients in South African shrub *Protea repens*

Melis Akman*, J.E. Carlson, K.E. Holsinger and A.M. Latimer

Presenting Author's Affiliation: University of California, Davis, Department of Plant Sciences

Understanding environmental and genetic mechanisms underlying local adaptations along a species' range is crucial for predicting species' responses to climate change. Combining mRNA-seq with common garden studies on populations spanning geographical and environmental gradients holds promise for identifying such mechanisms. South African shrub *Protea repens* displays diverse phenotypes along

drought and temperature gradients. In order to reveal associations between population level gene expression profiles with phenotypes and source site climate gradients, we grew plants (in a common garden) collected at 19 populations along this species' range. We found strong correlations between gene networks enriched for growth-related pathways and source site winter temperature and common garden leaf area, stem diameter and height. Other gene networks with enrichments for photosynthesis pathways correlated with source-site precipitation and leaf morphology. Our results strongly suggest this species displays population-level differences in gene expression that have been shaped by source population site climate, and that are reflected in locally adaptive trait variation. Additionally we performed a dry-down experiment on select *P. repens* populations in order to reveal differential responses in gene expression, morphology and physiology. Results of this study will also be presented.

August 7, 14:15

Fire-dependent seed germination in rare annual *Chaenorhinum rubrifolium* (Scrophulariaceae)

Çağatay Tavşanoğlu*, G. Ergan, S. Çatav, K. Küçükakyüz, G. Zare and B. Özüdoğru
Presenting Author's Affiliation: Hacettepe University, Department of Biology

Fire-related germination in woody species is well documented in the Mediterranean Basin (MB), but the effects of fire on the germination pattern of annual Mediterranean species are still unclear. We studied the germination response of *Chaenorhinum rubrifolium*, a rare annual species, to fire-related cues such as smoke, heat shock, nitrate, karrikinolide (KAR1), and mandelonitrile (a cyanohydrin analogue) under constant dark and light conditions. We also used many combinations of these treatments. Germination data in treatments were statistically compared with the corresponding control with analysis of deviance (GLM). Zero germination in controls indicated that *C. rubrifolium* has high-level seed dormancy. Smoke solutions, KAR1, mandelonitrile and nitrate significantly increased germination percentage, up to 33% in smoke and 47% in KAR1 applications under light conditions. The combinations of heat shocks + smoke treatments and KAR1 + mandenonitrile treatments further increased the germination percentage to 43% and 61%, respectively. The results suggest that germination is positively affected by multiple fire-cues, and these cues have synergetic effect on germination in *C. rubrifolium*. Result of our study is the first record of KAR1- and mandenonitrile-stimulated germination in MB. Our study supports the idea that fire is an important germination agent in annual species in MB.

August 7, 14:30

Biological Invasions: Many impacts, much research, and some controversies

Daniel Simberloff*
Presenting Author's Affiliation: Department of Ecology & Evolutionary Biology, Institute for Biological Invasions, University of Tennessee

Modern invasion biology is a very young field, beginning in the 1980s. Nevertheless, we now know of drastic ecological and/or economic impacts of hundreds of invaders. They eat native species, overgrow them, outcompete them, infect them, and have myriad other impacts. Impacts that affect entire ecosystems have been increasingly documented, particularly as ecological research on aboveground-belowground interactions has proliferated. Evolutionary research has increasingly become a prominent part of invasion biology, with many examples of invasive species hybridizing with native ones and changing their gene pools; sometimes these hybrids are particularly invasive. The past three years have seen several criticisms of the field of invasion biology. Among other bones of contention, critics charge that the field is infected with xenophobia, claim that the damage caused by biological invasions is overblown, and argue that, even if effects of biological invasions are very substantial, we cannot do much about the phenomenon in the face of globalization, so we should not waste our resources trying. I will review progress in the field and discuss the various arguments and their impacts on both science and policy regarding invasions.

Poster Presentations:

1.

Information theoretic approach for the DNA size and the protein length relation

Yekbun Adıgüzel*

Presenting Author's Affiliation: Istanbul Kemerburgaz University, Faculty of Medicine

Insights of the existing discussions on the evolutionary forces that are shaping the proteins' sizes and distributions in the modern organisms need to be broadened. For this purpose, an information communication theory based approach for the relation of the DNA and protein length is aimed to be presented here. DNA and protein are the molecules that carry information, the quantity of which can be calculated and related to the Shannon's entropy. If the information entropies in DNA and protein are assumed to be preserved, the equalization or the balancing can be achieved by introducing a protein length dependent variable in the calculations for the protein. The presented attitude is in line with the requirement of introns and the higher variation in the proteins' lengths due to the presence of introns in the eukaryotic genome.

2.

Characterization and molecular evolution of the serum albumin gene of the pool frog, *Pelophylax lessonae*

Çiğdem Akın Pekşen*, J.H. Grau, A.J. Poustka, T. Uzzell, C.C. Bilgin, J. Plötner

Presenting Author's Affiliation: Middle East Technical University, Department of Biological Sciences

Serum albumin (SA) is the most abundant plasma protein, and since SA is a highly polymorphic protein, it has been often used as a genetic marker for systematic, phylogenetic, and population genetic studies in western palearctic water frogs (WPWF). Here we report the complete sequence of the pool frog (*Pelophylax lessonae*) SA gene including all exons, all introns, the upstream sequence of the 5' UTR and the downstream sequence of the 3' UTR. By aligning the *P. lessonae* albumin gene with albumin genes of closely and distantly related amphibian species, potential regulatory elements and functional motifs in the 5' UTR and 3' UTR were documented. Comparison of exon and intron lengths of the water frog with other vertebrate species revealed strong length conservation in protein coding albumin exons among distinct vertebrate species, but large variation in intron lengths. Search of the entire scaffold for retroelements revealed several distinct classes of truncated retroelements upstream of the 5' UTR, downstream of the 3' UTR, and within individual albumin introns. These could be important drivers of albumin gene evolution. Phylogenetic analysis of WPWF (*P. lessonae*, *P. bergeri*, *P. ridibundus*, *P. cf. bedriagae*, *P. epeiroticus* and *P. shqipericus*) based on nucleotide sequence of protein-coding albumin exons supported previous findings of mtDNA and the first intron of the SA gene.

3.

Some population characteristics of Western Caspian Turtle, *Mauremys rivulata* (Valenciennes, 1833) from Gökçeada (Imbros), Turkey

Y. Bayrakçı, Dinçer Ayaz*, B.Y. Yakın, K. Çiçek, C.V. Tok

Presenting Author's Affiliation: Ege University, Faculty of Science, Department of Biology, Zoology Section

In this study, we present data on the population of Western Caspian Turtle, *Mauremys rivulata*, from Gökçeada located at the westernmost of Turkey. The species is distributed almost all around the island, particularly in the western part, with a very low density. From the healthy population in Büyükdere, the largest river of the island, a total of 73 individuals were captured and marked; population size was calculated as 135 individuals (SE = 11, range = 117-161) and density was calculated as 68 indiv./ha. Moreover, *Emys orbicularis*, another fresh water turtle species which the species cohabits with in West Anatolia, was observed again on the island after years. Tourism, creeks with irregular flow regime and

holding water in the dams negatively affects populations of aquatic species, primarily *M. rivulata* on the island.

4.

Putative function of mitochondrial tandem repeat sequences in stem borers (Cephididae: Hymenoptera)

Hasan H. Başbüyük*, M.N. Ördek, S. Durel and I. Sarı

Presenting Author's Affiliation: Cumhuriyet University, Department of Biology

Animal mitogenomes have a control region possessing an essential regulator segments in replication and transcription. Even if the animals have a compact and conserved mitogenomes, size variation is particularly common in insect due to the high rate of tandem repeat sequences in control region. Certain tandem repeat pattern in different lineages or higher taxonomic groups is considered as a result of convergent evolution. However, a considerable length variation is identified in mitochondrial control region of insects, even between closely related taxa. To test this, the mitochondrial control region of six species in Cephini are investigated. Multiple PCR applications revealed that the length variation of fragments ranges from 3500 to 6000 bp. The short tandem repeat length is between 100 and 140 bp with 10-17 repeats while the long tandem repeat length ranged from 300 to 320 bp with 3-5 repeats. The sequence information of repeats are highly divergent within the genus but almost conserved in the species. This notion is explained by concerted evolution which suggests a tendency to homogenization within the species due to their regulatory function. It is thought that these tandem repeats may be functional as replication fork barrier in insects. From ecological point of view, the concerted evolution acting on tandem repeats may contribute to diversification of insects.

5.

The role of natural and anthropogenic drivers shaping current fire regimes in the Mediterranean-type ecosystems of Turkey: A project proposal

İsmail Bekar*, Ç. Karacaoğlu, M. Türkeş, Ç. Tavşanoğlu

Presenting Author's Affiliation: Hacettepe University, Department of Biology

Extreme weather and climate events are of an important place in the occurrence of fires; however climate is rarely linked to fire regimes, especially in the Mediterranean Basin. In a project proposal, we intended to study the relative role of natural and anthropogenic factors shaping the current fire regimes in the Mediterranean biogeographical region of Anatolia. We hypothesized that natural factors explain the most of the variance in recent fire regimes in the study area, but human activities contribute less. Moreover, we expect a positive relationship between the climate change and variability and fire regime changes at local scale. Fire data will include both the ground fire records of the General Directorate of Forestry and satellite fire records of NASA. A total of 24 bioclimatic variables will be used to investigate the effect of the climatic factors on fire regimes. Road network, demographic data, agriculture and husbandry activities will be used to investigate the effect of anthropogenic factors on fire regimes. Other natural variables will be physical geographic data and forest/vegetation structure. The data will be analyzed by generalized linear models, principal component analysis, and regression techniques. The results of the project will contribute to the up-to-date discussion on whether fire regimes are anthropogenic or natural origin in the Mediterranean Basin.

6.

Ecological reconstruction of trophic state of Turkish shallow lakes using diatom sub-fossils

Gizem Bezirci*, S. Sayer, A. Çakıroğlu, E.E. Levi, H. Bennion and M. Beklioğlu

Presenting Author's Affiliation: Middle East Technical University, Department of Biological Sciences

Palaeolimnological records show that the intensity of human impact on lake ecosystems has been much greater over the last 200 years. Diatoms, being the most common types of phytoplankton in freshwaters, are widely used for detecting past environmental changes in lakes due to their well-preserved silica based shells, different environmental requirements and fast responses to environmental changes. 55 Shallow

lakes in Turkey were sampled along a latitudinal gradient for water chemistry and sediment samples using space for time approach. Redundancy Analysis (RDA) revealed that conductivity, total phosphorus (TP) and percent plant volume inhabited (PVI%) are the most important factors affecting the diatom distribution of the lakes and the first two axes captured about 78.5% information of species-environment correlations. Considering the acquired surface sediment diatom data, Lakes Karagöl-İzmir and Karagöl-Bolu were selected for ecological reconstruction of past lake status. It is found that Lake Karagöl-İzmir is dominated mostly with eutrophic and planktonic taxa till 1970's. Between 1970-1950, benthic diatoms became abundant that might refer to water level changes. In Lake Karagöl-Bolu, the distribution of the diatoms until 1900's shows the characteristics of shallow, nutrient rich turbid water. After that period the lake become abundant with benthic plant associated taxa.

7.

Cataloging the genetic diversity of bats (Order: Chiroptera) in Turkey

Zirve Yiğit, Ahmet Karataş, Raşit Bilgin*

Presenting Author's Affiliation: Boğaziçi University, Institute of Environmental Sciences

Turkey has three biogeographical regions namely; Anatolian, Mediterranean and Black Sea regions. Due to the high variety of different ecosystems, biological diversity is very high compared to the biodiversity of other countries in the temperate zone (IUCN). In this study, 26 bat species from Turkey and surroundings were investigated with the cytochrome-oxidase subunit I (CO1) barcoding method. Twelve CO1 sequences from Barcode of Life Database (BOLD) and Genbank, and 134 specimens from Turkey and surrounding regions were analyzed together. We found that *Eptesicus serotinus/nilssoni* species complex has high intraspecific divergence (4.25%) and five other species (*Myotis capaccinii*, *Pipistrellus pipistrellus*, *Rhinolophus euryale*, *Rhinolophus ferrumequinum*, *Rhinolophus hipposideros*) have phylogeographic splits and are good candidates for discovery of subspecies/species for the Turkish population. We found *Tadarida teniotis* to show high intraspecific divergence ; sequences from Genbank and BOLD fell into one of the two main clades in BOLD database, whereas Turkish samples fell into the other clade. *Plecotus macbullaris* showed phylogeographic split between the Turkish population and other populations from Iran and probably from Far East. We conclude that, at least for bats, CO1 barcoding is a promising method for discovery of new taxa and comparisons with previous studies reveal that further studies are needed to get a clearer picture of subspecies distribution for these species in Turkey.

8.

Future water availability of the largest freshwater lake of Turkey is at great risk

Tuba Bucak*, D. Trolle, H.E. Andersen, H. Thodsen, A. İ. Çakıroğlu, Ş. Erdoğan, M. Beklioğlu

Presenting Author's Affiliation: Middle East Technical University, Department of Biological Sciences

Lake Beyşehir, the largest freshwater lake of Turkey is under the stress of climate change in addition to heavy use of water for irrigation. In this study, Soil and Water Assessment Tool (SWAT) catchment model was used to model the current and future state of the catchment processes and outputs of SWAT model linked to support vector machine regression (ϵ -SVR) model to model future water levels of Lake Beyşehir. According to our results, climate change projections caused a noticeable temperature increase and precipitation decrease in the catchment which resulted in enhanced evaporation and reduced total runoff to the lake while the effects of land use was minor. MPI-ESM-MR model with RCP 8.5 scenario predicted the most dramatic decrease in total runoff up to 52%, while HadGEM2-ES model with RCP8.5 scenario predicted 24% decrease in total runoff at the end of the century. According to ϵ -SVR model, changes in hydrological processes caused a dramatic water level reduction for all the scenarios though MPI-ESM-MR model outputs were more prominent which showed that lake may dry out 2040s with the current outflow regime. However for HadGEM2-ES model, in 2070s and late 2090s extreme water level reduction was predicted. Our results imply that Lake Beyşehir can be under the risk of drying out if current outflow regulation is maintained.

9.

Gender determination in 77 bird species using CHD gene

Emel Çakmak*, Ç. Akın Pekşen, C.C. Bilgin

Presenting Author's Affiliation: Middle East Technical University, Department of Biological Sciences

Because many bird species are monomorphic or only sexually dimorphic in adult stages, it is difficult to determine their sexes, which cause significant problems in population and conservation studies; such as defining sex ratios, demographic studies, and captive breeding of endangered species in the field or in zoos. As aviculture is frequently developing, even individual owners wish to detect sexing of birds. Other methods of avian sex determination are generally based on behavioral and morphological observations. In DNA-based sexing, highly conserved CHD gene (chromo-helicase DNA binding gene) located on the W chromosome and its homologue on the Z chromosome were amplified using specific primer set, which gave an apparent single band in males and two bands in females on agarose gel because of length differences in intronic regions within this gene from 230 samples from 77 avian species. Since there is a high degree of conservation even among distant species, the CHD gene provides an opportunity for developing a universal method for molecular bird sexing, which is very reliable, fast and cost-effective method.

10.

Age and sex related change in the heritability of locomotor behaviour in *Drosophila melanogaster*

Hazal Çalışkan*, B. Efecik, A. Turan, M. Dizemen, N.C. Özcan, O. Düzgün, D. Aygün, E.D. Özsoy

Presenting Author's Affiliation: Hacettepe University, Department of Biology

Locomotor behaviour is a crucial and fitness related trait which has a polygenic basis. Here in this study we estimated basic quantitative genetic parameters of locomotion using isofemale lines of *D.melanogaster*. Negative geotaxis and startle response were used as component traits defining locomotion. We have estimated broad and narrow sense heritabilities and evolvabilities for three different age groups for both sexes. Our results show that these indices change in age and sex dependent manners, differently for geotaxis and startle response. We discuss the findings in light of the plasticity of the response of genetic variation for locomotor behaviour and its evolutionary implications."

11. will be presented as a talk

12.

Does the red-eared slider (*Trachemys scripta elegans*) breed in Turkey?

Kerim Çiçek*, D. Ayaz

Presenting Author's Affiliation: Ege University, Department of Biology

Here, we firstly report reproductive feral population of the red-eared slider (*Trachemys scripta elegans*) from Southern Anatolia (Anamur, Mersin). We detected a female laying 15 eggs in the morning of July 03, 2012 and a female digging nest on May 16, 2015. Moreover, two hatchlings 26.1mm and 28.4mm in length were observed on September 03, 2013. According to our observations, the Mediterranean coast of Turkey has the potential to provide the requirements of the species. The impact of the red-eared sliders on native turtles was competition for food and basking site.

13.

The complete mitogenome in *Corynis lateralis* (Hymenoptera: Cimbicidae)

Özgül Doğan*, B. Temel, B. Aydemir, E.M. Korkmaz, H.H. Başbüyük

Presenting Author's Affiliation: Cumhuriyet University, Department of Molecular Biology and Genetics

Mitogenome information contributes greatly to the studies of ecology and evolution. Such information can be used in understanding of Hymenoptera, one of the most important insect orders for their diverse life strategies and species richness. However, mitogenome information has been reported for only seven species of Symphyta suborder. Here, the mitogenome of *Corynis lateralis* is characterized for better understanding of its life strategy. The mitogenome is accomplished by new generation sequencing and *Allantus luctifer* is used as a reference. The dataset was annotated and characterized. The secondary structures of rRNA were predicted. Replication origin and known motifs were searched in the control region. The mitogenome content is consistent with most of previously determined animal mitogenomes. The most genes are located on the J strand except for four PCGs, two rRNAs and eight tRNAs. The nucleotide composition is A + T biased similar to other hymenopteran genomes. All the tRNA genes display a typical clover-leaf structure of mitochondrial tRNA. As a result, the motifs and organization of genes appears to be conserved in Symphyta when compared with Apocrita suborder.

14.

Investigation of tumor suppression systems in long-lived mammalian transcriptomes

Melike Dönertaş*, Ö. Gizlenci, M. Somel

Presenting Author's Affiliation: Middle East Technical University, Department of Biological Sciences

Each proliferating cell in the body means a risk for cancer development. As lifespan increases, time to accumulate mutations increases and suppression of somatic cancer evolution becomes challenging. However, there is no apparent correlation between lifespan and cancer across species - a phenomenon termed "Peto's Paradox". Diverse tumor suppressor mechanisms in different species may be contributing this phenomenon. Another possibility is that species with longer lifespan use common, conserved tumor suppression systems more efficiently. Here we addressed this latter hypothesis by analyzing liver transcriptome data from 23 diverse species of mammals. We compared expression differences among species with different lifespans, with gene expression changes in early stage cancer (ESC) in the same tissue. We find that genes upregulated in ESC have significantly lower expression levels in species with longer lifespans, compared to closely related but short-lived species. However, genes downregulated in ESC, as well as genes with known tumor suppressor functions, did not show higher expression in species with longer lifespan. We aim to continue the study by including two more tissues and using phylogenetic contrasts for comparisons among species. Our findings could contribute to resolving the paradox of lifespan and cancer incidence.

15.

A preliminary intra phylogeny of the genus *Sideritis* by morphology

Canan Dülgeroğlu*, O. Ünal

Presenting Author's Affiliation: Akdeniz University, Department of Biology

Genus *Sideritis* is ranged in Western Palaearctic by 193 species classified into two subgenus and seven sections. Its species diversity mainly concentrated in Mediterranean basin. The subgenera and sections in the genus were established by traditional taxonomy and their monophyly has not been tested. Using 19 representative species from seven sections belonging to subgenera *Sideritis* and *Marrubiastrum* we aimed to test monophyly of the subgenera. We defined and coded 26 morphological characters and applied a parsimony analysis choosing a *Stachys* sp. as outgroup. The majority rule consensus tree of the 9 equally parsimonious trees suggested the following relationships: ((((((*S. montana* + (*S. lanata* + *S. romana*) + (*S. barbellata* + (*S. discolor* + *S. cretica* + (*S. macrostachys* + (*S. nutans* + *S. gomerae*)))))) + *S. stachydioides*) + *S. scardica*) + *S. condensata* + (*S. sipylea* + (*S. cilicica* + (*S. hyssopifolia* + (*S. glacialis* + (*S. osteoxylla* + *S. bourgeana*)))))) + *S. syriaca*) + *Stachys* sp.. In the light of these data, the following main conclusions were raised: (i) Neither subgenera nor sections in the genus *Sideritis* are monophyletic, (ii) most of characters that were used for descriptions of subgenera and sections are homoplastic and (iii) as species in the *Empedoclia* section occupy the basal branches of the each main clades possibly this section represent ancestor.

16.

Impact of nutrient and water level changes on submerged macrophytes along a latitudinal gradient: A Pan-European mesocosm experiment

Zeynep Ersoy*, T. Bucak, E. Levi, M. Beklioğlu, E. Papastergiadou, K. Stefanidis, T. Nöges, T. Feldmann, J. Hejzlar, M. Sorf, D. Baho, C. Trigal, U. Scharfenberger, A. Mahdy, M. Søndergaard and E. Jeppesen

Presenting Author's Affiliation: Middle East Technical University, Department of Biological Sciences

Climate warming is affecting freshwater ecosystems by causing temperature rise, increased precipitation and nutrient runoff in Northern Europe, while decreased precipitation and intensified drought in Southern Europe and Mediterranean region. We conducted a controlled Pan-European mesocosm experiment in six countries (Sweden to Greece) along a latitudinal gradient to elucidate the effect of climate on macrophyte growth in shallow lakes with contrasting depths and nutrient levels (from May to November 2011). Water level didn't change much in north; whereas more than 40 cm drop occurred in south, having higher mean air temperatures (> 18 oC). Results indicated a significant effect of depth- nutrient and temperature-nutrient interactions on macrophyte growth (PVI%). Low nutrient levels in shallow mesocosms had higher PVI%, increasing with air temperature. Also, shallow high nutrient mesocosms of Turkey had higher PVI%, while macrophytes disappeared with extreme water level drop in Greece. We conclude that combined effects of water level drop and temperature stimulated macrophyte growth even under unfavorable light environment and high nutrient conditions. However, extreme water level had negative effects on macrophytes. Our results indicate that global climate warming and eutrophication may negatively affect macrophytes, if longer and intense drought periods become more common.

17.

The effect of coding sequence and expression polymorphism in testis specific genes in primates

Ayshin Ghalichi*, E. Özkurt, M. Somel;

Presenting Author's Affiliation: Middle East Technical University, Department of Biological Sciences

Intense sperm competition among promiscuous primate species has shaped male reproductive traits, such as testis size and sperm rate, in primates. In multimale species (e.g. chimpanzee, macaque), males have larger testis and faster sperm than single male (e.g. gorilla, human) species do. These differences could be explained by positive selection in chimpanzee or macaque, while they could also be explained by relaxation of constraints in single male species. A recent study on human non-synonymous polymorphism among tissue specific gene sets found an intriguing trend: dramatically higher frequencies of possibly damaging mutations in testis specific genes, compared to other tissue specific genes. This signals relaxation of constraint on human testis. However, this could be possibly resulted by balancing or positive selection on testis-related genes. To resolve this problem, here we analyze human SNP data from HapMap 28 to confirm the results of Grossman et al, and analyze SNP data in two other great ape species: chimpanzees and gorilla. To further supplement the analysis, we will continue with within-species gene expression data in humans, chimpanzees and macaques. In the end, we aim to figure out the role of selection versus relaxation in the maintenance of possibly damaging polymorphism accumulation in human testis genes.

18.

ATLAS and the cosmopolitan town Sigtuna in Lake Mälaren Valley

Anders Götherström*

Presenting Author's Affiliation: Stockholm University, Department of Archeology and Classical Culture

The ATLAS project is an ambitious project carried out in Stockholm / Uppsala where we generate massive amount of ancient human genomic data from prehistoric Swedish remains. We have geneticists, bioinformaticians, physical anthropologists, and archaeologists employed within the project, and with the joint purpose of generating and interpreting data, and exposing as much as possible of Northern Europe's genomic prehistory. Out of the many things we research is a project where the Iron Age part of the project work with inhabitants from the Scandinavian town Sigtuna. Sigtuna was founded in the mid 10th century,

and became a hub for power and demography already from its start. The material remains from the town are cosmopolitan, and now we use genomics to investigate whether this was the case with the inhabitants as well. I will present a few of the preliminaries from their work. Individuals excavated within the town appear to be from other parts of Europe when their genomic SNPs are compared to various populations from Europe and other parts of the world.

19.

Analyzing of conserved miRNAs on ruminants by computational approaches

Egemen E. Güler*, C. Ün

Presenting Author's Affiliation: Ege University, Department of Biology

MicroRNAs (miRNAs) are small (nearly 22 nucleotides) RNAs which regulate gene expression by a sort of mechanisms. They are mainly located on non-coding sequences of genome and therefore are conserved in evolutionary process. miRNAs play an important role in post-transcriptional regulation of gene expression and work as small degradation molecules. Also they have roles in stem cells differentiation, apoptosis mechanism and cell to cell communication. In addition, the association between miRNAs and diseases, lactation of farm animals and meat yields are known. In this study, we searched conserved miRNAs on sheep (*Ovis aries*), goat (*Capra hircus*) and cattle (*Bos taurus*) genomes by using computational approaches. For miRNA analysis, bioinformatics methods were used in this study. Firstly, cattle miRNAs were obtained from miRNA database (miRBase) and then these miRNA sequences were scanned in goat cDNA libraries by Blastn program to gain match sequences. Afterwards Blastx program was utilized to ensure that matched sequences are non-coding. Protein coding sequences were eliminated and non-coding sequences were analyzed by Mfold program to provide secondary structure. According to convenience of sequences, new pre-miRNAs and mature miRNAs were determined. The same procedure was repeated for sheep genome to analyze miRNAs by using new goat's miRNAs which were obtained. As a result of this study, 65 new miRNAs in goat genome and 35 new miRNAs in sheep genome were determined by computational approaches. Also 36 new miRNAs were found common in goat, sheep and cattle. These obtained miRNAs are conserved in the evolutionary process on ruminantes.

20.

The Anatolian Diagonal revisited: an environmental barrier to dispersal?

Hakan Gür*

Presenting Author's Affiliation: Ahi Evran University, Department of Biology

The Asian part (i.e. Anatolia) of Turkey (Türkiye) is the only region where three (Caucasus, Irano-Anatolian, and Mediterranean) of the world's 35 biodiversity hotspots meet and interact. This means that Anatolia has high biodiversity and high percentage of life found nowhere else on the planet, but has lost the most of its original natural vegetation. One of the most important biogeographic phenomena that helps in understanding biodiversity of Anatolia and has received increased attention in recent years is the Anatolian Diagonal. Although the Anatolian Diagonal has long been recognized as a biogeographic boundary between central and eastern Anatolian floras and faunas, processes (i.e. historical, ecological or some combination of these) responsible for its origin and maintenance have not been well understood. Thus, in this study, to assess whether the Anatolian Diagonal corresponds with a significant environmental barrier to dispersal, I used ecological niche modelling and associated comparative metrics. Accordingly, first, I created virtual records in the Anatolian part of Irano-Anatolian hotspot, and split these records into two groups by the Anatolian Diagonal. Then, I asked whether the Anatolian Diagonal is associated with an abrupt environmental transition or a steep environmental gradient. Ecological niche modelling suggested that the Anatolian Diagonal is associated with an abrupt environmental transition or a steep environmental gradient, and therefore corresponds with a significant environmental barrier to dispersal.

21.

Occurrence of gill parasites in the Turkish endemic fish, *Squalius fellowesii* (Cyprinidae); including new host records

M.C. Unal, D. İnnal*, K. Civiňová, M. M. Stavrescu-Bedivan, B. Koubková

Presenting Author's Affiliation: Department of Biology, Mehmet Akif Ersoy University

In this study, the occurrence of gill parasites in *Squalius fellowesii* (Cyprinidae) of Dođanbaba Creek (Yeşilova-Burdur) was investigated. The total of 152 *S. fellowesii* specimens were collected by electrofishing method between January 2014 and February 2015. At the end of study, two parasitic helminth species (*Lamproglena compacta*, *Paradiplozoon bliccae*) were recorded. *L. compacta* and *P. bliccae* are new records for helminth fauna of Turkey. Prevalence and intensity of infection, length classes and sex compositions of infected population, seasonality of infection, have been obtained and compared with other studies.

22.

Infestation of *Lernaea cyprinacea* (Copepoda: Lernaeidae) in two endemic and one non indigenous fish species from Düger Spring Creek (Burdur-Turkey)

Deniz İnnal*, A. Avenant-Oldewage, Bugrahan Dogangil

Presenting Author's Affiliation: Department of Biology, Mehmet Akif Ersoy University

A study was undertaken to assess the prevalence, mean intensity and seasonality of *Lernaea cyprinacea* infestation of fish in a natural spring creek (Düger Spring), southwest part of Turkey. A total of 283 fish specimens belonging to four families (Poecilidae, Cobitidae, Nemacheilida and Cyprinidae), four genera and five species were collected from the creek and examined for infestation by *Lernaea cyprinacea*. It was recorded from two endemic (*Pseudophoxinus burduricus*, *Oxynoemacheilus anatolicus*) and one non indigenous (*Gambusia holbrooki*) fish species. Prevalence, mean intensity and seasonality of infection have been recorded and is compared with other studies. This is the first parasitological record of *L. cyprinacea* on *Pseudophoxinus burduricus* and *Oxynoemacheilus anatolicus* from Turkey.

23.

Molecular phylogeny and divergence time estimates for the family Elateridae (Insecta: Coleoptera)

Mahmut Kabalak*, İ.K. Sađlam

Presenting Author's Affiliation: Hacettepe University, Department of Biology

Our main goal was to understand evolutionary history of the family Elateridae (Insecta, Coleoptera). In the scope of aim, Phylogenetic relationships between the 67 taxa were reconstructed using partial sequences from 16S, 18S and 28S mitochondrial rDNA regions and partial sequences from the COI mitochondrial gene. Species trees were estimated using these 4 partitions using the coalescence based MCMC program BEAST, under a Yule model of speciation. For divergence time estimates we entered the consensus species tree obtained from our full data set as fixed and estimated branch lengths by calibrating the tree using a mitochondrial divergence rate of 2.3% divergence per million years. Our results did not show major deviations from phylogenetic relationships estimated prior to this study but helped to revise incongruences between several taxa within Turkey and their taxonomic placement from a broader systematic view. In addition our results are the first attempt at obtaining reliable divergence times within this family and in evaluating the evolutionary history of Elateridae as a whole.

24.

The restraint of some exotic plant taxon over natural vegetation and utilization of these taxon by local population (case study of Trabzon)

Gökçe Kalankan*, D.U. Saraç, A. Egemen, N. Yıldırım and A. Ergül Bozkurt

Presenting Author's Affiliation: Karadeniz Technical University, Faculty of Forestry

It was confirmed that 31 naturalized/exotic plants which are benefited as herbal products around different regions of our country has also demonstrated an increase within the boundaries of Trabzon and some of these products are used by the locals though the traditions of using of natural herbal products diminished in conjugation with lack of interest in young generations. The present study which aimed to record these information has been conducted between 2014 and 2015 within the boundaries of Trabzon. In the study, face to face surveys were conducted with local population to determine the areas of usage and forms of utilization of herbs, which parts of the herbs are used and demographics of the participants. The surveys were conducted with 60 people – of the participants 39 were female and 21 were male. It was determined that from 19 plant families selected from the field of study, 8 were used as treatments, 13 as food, 12 as indoor ornamental plants and 13 were used as animal feed. According to these results, top three families are determined as Asteraceae family 6 taxon (%32), Poaceae 5 taxon (%26) and Fabaceae 3 taxon (%16). The plants, which were used for medical or other purposes by local people, *Zea mays* L., *Brassica oleracea* L., *Diospyros kaki* L., *Diospyros lotus* L., and *Robinia pseudoacacia* L. are cultured plants that are strikingly used as herbal products in recent years. Moreover, it was determined that residues of *Camelia sinensis* (L.), which is known as tea, are used as animal underlay and fresh fruits of *Diospyros kaki* L. are emptied out and used for stuffing.

25.

Phylogenetic analysis of *Petroleuciscus* species distributed in Turkey

Gökhan Kalaycı*, Y. Bektaş, D. Turan

Presenting Author's Affiliation: RTE University, Department of Fisheries

Petroleuciscus is one of the genus of Cyprinidae family distributed Black Sea and Eastern Aegean drainage and represented two species as *P. borysthenicus* and *P. smyrnaeus* in Turkey. To find out genetic relationship of *Petroleuciscus* species in Turkey, samplings were conducted in Aegean drainage, Gediz River (Uşak) for *P. smyrnaeus* and Black Sea drainage, Manyas Lake (Balıkesir), Istranca and Karaman Stream (Istanbul), Canbolu Stream (Bursa) and Yenice Stream (Çanakkale) for *P. borysthenicus*. Sequence analysis of partial mtDNA cytb gene (886 bp) was used to reveal phylogenetic relationship of *P. borysthenicus* and *P. smyrnaeus*. Alignment of nucleotide sequences was performed with Clustal W. Pairwise genetic distances and relationships among haplotypes were estimated using the NJ and ML algorithms with MEGA and the haplotype number, nucleotide and haplotype diversity were calculated using DnaSP software. At the result of alignment of cytb sequences, 48 and 41 characters were variable and parsimony informative. The nucleotide composition was 25.2% (A), 29.1% (T), 29.2% (C) and 16.5% (G). 10 haplotypes were determined also haplotype and nucleotide diversity was calculated as 0.863 and 0.017 respectively. Pairwise distance was calculated as 0.1-4.5% (mean 1.9%) and 4.2% for haplotypes and interspecies. Phylogenetic tree topologies were showed two lineages with high bootstrap values.

26.

An ecophysiological study: Time patterns of body temperature in Anatolian ground squirrel before hibernation

Mutlu Kart Gür*, G. Cornelissen, C.L. Gierke, H. Gür and T. Kankılıç

Presenting Author's Affiliation: Ahi Evran University, Department of Biology

Hibernation is a seasonal adaptation of small mammals to survive during times of cold exposure, drought, and/or food shortages. Despite many studies on hibernation, few have examined the time structure of body temperature (T_b) before hibernation, particularly under natural conditions. Herein, using advanced analytical methods, we aimed to understand the changes in daily rhythm structure of T_b before hibernation, with special interest to sex differences in adult Anatolian ground squirrels. We monitored T_b continuously from summer to spring using intraperitoneally implanted temperature loggers. Least squares spectral analysis identified prominent 24- and 12-hour components, which were concomitantly fitted to data in consecutive daily spans by chronobiologic serial section. Our results showed that important changes in time structure of T_b occur well before the start of hibernation in adult ground squirrels, with notable differences between males and females.

27.

Breeding ecology of two Tit species (Paridae) at METU campus: The importance of nest predation

Pınar Kavak*, E. Çakmak, C.C. Bilgin

Presenting Author's Affiliation: Middle East Technical University, Biodiversity and Conservation Lab, Department of Biology

Great Tit (*Parus major*) and Coal Tit (*Periparus ater*) are widespread passerine species that readily use man-made nest boxes. We aimed to determine the breeding phenology and breeding success of their local populations by placing artificial nest boxes (n=50) within METU campus and observing them for two years. For most attempted nests, predation events were documented by examining either nest remains or videos recorded with camera traps. A total of 9 and 15 nest boxes were occupied by either species in 2013 and 2014, respectively. Nesting success was 37.5% and 60% for Coal Tits (n=13), and 0% and 30% for Great Tits (n=11) in those years. Average number of fledglings per nest attempt was 2.69 and 1.27 for Coal Tits and Great Tits, respectively. Nest boxes away from man-made structures were more readily occupied by birds ($p < 0.05$). Predation was the most common cause for nest failure, accounting for at least 76% of the total nestling loss, and the main predator was identified as Magpie (*Pica pica*). Compared with the only major study in Turkey, breeding success at METU remained at 41% and 20% of those reported for Coal and Great Tits, respectively, at Beynam Forest (Kiziroğlu 1982). Lower use of nest boxes near buildings can be better explained by increased availability of nest locations around buildings since predation rate did not show a significant difference between proximate and distant nest boxes. Overall, our findings suggest that populations under study experience levels of predation so high that they possibly persist only due to immigration from elsewhere.

28.

Patterns of post-fire germination in Mediterranean plants of Turkey

Duygu Deniz Kazancı*, Ç. Tavşanoğlu

Presenting Author's Affiliation: Hacettepe University, Department of Biology

In Mediterranean-type ecosystems, many species have adapted to germinate just after fire via breaking of seed dormancy by fire-related germination cues. The purpose of this study is to determine the fire-related germination properties of plant species growing in Mediterranean Turkey, a less-known region in terms of fire ecology. Seeds of 76 species from Mediterranean vegetation (phrygana, maquis, Turkish Red Pine forest) were collected from southwestern Turkey. A series of germination experiments including an aqueous smoke and various heat shock (60, 80, 100, 120, 140 °C for 5 min.) treatments were conducted. Germination of almost half of the studied taxa (34 out of 76) increased with heat shock or smoke application. Germination responses of species to fire-related cues were strongly related to the families they belong to. Heat shocks increased the germination of the members of Cistaceae and Fabaceae, while the germination in Lamiaceae increased by aqueous smoke treatment. An association was found between the geographical distributions of taxa and their response to fire-related cues. Moreover, annual species were more prone to give a positive response to smoke. This study fills an important gap on fire-related germination in the eastern Mediterranean Basin, and the results have potential to be used in post-fire management and conservation of Mediterranean habitats.

29.

The role of biotic interactions in determining species ranges

M. Çisel Kemahlı*, A. Birand

Presenting Author's Affiliation: Middle East Technical University, Department of Biological Sciences

Species diversity and their geographic range size patterns across latitudinal gradients have been studied for decades. One generally accepted rule is Rapoport's rule, which states that temperate species may have larger geographic range sizes than tropical species, due to their tolerance of a broader range of environmental conditions. The generality of Rapoport's rule however, has been challenged by recent studies that used null models and simulations. Like Rapoport's rule, latitudinal gradient studies that

investigate the latitudinal gradient in species range sizes generally focus on the role of environmental factors, like temperature. The role of biotic interactions on species ranges is not well understood. In this study, we make inferences on the role of biotic factors in determining range sizes by studying the distribution of New World birds.

30.

Eco-physiological functioning of oak coppices in southeast terrestrial ecosystems in Turkey

Uğur Kezik*, F. Kocaçınar

Presenting Author's Affiliation: Karadeniz Technical University, Faculty of Forestry

Approximately 27.6% of Turkey's land area is covered by forests. This ratio is seems like near the averages in the world. But about half of the our forest assets are regarded as unproductive and degraded in terms of wood raw material. Degraded forestland in Turkey constitutes nearly 40% the oak species and coppice form and its occurring mostly in Southeastern Anatolia Region of Turkey. Oak coppices in Southeastern Anatolia has been destroyed and formed shrubby bunchy by anthropogenic effects for the several decades. Even if this forest may regarded as unproductive and degraded, it has ability to sequestrate atmospheric CO₂ with physiological activity as all other plants. It has not been studied so far that how much atmospheric CO₂ may be sequestered and how much O₂ and NPP (Net Primary Production) can be produced in oak coppice ecosystem. In this study, we measured photosynthetic properties such as net atmospheric CO₂ assimilation rate, O₂, NPP production rate and total leaf area properties of oak trees by using portable gas exchange device (Waltz GFS 3000) with leaf area meter (LI COR 3000C) device. It is found that Branth's oak coppice may produce 4.0 tonnes O₂ and 3.75 tonnes net primary production by assimilating 5.5 tonnes atmospheric CO₂ per year in one hectar. Consequently, In contrast to popular belief, this oak ecosystem, in reducing CO₂ which is one of the most significant of the greenhouse gases causing global warming, play an important role.

31.

Genomic investigation of the Neolithic Revolution in Near East

Gülşah M. Kılınç*, F. Özer, A. Omrak, R. Yaka, N.D. Dağtaş, E. Yüncü, S.C. Açıkan, A.M. Büyükkarakaya, Y. Erdal, E. Bıçakçı, D. Baird, I. Hodder, C. Knüsel, C. Larsen, Ö. Taşkent, M. Dönertaş, C. Alkan, M. Jakobsson

Presenting Author's Affiliation: Middle East Technical University, Department of Biology

The Neolithic transition began ~12,000 BP in the Near East (NE) and from there it spread throughout Europe. This episode which is defined as the replacement of hunting and gathering way of life with another one based on farming and herding, transformed the global demography, social organization and structure. Therefore, understanding the dynamics behind the establishment and spread of the Neolithic has been a core interest in archaeogenomics studies. Outstanding progress of the sequencing technologies has facilitated the investigation of ancient genomes and led to the discovery of the migration-based diffusion of the Neolithic from NE into Europe. However, several questions as to how this period started within the NE and which processes prompted the spread of it inside the region have remained unknown. Hence, we have started to investigate human remains from Anatolia and Cyprus through exploiting ancient genomics approaches to answer these questions, to describe the Near Eastern Neolithic, as well as to delineate the characteristics of Near Eastern populations. To date, we sequenced 21 Neolithic samples excavated from 4 different sites and discovered the presence of authentic DNA conservation at high level in 4/21 samples. This study will reveal the processes behind the establishment of Neolithic within the NE and dynamics behind the spread of the culture within the region.

32.

Computational identification of conserved miRNAs and their target genes in faba bean (*Vicia faba*)

Dilek Koptekin*, L.Y. Aktaş

Presenting Author's Affiliation: Ege University, Department of Biology

microRNAs (miRNAs) are a class of endogenous, non-coding short RNAs, around 21 nucleotides (nt) in length found in eukaryotic cells. To date, they are identified in several plants through experimental and computational approaches where they play important roles in growth, development and stress responses by guiding mRNA cleavage or by repressing translation. However, not a single miRNA has been identified in faba bean (*Vicia faba*) up till now, which is an important source of protein widely used for human and animal nutrition. The aim of this study is to identify conserved plant miRNAs in faba bean by using homology analysis. 262 candidate miRNAs belonging to 143 miRNA families in faba bean from 20697 expressed sequence tags (EST) and 577 genome survey sequences (GSS) have been found through computational identification of miRNAs using EST based homology analysis approach. All candidate miRNAs were recognized following the miRNA criteria of secondary structure and biogenesis. Moreover, potential targets of these candidate miRNAs were predicted from faba bean ESTs, some of which seem to encode genes in regulation several important biological processes such as development, metabolism, transport, signal transduction and stress response. The results of this study will contribute to further research on miRNAs, leading to an improved understanding of the role miRNAs play in biological processes and the underlying molecular mechanisms of faba bean.

33.

Effects of river type hydropower plants on some water quality parameters

Necla Koralay*, O. Kara and U. Kezik

Presenting Author's Affiliation: Karadeniz Technical University, Faculty of Forestry

River Type Hydropower Plants (HPPs) which set on main stream in one watershed may affect water quality parameters and aquatic ecosystems. Owing to the geographical and ecological features, Northeast of Turkey has high potential of the hydropower energy. In this study, we determined monthly some water quality parameters by using YSI Professional Plus instrument for one year in two hydropower plants (Çamlıkaya HPP and Arca HPP) constructed on Solaklı River in Trabzon province, Turkey. Temperature (°C), pH, electrical conductivity (mS cm⁻¹), dissolved oxygen (ppm) and total suspended solids (TSS, mg l⁻¹) were measured at the samples points. Results demonstrated that the quality and quantity of water in the main stream were negatively affected by HEPPs in both operational and constructional phases. Statistically, significant changes were occurred in water quality parameters such as TSS, pH and temperature. It was concluded that these negative changes were caused by the sand mine in construction phase of HEPPs. Furthermore, aquatic ecosystems and riparian zone may negatively affected by the decrease of the amount of water released into the river during the operational phase of HEPPs.

34.

Identification of *Tenthredopsis* (Hymenoptera: Symphyta) species based on predicted ITS2 secondary structure

M. Budak, M. Güler, F. Tokgöz, S. Hastaoğlu Örgen, E. Mahir Korkmaz*, Hasan H. Başbüyük

Presenting Author's Affiliation: Cumhuriyet University, Department of Biology

Identification of *Tenthredopsis* species is often difficult because of variable and insufficient morphologic characters. Recently, the internal transcribed spacer 2 (ITS2) secondary structure has been reported to be useful in identification at species level and its utility is here tested in *Tenthredopsis*. A total of 42 specimens representing 5 species were used to extract DNA and the 5.8S-ITS2-28S region was amplified and sequenced. The ITS2 regions were annotated using ITS2 Database and the secondary structures were predicted and characterized. A NJ tree was constructed based on secondary structures and the detected CBCs were compared among species. The lengths of the ITS2 sequences vary among species. The nucleotide similarities within species range from 96.61 to 99.27%. However, the low level of nucleotide similarity is observed between species, with an 83% in average. The extremely low levels of nucleotide variation within species strongly indicate a pattern of concerted evolution contrary to opinion that many mutations become fixed in a population under selection and/or genetic drift. The tree based on ITS2 secondary structure and CBCs analyses revealed the presence of six taxa (species) contrary to five morphologically identified species.

35.

Bioinformatic analysis of *Conus species*-Conotoxin to understand evolutionary diet-toxin modification interactions

Ahmet Efe Köseoğlu*, Z. Osmanlı, M. Uslupehlivan, C. Ün
Presenting Author's Affiliation: Ege University, Department of Biology

Cone snails (*Conus species*) are phylogenetically and ecologically highly diverse prosobranch predatory marine gastropods distributed throughout the world's tropical oceans in the regions of Indo-Pacific, Eastern Pacific and Atlantic. Many specialized envenomation strategies are widely evolved across worm, mollusk and fish-hunting cone snails for predation, defense and competition. Each *Conus* species contains 100-200 small, biologically active venom peptides known as conotoxins or conopeptides. There are different types of conotoxins called the *alpha*, *delta*, *kappa*, *mu*, and *omega* according to the differences in the number and pattern of disulfide bonds. In this study, we have compared 30 *Conus* species by analyzing the nucleotide and amino acid sequences, conserved regions, phosphorylation and glycosylation profiles of -conotoxins that inhibit nicotinic acetylcholine receptors at nerves and muscles. The results of our bioinformatic studies had shown close relationship between toxin modifications (glycosylation and phosphorylation) and snail diets. Our comparative analysis provides new insights into the complexity of the processes that drive the evolution and diversification of *Conus* species, conotoxins, and their diets.

36.

Effects of ammonium sulfate exposure on *Bufo bufo* tadpoles gonadal histopathology

Gülşah Köseoğlu*, T. Ergül Kalaycı, Y. Kalkan, B. Karaca, L. Tümkaya, N. Özdemir
Presenting Author's Affiliation: RTE University, Department of Biology

In this study, we evaluated the gonadal histopathology of *Bufo bufo* tadpoles after acute toxicological test for different concentrations of ammonium sulfate (0, 250, 500, 750 and 1000 mg/L). For ecological risk assessment, these kinds of tests are needed for Amphibia and other aquatic vertebrates. Before the histopathological examination, tadpoles were exposed to ammonium sulfate solution for 96 hrs and 5 replications per concentration were performed. Histopathological changes between groups were tested by Kruskal-Wallis test. In high concentrations; deterioration was seen in tissue integrity. Germ cells were lost their characteristic appearance. Vacuolization, dilatation and pigmentation was seen intensely. Also, there are significant differences between groups in terms of germ cell degeneration, vacuolization, edema and pigmentation ($p < 0.05$). We revealed that the acute toxicological exposure of ammonium sulfate had a major impact on the urogenital system of *Bufo bufo* tadpoles. Exposure to agricultural chemicals, like fertilizers or herbicide, together with other factors, such as habitat fragmentation, introduction of predatory species, wetland losses, UVB radiation and diseases have been postulated as possible causes for world-wide declines of amphibian populations.

37.

Spontaneous mutation rate and spectrum in mismatch repair-deficient *Mycobacterium smegmatis*

Sibel Küçükyıldırım*, H. Long, W. Sung, S.F. Miller, M. Lynch
Presenting Author's Affiliation: Hacettepe University, Department of Biology

Mycobacterium smegmatis is a bacterium naturally devoid of the conserved DNA mismatch repair (MMR) pathway, and this provides great opportunity to estimate spontaneous mutation rate and spectra without bias from the MMR system. Our mutation accumulation experiments yielded a base-substitution mutation rate of 4.70×10^{-10} (Standard Error: 4.25×10^{-11} ; whole genome rate: 0.003 per generation) per site per generation, which is surprisingly close to other MMR functional organisms. Transitions dominates transversions, with the A:T>G:C transition rate higher than the G:C>A:T rate. We also found that insertion-deletion mutations unusually biased towards insertions which is not consistent with the idea that deletion pressure reduces prokaryotic genome sizes. Since *M. smegmatis* does not have any homologs to known mutS and mutL genes, *M. smegmatis*' mutation rate and unusual mutation spectrum may be shaped by several processes involved in replication and repair. Firstly improved replication fidelity could be one potential explanation for mutation rate that is in normal range in MMR deficient organism. For this reason

we compared DNA polymerase sequences with the other prokaryotes and we observed some differences on the catalytic site of DNA polymerase alpha subunit. Secondly, improved DNA mechanisms could decrease the mutation rate that involved in cytosine deamination repair, anti-oxidation mechanisms, and DNA methylation. Also, Mycobacteria have an effective UDG system and especially have an UdgB ortholog, they can effectively protect their GC-rich genomes against the threat of deamination and reactive oxygen and nitrogen species.

38.

Effect of water level change on sedimentary proxies: Lakes Beyşehir, Marmara and Uluabat

Eti Levi*, S. Turner, G. Bezirci, A. Çakıroğlu, M. Kernan, H. Bennion, E. Jeppesen and M. Beklioğlu
Presenting Author's Affiliation: Middle East Technical University, Department of Biological Sciences

Strong natural or human induced water level fluctuations have been known to influence shallow lakes, especially in semi-arid to arid Mediterranean climate regions. In the absence of historical data, sedimentary remains may provide information on long-term dynamics of the lakes. For a reliable interpretation of past conditions and forecasting of future patterns it is important to understand the response of the sedimentary proxies to environmental changes. Therefore, in an EU-FP7 project (REFRESH), three large shallow lakes were chosen in order to investigate biological and non-biological sedimentary proxies together with existing long-term instrumental water level data. Core samples from littoral of the three lakes were retrieved with a Livingstone Piston Corer. ²¹⁰Pb-dated cores were analyzed for X-ray fluorescence and loss-on-ignition, also sub-fossil cladocerans, diatoms and plant remains were identified. Results from Lakes Beyşehir and Uluabat indicated a change from benthic associated communities to more pelagic ones. The core from Lake Marmara, on the other hand, indicated a more benthic ecosystem structure throughout the comprised period. However, our data indicates that the noisiness of short-term cyclical water level changes and the anthropogenic impact blur the accuracy between actual and recorded change, and highlights the care required in using recent sediment records.

39.

Resource availability versus resource use: diet assessment of subterranean rodents using DNA metabarcoding

Carla Lopes*, M. De Barba, F. Boyer, C. Mercier, D. Galiano, B. Kubiak, P. Filho, L. Gielly, E. Coissac, T. Freitas, P. Taberlet
Presenting Author's Affiliation: Universidade Estadual Paulista, Department of Zoology

The subterranean rodents of the genus *Ctenomys* are herbivorous species referred as ecosystem engineers, developing an important role in the environment where they occur. We analyzed the diet composition of 6 described and 1 undescribed Brazilian ctenomyid species (*C. minutus*, *C. lami*, *C. torquatus*, *C. ibicuiensis*, *C. flamarioni*, *C. bicolor*, and *C. sp*), and some hybrid individuals, as a first step to better explore questions related to their impact in the dynamics of the environment and their interaction with other organisms. We also analyzed the environmental DNA of soil samples to assess the availability of plant resource around the burrows. We applied the DNA metabarcoding approach combined with the next-generation sequencing to amplify the DNA of plants from soil and scat samples. From 3 to 14 plant families were identified in the diet composition of the ctenomyid species. The Poaceae family was highly used as food resource by all species. From 3 to 9 plant families were identified in each soil sampling site. Asteraceae and Poaceae sequences were retrieved in all soil sites. The rodents showed, in general, a varied diet pattern, influenced by the availability of food resources in the environment. However, not all plants available were used as food resource. Some dietary preference for Poaceae, Asteraceae and Fabaceae families can be suggested for the species analyzed.

40.

A new hypothesis for why mole rats have so many cytotypes

Ferhat Matur*
Presenting Author's Affiliation: Bülent Ecevit University, Department of Biology

Structurally, Turkey is located within the geologically recently-folded mountain zone of Eurasia. Turkey's varied landscapes are the product of a wide variety of tectonic processes that have shaped Anatolia over millions of years and continue still as evidenced by frequent earthquakes. It is known earthquakes release radon gas from fault lines, which is radioactive and highly mutagenic. Some studies claim that ionizing radiation induces a variety of chromosome aberrations. Because mole rats live underground in their tunnels, and they have more limited movement/dispersal ability than other rodents or mammals so that they may have exposure the radon gases longer than other rodents. It causes more aberrations in mole rats than other rodents. If aberrations fix, the individual will have a new chromosome sets that may dispersal population through sexual reproduction. In this study I briefly summarize former mole rats studies that give a clue for my new hypothesis: fault lines form cytotypes distributions of mole rats.

41.

Species boundaries of an asexual fungal genus

Hilal Özkılınç*, F. Rotondo, B.M. Pryor and T.L. Peever

Presenting Author's Affiliation: Çanakkale Onsekiz Mart University, Department of Molecular Biology and Genetics

The fungal genus *Alternaria* comprises a large number of asexual taxa with diverse ecological, morphological and biological modes ranging from saprophytes to plant pathogens. Species concepts can vary depending upon criteria selected and the applicability of those criteria across related taxonomic groupings. For example, the biological species concept is not applicable to asexual organisms, and other definitions such as the phylogenetic species concept are required. This study included 123 isolates of *Alternaria* representing five morphologically defined species in two sister sub-generic groups; Section Porri (*A. dauci*, *A. solani* and *A. limicola*) showing host specificity and Section Alternata (*A. alternata* and *A. arborescens*) having wider host ranges. For each isolate, sequences from four genes (Allergen a1, ATPase, Calmodulin, Endo_PG) were analyzed using Bayesian phylogenetic approaches. An initial species tree was inferred using a Yule Speciation model and a molecular clock assumption. Species boundaries were well defined within Section Porri. But, species boundaries within Section Alternata were partially resolved indicating incomplete lineage sorting and/or recombination. This study compares evolutionary patterns within two Sections of *Alternaria* and suggests approaches for phylogenetic study that will be useful for further defining species boundaries in asexual organisms.

42.

The effect of *Buddleja davidii* on dendroflora in Degirmendere Valley (in Trabzon)

Murat Öztürk*, A. Ergül Bozkurt and N. Yıldırım

Presenting Author's Affiliation: Karadeniz Technical University, Faculty of Forestry

Buddleja davidii is grown outside of his native land China for landscaping purposes because of its beautiful appearance and having flowers with nice scent. Because the invasive features of the species have not been taken into consideration at first, it has come to endanger the natural biodiversity where it is grown as an exotic species. It threatens large areas in riparian zone throughout Trabzon Degirmendere basin. Observations and investigations which were conducted in these areas sought to reveal the threatened dendroflora and the age distribution of the species per elevation level. The expanse and population density of the species, the time it settled the area and the dendroflora elements it threatens in the area were tried to suggested there by. According to observations and investigation results, it was determined that the species threatens some of the plant taxon especially in basin vegetation primarily *Alnus glutinosa* and *Salix* sp. and that it has begun to replace the natural vegetation. With respect to the fact that it has spread to a large are over a very little period of time it is clear that necessary measures should be taken to stop its expand.

43.

Phylogeography of Anatolian diagonal endemic *Ricotia aucheri* (Boiss.) Burt. (Brassicaceae)

Barış Özüdoğru*, S. Erik, G. Akaydın

Presenting Author's Affiliation: Hacettepe University, Department of Biology

Current distribution pattern and genetic diversity of living organisms are the results of climatic oscillations and multiple expansion / contraction events in Pleistocene. Although this phenomenon was tested many times by scientists for European Flora, responds of Anatolian high mountains taxa to climatic oscillations are still unclear. *Ricotia aucheri* was used as a model species to find a pattern that may have taken place in Anatolian high mountain plant taxa in respond to changing historical environmental conditions. This study was conducted by using Ecological Niche Modelling (ENM) and molecular phylogeographical test and analyses (e.g. haplotype networks, mismatch distribution, Tajima's D, Fu's Fs and recently developed "Extended Bayesian Skyline Plot" etc.). Despite ENM results indicate three potential refugial areas (this is generally interpret a signal for a contraction event) in Last Glacial Maximum, the results of phylogeographical analyses clearly indicate demographic stability for *R. aucheri* through time. Therefore, phylogeographical results together with ENM output were discussed carefully taking into account habitat preferences and dispersal ability of *R. aucheri* to infer species history.

44.

Statistical analysis of expression divergence in paralogous zebrafish genes

Huma Shehwana*, Ö. Konu

Presenting Author's Affiliation: Bilkent University, Department of Molecular Biology and Genetics

The zebrafish (*Danio rerio*) is an emergent model organism for the study of several vertebrate biology aspects including developmental and genetic analysis. Recent studies have identified hundreds of mutant zebrafish phenotypes many of which resemble human clinical disorders. Despite many similarities, unlike humans, genome of zebrafish has undergone an additional genome duplication event during evolution. Whole genome duplication (WGD) has important consequences one of which is novel gene generation through neofunctionalization or subfunctionalization. Main objective of this work is to identify zebrafish paralogs that have an ortholog in humans to analyze paralogous expression divergence. To achieve the aim, microarray expression datasets, human-zebrafish orthologs, zebrafish paralogs information has been retrieved from publicly available resources. R platform along with bioconductor package, Limma was used to calculate expression divergence of zebrafish paralogs based on microarray dataset. Results are integrated in a shiny web application. Web application was designed such that user can query a human gene with a unique name/ID before processing the query to retrieve zebrafish orthologs and associated paralogs annotation. The application then allows for comparison of the expression changes in paralogous genes in different microarray datasets. Graphical visualization of expression analysis could then be performed. Work will be extended to include large array of microarray datasets having different test conditions including expression variation in maternal and zygotic gene expression.

45.

Phylogeography of the water vole, *Arvicola amphibius* (Mammalia: Rodentia) in Turkey

Perinçek Seçkinozan Şeker*, E. Çolak

Presenting Author's Affiliation: Artvin Çoruh University, Department of Biology

The aim of the current study was to reveal phylogeographic pattern of genetic diversity in water vole, *Arvicola amphibius* in Turkey, by using control region of mitochondrial DNA (mtDNA). A total of 120 samples from 26 different localities within Turkey were evaluated in the study. Genetic variation in mtDNA control region revealed 28 haplotypes. Distance, model, and network analyses revealed that *A. amphibius* has five highly differentiated genetic lineages in Turkey. These lineages were Thrace (T), Central and West Anatolia (CWA), Central and North Anatolia (CNA), Southeast Anatolia (SEA) and East Anatolia (EA) lineages. When two shared haplotypes between T and CWA lineages were excluded, all lineages had substantially nonoverlapping geographic distributions. It was detected that *A. amphibius* populations in Turkey have approximately one and a half fold nucleotide diversity in control region than

those in Europe, when populations constituting all lineages were evaluated together. This case and presence of two shared haplotypes between T and CWA lineages pointed out that Anatolia might have served as a refuge in Quaternary for this species. High genetic differences among those lineages showed that geomorphological conglomeration process shaping current geology of Turkey and climatic oscillations in Quaternary may have had an impact for differentiation of *A. amphibius* lineages.

46.

Small RNA sequencing based identification of microRNAs in *Daphnia magna*

Murat Telli*, E.S. Ünlü, D.M. Gordon

Presenting Author's Affiliation: Abant İzzet Baysal University, Department of Biology

Small RNA molecules are short, non-coding RNAs identified for their crucial role in post-transcriptional regulation. A well-studied example includes microRNAs (miRNA), which have been identified in several model organisms including the freshwater flea *Daphnia*. A model for epigenetic-based studies with an available genome database, the identification of miRNAs and their potential role in regulating *Daphnia* gene expression has only recently garnered interest computational-based work using *Daphnia pulex*, has indicated the existence of 45 miRNAs, 14 of which have been experimentally verified. To extend this study, we took a sequencing approach towards identifying miRNAs present in a small RNA library isolated from *Daphnia magna*. Using Perl codes designed for comparative genomic analysis, 815,699 reads were obtained from 4 million raw reads and run against a database file of known miRNA sequences using Perl blast code. We identified 205 putative mature miRNA sequences belonging to 188 distinct miRNA families. This study provides critical information necessary to begin an investigation into the role for these transcripts in the epigenetic regulation of *Daphnia*.

47.

Transcriptome conservation changes during mammalian brain aging

Zeliha Gözde Turan*, P. Parvizi, M. Somel

Presenting Author's Affiliation: Middle East Technical University, Department of Biological Sciences

Aging is a complex phenotype determined by wide range of genetic and environmental factors. More than 300 theories were postulated to explain aging to date, and mutation accumulation theory is among the keystones of such theories, attempting to explain aging in evolutionary context. It states that mutational load of genes (i.e. damaging germline mutations in a gene) increase with age due to declining force of negative selection. The idea was previously tested by conducting experiments in *Drosophila* sp., with mixed results. But to our knowledge, it was not tested yet using transcriptomic/genomic data. Here we analyzed different transcriptome datasets in human, chimpanzees, and macaques. These datasets include both mitotic and non-mitotic tissues, which deteriorate through different mechanisms in aging. We found that transcriptome conservation level starts to decline after sexual maturity in brain regions for three species, but in other tissues, such as human skin and human skeletal muscle, we found no such trend. Indeed, this result is consistent with the developmental theory of aging which states that evolution optimizes genomes for reproduction, and physiological and molecular damage might increase after sexual maturity. However, why we observe this trend in only brain, remains to be investigated.

48.

The Pleistocene history of a passerine bird species: phylogeography and ecological niche modeling of the blackcap

Onur Uluar*, C. Elverici, E. Ada, U. Perktas

Presenting Author's Affiliation: Hacettepe University, Department of Biology

Global climate oscillations through the Quaternary glacial–interglacial cycles have had significant impacts on the geographic distribution and genetic structure of bird species. The effects of these climatic fluctuations have been well documented by numerous different phylogeographic studies. In this study, we would like to test whether multiple refugia existed for the blackcap (*Sylvia atricapilla*) during the Last

Glacial Maximum. To achieve this aim, an ecological niche modeling was developed to predict the geographic distribution of breeding populations of the blackcap under reconstructed past and present. In addition, we also performed coalescent analyses based on Bayesian approach to understand historical demography of the blackcap. Results are discussed with regard to ecological niche modeling and phylogeography.

49.

Ancient DNA Isolation and mtDNA Analysis of approximately 2500-year-old Human Teeth and Phalanx Samples from Çemialo/Batman in Southeastern Anatolia

Reyhan Yaka*, C. Berkman, S. Gündüzalp, Y. Yılmaz, M. Somel, A.E. Özdoğan, İ. Togan
Presenting Author's Affiliation: Middle East Technical University, Department of Biological Sciences, Population Genetics Laboratory

In the proposed study, the mtDNA HVI and HVII region sequences (354 and 217 bp, respectively) of seven ancient samples collected from Cemialo Sirtı (Batman) excavation site in the southeastern of Anatolia were successfully obtained. The mtDNA HPG compositions of these ancient human samples were determined. The mtDNA haplogroups of seven ancient individuals were assigned as H1z1, M1a, U2b1, H1a, HV, R2 and R6 and PhyloTree (http://www.phylotree.org/) was used for determination of the mtDNA haplogroups.

Furthermore the mtDNA HVI - HVII region sequences of seven samples were comparatively analyzed with some modern human populations and various Neolithic populations that were retrieved from databases from Northern Syria (8000 BC), Central Europe (6000-1550 BC) and Southern Paris (5000-4000 BC), including the Sagalassos population which is an ancient Byzantium population (11th–13th century Common Era (CE)) near from Ağlasun/Burdur in the Southwestern Anatolia. This study is the first study where the questions about the human ancient DNA (aDNA) are addressed in the dedicated ancient DNA laboratory of Middle East Technical University (METU), Ankara, Turkey.

50.

Breeding and foraging ecology of semi-wild Northern Bald Ibis (*Geronticus eremita* Linnaeus, 1758) in Turkey

Can Yeniurt*, S. Opper, S. İsfendiyaroğlu, C. Bowden
Presenting Author's Affiliation: Doğa Derneği (BirdLife Turkey)

The Northern Bald Ibis is a critically endangered, migratory bird species. Once a common bird in South-Eastern parts of Turkey, recently a colony of approximately 160 individuals live at a captive breeding center in Birecik (Şanlıurfa, Turkey). The colony roams freely during the breeding season. The aim of the study was to quantify the breeding performance, and estimate to what extent foraging in the surrounding landscape influences breeding success. Breeding success in 2013 and 2014 was measured, and the presence of individual birds at daily feeding events to relate attendance rate to breeding success was observed. Also, individuals in surrounding habitats were observed sightings in different habitats were related to breeding success. Lastly, foraging success was quantified to assess which habitats provided easier food. There was no correlation between attendance at feeding events and breeding success. Birds that were frequently observed at a local tree nursery raised fewer offspring. Foraging success was highest in agriculture fields, followed by meadows and poldered cultivation, and lowest at the tree nursery, explaining why birds frequently seen there had lower breeding success. Northern Bald Ibis use wild food during the breeding season, and establishing a second breeding center in Turkey will require a careful assessment of wild foraging habitat.

51.

The morphology and ecology of *Cyclamen coum* var. *coum* (Trabzon-Solaklı Basin Example)

Nebahat Yıldırım*, A. Ergül Bozkurt, İ. Turna, E. Doğan and E. Benli
Presenting Author's Affiliation: Karadeniz Technical University, Faculty of Forestry

Cyclamen coum, which has a wide propagation in Turkey, ranges from Istranca Mountains in Trakya to Russian border along the coast of Black Sea and to the Caucasus. In the South, it propagates in Amanos Mountains, around Osmaniye and also in Bilecik, Kütahya, Eskişehir and Bursa. In this study, there are two examples of *Cyclamen coum* var. *coum* picked up from two different altitudes (1020 meter and 1235 meter) of Solaklı Basin of Of Province, Morphological measurements and investigations were made on the *Cyclamen coum* var. *coum* examples. Moreover, soil characteristics were determined by taking topsoil examples from these altitude levels. Taking fifteen *Cyclamen coum* var. *coum* examples from each altitude levels, the necessary measurements were made. As a consequence of the study, average tuber diameter, tuber height, tuber weight, length and width of a leaf, leaf number per plant and flower number per plant were calculated. When the results were evaluated, it was seen that other parameters except for average tuber weight were higher in 1020 meter altitude level. It was found that this state mainly stems from altitude difference at which *Cyclamen coum* var. *coum* exists, soil characteristics and exposure differences.

52.

Threatened raptor species in Turkey

Gizem Yılmaz*

Presenting Author's Affiliation: Hawk Mountain Sanctuary, Pennsylvania

Thirty six species of diurnal raptors occur in Turkey. All of those, *Neophron percnopterus* and *Falco cherrug* are endangered species; *Clanga clanga* and *Aquila heliaca* are vulnerable species; *Circus macrourus*, *Falco vespertinus*, *Milvus milvus*, *Aegypius monachus* are near threatened species. Despite the fact that, knowledge on raptor ecology and their conservation in Turkey is limited. Ten studies were reviewed about these 8 species; of which 6 were treated on breeding, 2 on population dynamics, 1 on distribution, 1 on movement and habitat use, 1 on diet and conservation. My objective is to assess the knowledge on ecology and conservation of threatened raptor species and identify the gaps and prioritize researches about raptor conservation in Turkey.