1st Ecology and Evolutionary Biology Symposium, Turkey

July 12th-13th, 2014

Symposium Programme

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Abstract Book

Boğaziçi University

İstanbul, 2014

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Symposium Program

July 12th-13th, 2014

Ecology and Evolutionary Biology Symposium (EEBST), July 12-13, 2014

JULY 12TH 2014 *(Venue: Albert Long Hall)*

08:00-12:00 *Registration*

09:00-09:15 *Welcome Address*

Ecology Session Part 1

09:15-10:00	**Juli Pausas [Keynote Speaker]**	"Fire and Biodiversity"
10:00-10:15	**Çağatay Tavşanoğlu**	"Comparing Patterns of Post-Fire Germination in Central Anatolian Steppe and Mediterranean Plants: Implications For Pyrogeography"
10:15-10:30	**Ayşegül Birand**	"Ecological Co-optation in Birds"
10:30-11:00	*Coffee break*	
11:00-11:15	**Burçin Yenisey Kaynaş**	"Pollination Strategies of Plant Species in Phryganic Ecosystems of Southwestern Turkey "
11:15-11:30	**Melike Bor**	"Gamma-amino Butyric Acid (GABA) Shunt in Phylogeneticaly Divergent Plants"
11:30-11:45	**İstem Fer**	"Vegetation Dynamics in East Africa: Past, Present and Future"
11:45-12:00	**Tuba Bucak**	"Zooplankton Avoidance Strategies Against Predation in Turkish Shallow Lakes: Experimental Approaches"
12:00-12:15	**Oğuzhan Kanmaz**	"Spatial and Temporal Patterns of a Zebra Mussel Invasion: An Individual Based Modelling Study"
12:15-12:30	**Eti Ester Levi**	"Congruence Between Modern Vegetation and Plant Remain Assemblages in the Sediment Surface for Assessing Lake Ecological Status"
12:30-14:00	*Lunch Break*	

Evolutionary Biology Session Part 1

14:00-14:45	**Jennifer Leonard [Keynote Speaker]**	"Dynamic Populations in Late Pleistocene Beringia"
14:45-15:00	**Elizabeth Hemond**	"Transcriptomic Variation Between Day and Night in the Coral Endosymbiont Symbiodinium "
15:00-15:15	**Mehmet Somel**	"A Novel Fixation Bias for Extended Homopolymers in the Human Genome"
15:15- 15:30		
15:30-16:00	*Coffee break*	
16:00-16:15	**Tsegazeabe Hadush Haileselasie**	"Population Genetic Structure of the Water Flea along an Age-Gradient of Novel Habitats Created by Ice Retreat in Greenland"
16:15-16:30	**Öncü Maracı**	"Evolutionary Relationships and History of Rye (Secale spp.)"
16:30-16:45	**Çiğdem Akın Pekşen**	"Do Discordant Mitochondrial and Nuclear Distribution Patterns Indicate Introgression Following Secondary Contact between Anatolian Water Frog Lineages (Pelophylax Cf. bedriagae) and European Water Frog Lineage (Pelophylax ridibundus) In Anatolia?"
16:45-17:00	**Tom Ellis**	"Mechanisms of Selection in an Antirrhinum Hybrid Zone"
17:00-18:30	**Poster Session (Venue: Özger Arnas Hall)**	
19:30-21:30	**Cocktail (Venue: Kennedy Lodge)**	

JULY 13TH 2014 (Venue: Albert Long Hall)

Ecology Session Part 2

09:00-09:45	**Luigi Boitani [Keynote Speaker]**	"Where is a Species? Representing Species on a Map"
09:45-10:00	**Vassiliki Kati**	"Forest Management for Woodpecker's Conservation: A Lesson from Epirus Sacred Groves, NW Greece "
10:00-10:15	**Anıl Soyumert**	"Species Richness and Relative Abundance of Large Mammals in Protected Areas of Northern Anatolia"
10:15-10:30	**Kaan Kerman**	"Avoiding Pitfalls in Detecting Behavioral Syndromes in Previously Untested Species: A Case Study on Monk Parakeets"
10:30-11:00	*Coffee break*	
11:00-11:15	**Haritakis Papaioannou**	"Conservation Management of the Balkan Chamois in Timfi Mount, NW Greece"
11:15-11:30		
11:30-11:45	**Mert Elverici**	"Compositional Changes in Ground Spider Fauna Over the Seasons: An Additional Case from the Mediterranean"
11:45-12:00	**Bahar Patlar**	"The Longer is The Better: The Role Of Testis and Sperm Size on Sperm Competition in Animals"
12:00-12:15	**Korhan Özkan**	"Long-term Trends in Danish Lake Plankton and The Effects of Nutrient Reduction and Climatic Changes"
12:15-12:30	**Deniz Innal**	"Seasonal Variations in Species Diversity and Relative Abundance of Fishes in Belek Coast of Antalya Gulf-Turkey"
12:30-14:00	*Lunch Break*	

Evolutionary Biology Session Part 2

14:00-14:45	**Nick Barton [Keynote Speaker]**	"Modeling Evolution"
14:45-15:00	**Eren Yüncü**	"Gaining Insight into the Evolutionary History of Sheep in Anatolia"
15:00-15:15	**Gönensin Ozan Bozdağ**	"Genetic Analysis of Hybrid Sterility in Yeast"
15:15- 15:30	**Kübra Karaman**	"A Genetic Investigation on the Evolution and Taxonomy of the Genus Nannospalax in Turkey"
15:30-16:00	Coffee break	
16:00-16:15	**Ekin Sağlıcan**	"Mechanisms of Testes Expression Divergence in Humans and Chimpanzees"
16:15-16:30	**Zeycan Helvacı**	"Geographic Structure of the Edible Dormouse in Turkey"
16:30-16:45	**Can Bilgin**	"Brown Bears from Turkey Show Exceptionally High Maternal Lineage Diversity"
16:45-17:00	**Jacob Moorad**	"Polygamy and Sexual selection for Long-life"
17:00-17:15	**Golshan Zare**	"Molecular and Morphological Phylogeny of the genus Orobanche L. (Orobanchaceae) with Emphasis on Turkish Taxa"

17:15-17:45 **Announcement of Student Awards & Final Remarks**

ECOLOGY ORAL ABSTRACTS

Ecological Co-Optation in Birds

Gökçe Aköz[1] and Ayşegül Birand[2]*

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Natural selection is commonly thought as the engine of ecological diversification, where sexual selection has a secondary role in promoting speciation. Sexual selection is also attributed a primary role in the origin of species, where it produces divergence not in ecological traits, but in sexually selected traits. Ecological co-optation suggests an alternative to these prevailing ideas. Sexual selection alone could drive ecological diversification, where a sexually selected trait is co-opted for a novel viability trait. Such an ecological co- optation will then enable species with newly co-opted trait to exploit a novel niche. In the present study, we test the prediction of ecological co-optation in antbirds, tanagers, and blackbirds. We use sexually selected plumage coloration in these groups, and check whether the birds with colorful plumage differ in their niche use (i.e. habitat range, altitudinal range, and distributional range), by using phylogenetically independent contrasts method, and sister taxa comparisons. Our results show that increasing plumage coloration produces changes in niche uses. Similarly, increasing plumage color differences between sexes leads to changes in niche width, which is a trend consistent with ecological co-optation hypothesis.

Testing the Assumptions of Relative Abundance Indices Used in Camera-trapping Studies

Batur Avgan[*1], Marcel Güntert[2] and Urs Breitenmoser[3].

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Relative abundance index (RAI) is a widely used method in analyzing camera-trapping data for estimating the relative abundance, habitat use, activity patterns and population changes of a species. Based on percent event of target species at sampling units, the method does not take into account imperfect or variable detection, and simply assumes the detection probability as either constant or equals to 1. By explicitly modeling detection probability from empirical data collected in 3 consecutive camera-trapping surveys at Düzlerçamı Game Reserve in Antalya-Turkey, we tested the RAI assumptions on detection probability and calculated the relative abundance of caracal (*Caracal caracal)* between the survey periods. Results revealed that the detection probability was not constant and could vary up to 5 times between trap sites within the same survey. The relative abundance results also brought unrealistic values; a 3 times increase in the caracal abundance in only 9 months. Although the pitfalls of RAI have already been demonstrated by several studies worldwide, it has not been discussed critically within the local scientific community This is a serious problem, since these "easy to apply" indices are used as the basis of protection area management plans of the Ministry of Forestry and Water Affairs, the main decision maker on Turkish wildlife. As local scientists, we must consider using more reliable survey methods, which should explicitly model detection probability in analyzing camera-trapping data and guide the government agencies accordingly.

Compositional Changes in Ground Spider Fauna over the Seasons: An Additional Case from the Mediterranean

Mert Elverici[1,2], C. Can Bilgin[1], Aykut Kence[1].*

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Community level arachnological data are scarce in the eastern Mediterranean and largely rely on studies from southeastern Europe or several Aegean islands; while Anatolia has remained untouched in this context. Aiming to gather the first comprehensive set of community level faunistic data on a Mediterranean spider assemblage from Turkey, a semi-natural olive grove and associated shrubland at Kıyıkışlacık (Muğla) was sampled monthly during a period exceeding one year. We report here the findings of a one year long pitfall trap survey (2010 & 2011), and reveal the effects of seasonality over composition and surface activity of the ground spiders in the assemblage. Among the 3469 specimens sampled, 1392 were adults, in which 106 species from 26 families were identified. Detrended correspondence analyses (DCA) and an analysis of similarity were used to explain compositional changes among samples. DCA revealed close associations between consecutive samples among seasons and explained species turnover in the course of a year, while segregating winter samples from rest of the year. Similarity analysis also indicated activity of a distinct fauna in winter, and revealed a 'winter inactive' fauna absent in winter samples but well represented in both November and March samples. Adult percent representation and crude abundance data among samples indicate differences between winter samples and those from rest of the year, supporting the results of previous analysis. Further studies focusing on ecological or bio-geographical gradients over spatial space in Anatolia are necessary for a better understanding on seasonal changes.

Vegetation Dynamics in East Africa: Past, Present and Future

Istem Fer[1], Florian Jeltsch[1] and Britta Tietjen[2]*

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Temporally and spatially extensive understanding of the evolution and response of ecosystem dynamics under the changing climate is of vital importance for human populations and nature conservation efforts, especially in regions like East Africa which has one of the fastest growing populations in the world and hosts a broad variety of ecosystems including globally important biodiversity hotspots. One of the ways of achieving such an understanding is, studying past, present and future environmental changes with predictive tools such as dynamic vegetation models (DVMs). Here, we have applied a dynamic ecosystem model, LPJ-GUESS for simulating the past (6 kyrs BP), present (1901-2011) and future (2011-2100) distribution and composition of East Africa's vegetation. The simulated modern biomes are in agreement with observational data such as vegetation maps and pollen records. Our results regarding the past and future scenarios suggest that different biomes of East Africa show different sensitivities to the changing precipitation regimes and not only the changes in the total precipitation amount but also the timing of this precipitation have a combined effect on these responses. Although LPJ-GUESS does not include the anthropogenic influence, the simulated dynamics of the vegetation should be taken into consideration for a

proactive conservation of the vulnerable biodiversity and an adaptive management of the limited resources in the region.

Seasonal Variations in Species Diversity and Relative Abundance of Fishes in Belek Coast of Antalya Gulf-Turkey

*Deniz Innal**

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Seasonal variations in species diversity and relative abundance of fishes in Belek Coast of Antalya Gulf was investigated. Fish sampling at two stations was conducted monthly from October 2006 to March 2008 using gill nets. The fishes were counted and identified to the family and species levels. Species diversity index, dominance, evenness and catch per unit effort (CPUE) were calculated to evaluate the fish distribution. A total of 1765 individuals (145.1 kg total biomass) from 75 species were collected in this study. Fish species distributed among 55 genera and 36 families were identified. Sparidae was the family most represented in terms of number of species. The most abundant fish species collected were *Diplodus annularis* (6.6 %), followed by *Sardinella aurita* (6.1 %) and *Lithognathus mormyrus* (5.6 %). Lessepsian (Red Sea) immigrant fish species [*Lagocephalus spadiceus*, *Pempheris vanicolensis*, *Sargocentron rubrum*, *Siganus luridus*, *Siganus rivulatus*, *Sillago sihama*, *Sphyraena chrysotaenia*, *Stephanolepis diaspros*, *Upeneus moluccensis*] comprised 12% of the catches in terms of number of species. Among them, *Upeneus moluccensis* was the most dominant species with 67 individuals. Number of species varied from 17 (January, 2008) to 43 (May, 2007). Shannon-Weiner diversity index showed considerable variation among the months and ranged from 2.57 to 3.57. The dominance range was 0.033–0.087, and the evenness estimated ranged was 0.74–0.94 Issues related to various threats to aquatic environment and conservation management strategies have been discussed. It is thought that the results of this study will make a major contribution to the management of fisheries sources of Antalya Gulf, Turkey.

Congruence between Modern Vegetation and Plant Remain Assemblages in the Sediment Surface for Assessing Lake Ecological Status

Eti Ester Levi[1], Ayşe İdil Çakıroğlu[1], Tuba Bucak[1], Bent Vad Odgaard[2], Thomas Davidson[3,4], Erik Jeppesen[3,5,6] and Meryem Beklioğlu[1,7].*

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Since macrophytes have direct and indirect effects on biological, physical and chemical processes, they are commonly used in assessing the ecological conditions of lakes. Moreover, when historical data from the lakes is absent, plant remains, like fruits and vegetative fragments, found in the lake sediments

can be used to acquire information on past lake conditions. However, for a relible interpretation of the past conditions it is important to confirm the congruence between contemporary and fossil assemblages. This study investigated such relationship between plant remains from surface sediments and present lake vegetation. Thirty-five shallow lakes, spanning around six degrees of latitude were sampled for aquatic plants, surface sediment plant remains and a range of in-lake environmental variables. The results showed that around 50% of the taxa recorded in the modern vegetation were represented by the sedimentary remains. Despite sedimentary macrofossils of some taxa were under- or over-represented relative to their frequency in the modern vegetation, a good accord between the assemblage composition of the modern and sedimentary samples was found. Furthermore, conductivity and trophic state (as indicated by total nitrogen, total phosphorus and chlorophyll-*a*) were identified as the environmental variables most clearly correlated with both the contemporary and macrofossil assemblages in these lakes. We conclude that, aquatic macrophyte remains can be used as reliable indicators of ecological status and to determine qualitative changes in aquatic plant community composition consequent upon environmental change.

Spatial and Temporal Patterns of a Zebra Mussel Invasion: An Individual Based Modelling Study

*Oğuzhan Kanmaz**

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Zebra mussels (*Dreissena polymorpha*) are one of the most notorious and well-known invasive species. After they have been introduced to out of their native habitat, Caspian Sea, they have reached to places like Mediterranean Sea, England, Sweden and even Great Lakes in western America in about 200 years. Because of their tremendous economical cost and ecological impact, they always been an important subject for researchers. Many different modelling methods have been applied to understand their invasion dynamics. In last two decades individual based models have been used in various ecolological studies. Despite their relatively simplistic nature, their applicability to complex systems makes them a strong alternative to the conventional models. Individual based models contains autonomous agents which have parameters that effect or be effected by the environment or the other agents. In this study, observational and theoretical results of many previous researches were used to create an individual based model in NetLogo environment, in order to reconstruct former invasions and also to help forecasting possible invasion scenarios.

Forest Management for Woodpecker's Conservation: A Lesson from Epirus Sacred Groves, NW Greece

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Sacred groves are small old-growth woodlands preserved through religion and maintained by local communities. We selected 20 oak sacred groves in Epirus region (NW Greece), and we employed a random selection algorithm to select an associated set of 20 control sites in the broader area, namely oak woodlands that are regularly managed by National Forest Service for wood harvesting. We sampled woodpecker's presence during early spring (2011) in terms of species calls (playback method), nests and tree holes from drumming (2782 trees examined overall), considering a standard quadrat (1ha) in the middle of each site.

Woodpecker's presence was recorded in all sacred groves (7 species, 55 ind.) and in 25% of control sites (2 species, 7 ind.). Sacred groves hosted significantly more woodpecker species and individuals than control sites (Friedman rank tests; $p<0.01$). Similarly, sacred groves included significantly more trees with woodpecker nests and tree holes from drumming (Friedman rank tests, $p<0.05$). These trees had significantly greater median tree diameter in breast height (dbh) as well as tree height than managed oak woods (Wilcoxon tests, $p<0.05$). Our results (violin plots) showed that forest management should maintain forest stands of mature oak trees within managed oak forests, with a median tree diameter (dbh) of 45-85 cm and median tree height of 8-14m, in order to conserve woodpecker diversity and nests.

Pollination Strategies of Plant Species in Phryganic Ecosystems of Southwestern Turkey

*Burçin Yenisey Kaynaş**[1], *Sinan Kaynaş*[2], *Çağatay Tavşanoglu*[3]

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Phryganic vegetation consists of plants mostly pollinate with insects. Plants and their pollinators provide an excellent system for studying competition since an increase in the number of the shared pollinators for a given set of plant species may reduce the flower visitation rates. In this study the plant-pollinator systems of phryganic plant species was investigated in a phryganic ecosystem in the South-west of Turkey. Six phryganic plant species, *Cistus creticus*, *C. parviflorus*, *C. salviifolius*, *Lavandula stoechas*, *Thymus cilicicus* and *Salvia fruticosa*, were selected to study. To determine which agents are responsible for the pollination, twenty individuals from each species were randomly selected, and ten enclosure with a large piece of 1 mm mesh tulle before the flowering period. The pollinator insects visiting the flowers of the selected individuals were observed for 30 minutes in total in each species during the flowering period of 2010. The results indicated that the *Cistus* species included in this study are obligate entomophilous species since none of the closed *Cistus* individuals produce any seeds. For *L. stoechas* and *S. fruticosa*, seed production success substantially decreased when pollination by insects was prevented. *T. cilicicus* is the only species in which the pollination is not depending on the presence of the insects. Two main flower visitor groups on phryganic plant species were determined: bees and beetles. In *Cistus* species, whilst beetles are the dominate visitors, visitation rates of bees were relatively lower. *L. stoechas* and *S. fruticosa* pollinated mainly with bees. Moreover, the difference of the dominated visitor groups in three *Cistus* species suggested that a specialization of visitor groups exists in *Cistus*. In conclusion, we found that the pollination process in the phryganic ecosystems conducted substantially by insects. Divergence and specialization in pollinator use of plant species is possibly a result of pollinator competition.

Avoiding Pitfalls in Detecting Behavioral Syndromes in Previously Untested Species: A Case Study on Monk Parakeets

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Behavioral syndromes are consistent differences among individuals that are stable over time and across different ecological contexts. Methods to diagnose syndromes have converged on a set of standardized experimental settings, each of which focuses on one or two commonly used measures to reflect the underlying context. These measures from separate experimental settings are then combined to express how individuals' behaviors are correlated across contexts. Although comparative work can be facilitated by using single, well- established measure for each experimental setting, failing to critically examine the choice of context-specific measures can carry some risks. Here we address the problem of correctly characterizing proactive-reactive syndrome for a previously un-diagnosed species by selecting the most appropriate measures, along with a sufficient number of measures across two experimental settings. We recorded a total of 10 different measures on 30 monk parakeets *(Myiopsitta monachus)* subjected to two experimental settings: presentation to a novel environment, and presentation of a novel object. In analysis we compared two approaches. We assessed the performance, in detecting a syndrome, of using (1) only the most commonly used measure, and (2) only the influential measures (i.e. measures that have the highest contribution on the principal component) for each of the three experimental settings, by comparing it to using all 10 measures (these were identified *a priori* from the literature). Principal component scores derived from commonly used measures approach correlated strongly with the inclusive approach ($r = 0.83$, $p << 0.05$), whereas scores from the influential measures approach resulted in a weaker correlation with the inclusive approach ($r = 0.18$, $p=0.34$), suggesting that commonly used, but not influential, measures approach can be adequate enough to detect proactive-reactive syndrome in monk parakeets. We conclude that it is critical to assess the performance of several methods if the focus is on a never-before tested species.

Long-term Trends in Danish Lake Plankton and the Effects of Nutrient Reduction and Climatic Changes

Korhan Özkan[12], Erik Jeppesen[134], Thomas Davidson[12], Rikke Bjerring[1], Liselotte Johansson[1], Martin Søndergaard[1], Torben Lauridsen[15], Jens-Christian Svenning[2].*

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A two-decade (1989-2008) bi-weekly time series of lake phyto- and zooplankton in 17 Danish lakes were analysed for long-term temporal changes. Time-series of lake water characteristics and climatic variables were also analysed to elucidate their role in driving the changes in lake plankton. Each time series

was analysed using the Mann-Kendal test for long-term trends, and temporal change in annually-pooled plankton genera composition was analysed using Non-metric Multidimensional Scaling. Six lakes, which were previously eutrophicated, had strong decline in their total phosphorus (TP) concentrations with a strong corresponding decline in phytoplankton biomass and a shift from Chlorophyta dominance in phytoplankton towards more heterogeneous communities, as well as an increase in plankton genera richness. Furthermore, plankton composition of these lakes changed towards that of lakes, which were not previously eutrophicated, indicating recovery of plankton community composition in response to improved ecological conditions. Notably, a widespread significant positive trend in plankton richness was observed across all lakes. The increase in plankton richness coincided with widespread nutrient reductions (re-oligotrophication), specifically with decreased phosphate and total nitrogen concentrations. These trends in plankton and water chemistry also coincided with significant increases in mean annual air temperature and precipitation and a decrease in wind speed during two decades of monitoring. Although the effects of lake chemistry and climate could not be separated due to their collinear changes, the climatic trends did not result in a strong corresponding trend in lake water characteristics, like surface temperature and stratification, and the trends in plankton variables were more consistently associated with the widespread nutrient reductions. Overall, the nutrient loading reduction across Danish landscape mostly due to the implementation of better agricultural practices have probably resulted in a widespread increase in plankton diversity, and resulted in marked recovery from eutrophication, especially in lakes with strong TP reduction.

Conservation Management of Balkan Chamois in Timfi Mount, NW Greece

Haritakis Papaioannou[1], Vassiliki Kati[1], Stefanos Sgardelis[2], Basilios Chondropoulos[3], Dimitrios Vassilakis[1] and Panayotis Dimopoulos[1]*

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The annual range of Balkan chamois (*Rupicapra rupicapra balacanica)* in Timfi Mt, exhibits a double pattern of habitat use: Winter/ Spring pattern includes areas at low and medium altitudes of 650m-1800m, mainly in forest with pines, whereas the Summer/ Autumn one includes areas in medium and high altitudes (1300-2500m), where sub-alpine heaths, pine forests and secondly rocky slopes and screes are in use. Winter and spring range areas are smaller than the summer and autumn one. The distribution of the species in Timfi Mt includes the most inaccessible parts of the mountain and the species presents a population density of 2 individuals /100ha. Females (38%) outnumber males (30%). Kids and juveniles represent 23% and 9% respectively of the total population. Although fecundity rate (0,60) and sex adult rate (0,80) is more or less similar to other European chamois populations, the Timfi Mt chamois population has just started to present a light increasing tendency. The dirt road network, together with the chamois poaching and the disturbance of the intensive legal hunting as well as the limited wardening of the area, seem to keep the total chamois population size in low numbers. Further research and urgent actions to solve these problems are needed in order to ensure the future of the Timfi Mt chamois population.

The Longer Is the Better: The Role of Testis and Sperm Size on Sperm Competition in Animals

Bahar Patlar[1*]

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Sperm competition is a form of sexual selection occurs when more than one male inseminates a female and then the physical competition between the sperms of different males to fertilize eggs. The selection pressure of sperm competition drives the evolution of traits that promote male mating success. Being primary structures of reproduction, sperm and testis morphology, particularly the sizes vary considerably across taxa and/or populations, and postcopulatory sexual selection is thought to be one of the main forces responsible for this diversity. Predominantly, selection to produce more and/or longer sperm can also select for the evolution of larger testis in many species. Phenotypic and genetic relationships between testis size and other mating success components (such as body size, copulation duration, ejaculate size, offspring number, etc.) are well documented across many groups of animals. Thus, in the field of evolutionary biology, researchers have greatly contributed to understanding the causes and consequences of diversification of testis and sperm size to be used as a model for understanding the evolutionary genetics of sexual selection. In this respect, the aim of this oral presentation is to emphasize the importance and role of testis and sperm size in sperm competition with giving examples of researches from this area.

Species Richness and Relative Abundance of Large Mammals in Protected Areas of Northern Anatolia

Anıl Soyumert[1†]*, *Alper Ertürk*[1†] *and Behzat Gürkan*[2]

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Protected areas are playing an important role for conservation of large mammal populations because of the serious threat on these species throughout the world. Black Sea region of Turkey has some of the major protected forest habitats of Anatolia that consist a diverse large mammal fauna. In the present study, three protected areas in the Black Sea region, northern Anatolia, were studied to evaluate the species richness and relative abundance of the large mammals. Küre Mountains National Park, Kartdağ Wildlife Development Area (equivalent to a Wildlife Reserve) and Sökü Wildlife Development Area were surveyed from 2008 to 2010 with 48 camera-trap stations, and 12 large mammal species were detected such as brown bear (*Ursus arctos*), gray wolf (*Canis lupus*), wild cat (*Felis silvestris*), red fox (*Vulpes vulpes*), red deer (*Cervus elaphus*), wild boar (*Sus scrofa*) and roe deer (*Capreolus capreolus*) in 13,432 camera-trap/day. Camera-trap stations were located with

~2 km interval and surveys continued for at least one year including four seasons in each study area to be able to obtain standard and unbiased data. Roe deer and wild boar were detected as most common target species in the study areas, and the lowest large mammal richness detected in Sökü WDA. Analyses were also conducted to evaluate the difference between protected and unprotected areas in the region; and certain areas were revealed to require further conservation status assessment due their high values of large mammal

abundance. Various human activities disturbing the wildlife were observed in the region during the field surveys, but the main threat in the protected areas for large mammals is detected as poaching. Consequently, conservation statuses and implementations should be reassessed in the region.

Zooplankton Avoidance Strategies against Predation in Turkish Shallow Lakes: Experimental Approaches

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Predation is often the key factor shaping the composition and body size distribution of zooplankton communities in lakes. Predation can also be a strong selective factor shaping avoidance and escape behavioral responses of planktonic prey. In north temperate lakes, zooplankton seek refuge among macrophytes, whereas in warm lakes fish may aggregate within macrophytes, thereby weakening their role as a daytime refuge for zooplankton and altering the zooplankton size structure. To elucidate the prey-predator interactions including the role of macrophytes as a refuge, we performed i) 'habitat choice' laboratory experiments to test the response of large-bodied *Daphnia magna* to predation cues at horizontal and vertical level in controlled laboratory conditions ii) artificial plant experiments, using three plant beds, conducted in eleven lakes in Turkey to determine the behavioural response *in situ* conditions. In artificial plant experiment, zooplankton samplings were performed during day and night in open water and within artificial plant beds. Fish were sampled in the littoral zone and in open water. The results revealed that under the predation pressure, large-sized *D. magna* prefered to move sediment not into the plant thereby the artificial plant experiment was also confirmed that dominant anti- predator behavioural response was mostly vertical migration both reverse and direct, depending on the predators. Under the predation risk intraspecific size-based migration was observed in large and medium sized zooplankton taxa, in contrast to small-bodied forms. There were also no migration observed in turbid conditions, due to the low encounter rate between prey and visual predator. Our results suggest that diel vertical migration is the common anti-predator avoidance behaviors and is notably affected by predators and, the response being size and water clarity dependent in shallow warm lakes.

Comparing Patterns of Post-Fire Germination in Central Anatolian Steppe and Mediterranean Plants:

Implications for Pyrogeography

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Fire regimes shape many plant traits, but fire-response of the plants under different fire regimes has rarely been compared. The aim of the study is to compare the germination response of plants to fire-related germination cues (heat shock and smoke) in Central Anatolian Steppe (CAS) and Mediterranean vegetation regions of Turkey, as the former has a history of low-intensity surface fires but the latter has frequently subjected to high-intensity crown fires. We collected seeds of 102 plant taxa from many localities in the selected regions between 2008 and 2012, and germination experiments including various heat shock treatments (60, 80, 100, 120, 140 °C for 5 min.) and an aqueous smoke treatment were conducted. We hypothesized that there should be clear differences in post-fire germination patterns in CAS and Mediterranean plants, as we expected more fire- stimulated germination in the Mediterranean taxa. The probability of germination stimulation was tested by analysis of deviance (GLM) with binomial error distribution, and germination patterns of plants were further analyzed using ANOVAs as region, treatment, distribution range and life form were considered as fixed factors. Only a few CAS taxa positively responded to low heat shocks, but seeds of many could resisted those treatments; whereas high mortality ratio was observed above 100 °C heat shocks. Conversely, seed germination was stimulated in 100, 120, and 140 °C heat shock treatments in many Mediterranean plants. Smoke application positively affected germination in only a few taxa from CAS, but germination percentage of many taxa from Mediterranean region increased in smoke treatment. The results suggest that the observed differences in post-fire germination patterns between CAS and Mediterranean plants can be explained by different fire regimes proceeding in these regions. Studying fire response of plants with a pyrogeographical approach is needed to understand how fire regimes shape plant traits.

Gamma-amino Butyric Acid (GABA) Shunt in Phylogeneticaly Divergent Plants

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The non-protein amino acid, GABA found in a wide range of organisms including plants. Due to its presence in diverse classes of organisms from prokaryotes and eukaryotes, GABA and components of GABA metabolism can be used as important tools for evolutionary analysis. Different roles in plant metabolism including carbon-nitrogen metabolism, energy balance, signaling and development had been attributed to GABA and constitutive and induced levels showed variations within several plant species. Research on GABA biosynthesis and GABA levels within an evolutionary concept are restricted to model plants such as *Arabidopsis thaliana* and tobacco. In order to understand and address the evolution of GABA shunt in plants we aimed to compare the levels of GABA shunt components such as activities of GDH and

GAD enzymes and total nitrogen, total soluble protein, succinate, glutamate, proline and GABA contents in plants from different phylogenetic levels such as *Ulva lactuca, Pseudevernia furfuracea, Nephrolepsis exaltata, Ginkgo biloba, Pinus pinea, Magnolia grandiflora., Nymphaea alba, Urtica dioica, Portulaca oleraceae, Malva sylvestris, Rosa canina, Lavandula stoechas, Washingtonia filifera, Avena barbata, Iris kaempferi*. Within the plant species that we have studied there were discrepancies between the activities of GABA biosynthetic enzymes (GAD and GDH) and GABA levels. However, the trends (increase-decrease) in the enzyme activities were not always parallel to GABA accumulation. Succinate and GABA contents were remarkably different in higher and primitive plants. Glutamate levels were high with a few exceptions and proline contents were at similar low values as compared to other amino acids. Our results support the hypothesis that GABA shunt plays a key role in carbon and nitrogen partitioning via linking amino acid metabolism and TCA cycle which is more essential for higher plant species.

EVOLUTION ORAL ABSTRACTS

iPBS Retrotransposons Marker For Diversity Analysis Among Wild Lens Species From Turkey

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The genetic diversity and relationship among wild Lens species from Turkey has received little attention and seldom been investigated. Lentil is the crop with low number of developed markers to be used in in breeding and genetic studies. Here genetic diversity and relationship among 50 accession belonging to six wild Lens species and one cultivated species, mostly from Turkey (core area of diversity and domestication), were assessed using newly developed iPBS retrotransposons and ISSR markers. The ten iPBS primers generated a total 151scorable bands and 150 of these were found polymorphic (99.3%), with an average of 15.0 polymorphic fragments per primer, while 138 scorable bands were detected using 10 ISSR primers with 100% polymorphism with an average of 13.5 bands per primer. The average polymorphism information contents value for ISSR marker (0.97) was higher iPBS marker (0.90). *L. orientalis* was the most diverse species showing the possibility of wide crosses with cultivated species *L. culinaris*. Cultivated varieties also showed high level of polymorphism with percentage of 82.92% and 51.92 with ISSR markers and iPBS marker. *L. lamottei* and *L. tomentosus* were the least polymorphic species with iPBS and ISSR markers respectively. The grouping of accessions and species within clusters were almost similar when iPBS and ISSR neighbor net planner graphs were compared. We have demonstrated that genetic diversity and relationship among seven Lens species from Turkey corroborated by two different genetic marker systems and adds strength to the taxonomic classification proposed genus *Lens*. Our data also suggested the role of iPBS-retrotransposons, 'a universal marker' for molecular characterization and genetic diversity studies in wild and cultivated *Lens* species.

Genetic Analysis of Hybrid Sterility in Yeast"

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Haploid cells of *Saccharomyces cerevisiae* and *Saccharomyces paradoxus* can fertilize, and form mitotically viable diploids. However, when diploid hybrids undergo meiosis, only 1% of the gametes they produce are viable. There are three potential explanations for this phenomenon of hybrid sterility in the scientific literature. The first hypothesis is the Dobzhansky-Muller model of incompatibility, which suggests that genes from one species do not function with the genes from another and therefore, if the products of those genes are essential for survival, hybrids are inviable. The second hypothesis that has been suggested is inviability through chromosomal rearrangements. The third hypothesis, which we suggest is an important factor in yeast hybridization, is the lack of recombination. There is a high degree of sequence divergence between yeast chromosomes, which potentially leads to the inhibition of crossover events and

therefore recombination. Here we have tested this hypothesis by inserting an artificial recombination hotspot (a double-strand break point) into the *Saccharomyces cerevisiae* chromosome III, and measured the change in chromosome III crossover and aneuploidy rates within the hybrids. A 4-fold increase in crossover rates decreased chromosome III aneuploidy rates from 28% to 15%. We have further testes this hypothesis by repressing anti-recombination proteins those prevent homeologous recombination events. Chromosome III crossover rates increased 10-fold, and aneuploidy rates decreased down to 11% in the hybrid spores, which further supported the anti-recombination hypothesis. Here we argue that the lack of recombination in yeast might be the major cause of the post-zygotic reproductive isolation in *Saccharomyces* yeast.

Brown Bears from Turkey Show Exceptionally High Maternal Lineage Diversity

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The genetic diversity and phylogeography of brown bear (*Ursus arctos*) maternal lineages have been studied extensively over the last two decades. However, sampling was so far largely limited to the northern Holarctic, and possibly biased towards lineages that recolonized the vast expanses of the north as the Last Glacial Maximum (LGM) ended. Here we report the genetic diversity and maternal phylogeography of non- invasively sampled 35 brown bear individuals, including 5 captive bears, from Turkey. Phylogenetic analyses based on a 269 bp long piece of bear mitochondrial DNA revealed 14 haplotypes belonging to four divergent lineages. The most widespread lineage was found to be the Holarctic clade 3a, while a specimen from the Taurus range (southern Turkey) belonged to a lineage previously only reported from presumably extinct bears from the Lebanon. Individuals from western Turkey are related to south European bears while the "Iran" clade occurs also in eastern Turkey. Despite limited sampling, our study demonstrates a high level of diversity among Turkish brown bears, extends the ranges of both European and Middle Eastern clades into Turkey, and identifies a new divergent lineage. The designation of the so-called Syrian bears, *U. a. syriacus*, as a separate evolutionary unit is not supported. Our study thus establishes the value of proper sampling from regions that have not been significantly affected by the LGM.

Gaining Insight into the Evolutionary History of Sheep in Anatolia

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Recent archaeozoological studies indicated that perhaps the oldest (11.000 years before present) and may be the only sheep domestication center was in Southeast Anatolia. In the present study, to contribute to the understanding of the evolutionary history of sheep, mitochondrial (mt) DNA polymorphisms found in modern Turkish domestic (n = 628), modern wild (n = 30) and ancient domestic sheep from Oylum Höyük in Kilis (n =
33) were examined comparatively with the accumulated literature data. The lengths (75 basepairs (bp)/76 bp) of the second and subsequent repeat units of the mtDNA control region sequences differentiated the five haplogroups (HPGs) observed in domestic sheep into two genetic clusters (the first cluster being composed of HPGs A, B, D and the second one harboring HPGs C and E) as was already implied by other mtDNA markers. To manifest genetic relatedness between wild and domestic sheep haplogroups, their partial cytochrome *b* sequences were examined together on a median-joining network. The two parallel but wider aforementioned clusters were observed also on the network of the wild individuals, within which domestic haplogroups were embedded. The *Ovis gmelinii* wilds of the present day appeared to be distributed on two partially overlapping geographic areas parallel to the genetic clusters that they belong to (the first cluster being in the western part of the overall distribution). Thus, the analyses suggested that the domestic sheep may be the products of two maternally distinct ancestral *Ovis gmelinii* populations. Further studies should include more samples distributed spatiotemporally on Anatolia to better understand the sheep evolutionary history in the area.

Mechanisms of Selection in an Antirrhinum Hybrid Zone

Tom Ellis, Austria.

Hybrid zones, where two populations meet, interbreed, and exchange genes, represent natural evolutionary laboratories. Alleles from either population recombine into new combinations which have never been exposed to selection, and as such are testing grounds for the effects of genes and haplotypes on fitness. In the Spanish Pyrenees snapdragons (*Antirrhinum magus*) with yellow and magenta flowers form a stable hybrid zone with recombinant flower colours, suggesting a selective role for pollinators. We are using SNP data to construct a multi-generation pedigree to determine the distribution in fitness for the entire fitness, but the pedigree itself cannot explain the mechanism underlying selection. I will present field and experimental data showing that bumblebees prefer locally-common phenotypes, leading to assortative mating. This contributes to the maintenance of the hybrid zone, because the more common yellow and magenta forms are favoured on their respective side. However pollinators cannot explain all the selection

which seems to be acting, and I will discuss other experiments we are carrying out to elucidate other mechanisms.

Population Genetic Structure of the Water Flea along an Age-Gradient of Novel Habitats Created by Ice Retreat in Greenland

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In response to climate change, glaciers are retreating at a high rate in Greenland. Glacier retreat has been well documented in the Jakobshavn-glacier region of Greenland. We investigated how the pond and lake habitats that became inhabitable due to this retreat are colonized by a key plankton organism, the water flea *Daphnia.* We assessed the spatial genetic structure of the Metapopulation of the *Daphnia pulex* spp. complex along the age gradient of lakes and ponds in the Jakobshavn Isbræ region of Greenland. We sampled 61 populations from 21 lakes and 40 ponds that varied in environmental variables, altitude and depth. A total of 1420 individuals were genotyped at 9 microsatellite loci, and we screened several individuals from each multilocus genotype for sequence variation at the mitochnoderial-COI gene. We identified two species of the *Daphnia pulex* spp. complex, *D. pulicariaand*, less abundant, *D.middendorffiana*. Both these species are obligately parthenogenetic and polyploid. We identified 42 clones that widely varied in spatial distribution. There were 1-9 clones per population, with clonal diversity ranging from 1.0 to 3.72. What is more, Older systems (>150 years) showed higher clonal richness and clonal diversity than younger systems (<150 years). Furthermore, genetic differentiation among populations was higher in older (mean Sorensen similarity index 0.52) than in younger systems. The genetic distance among 40 clones ranged from 0.02 to 0.70. Overall, we observed that the relative abundance of clones in habitats was strongly related to environmental rather than to spatial variables, providing evidence for strong sorting along environmental gradients (i.e. conductivity and nutrients). This shows that dispersal limitation was not important in this system, even not in the young habitats of age approx 10 - 150 years.

Geographic Structure of the Edible Dormouse in Turkey

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The use of morphometric methods allows a more accurate quantification of a broad range of

phenotypic, such as teeth. Beyond their value as taxonomic characters for species identification, intra-specific patterns of differentiation in tooth shape can thus be addressed. The present study illustrates the potential of fine- scale morphometric analyses for improving our understanding of geographic structure of a hibernating forest species, the edible dormouse (*Glis glis*) in a seldom investigated zone of its distributing area: the Northern part of Turkey (Thrace, Marmara and Black Sea regions). Two complementary approaches were combined: genetics (mtDNA) and morphometrics (tooth size and shape). Morphometric results evidenced a complex pattern of differentiation. A major signal opposed Western vs. Eastern parts of Northern Turkey. A secondary differentiation occurred along the Eastern part of the Black Sea coast. In contrast, mitochondrial DNA revealed a surprising homogeneity amongst Turkish and European populations, all sharing the same haplotype. We interpret these apparently discrepant results as the consequence of a complex history: (1) post-glacial recolonization from a single refuge; (2) isolation of populations in different forest blocks. This may be the results of changes in the composition of the forest, driven by climatic and topographic factors, as well fragmentation of the forest, due to local climatic variations but also possibly to anthropogenic factors.

Transcriptomic Variation Between Day and Night in the Coral Endosymbiont Symbiodinium

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The unicellular photosynthetic dinoflagellate symbionts that inhabit the cells of scleractinian corals, *Symbiodinium* sp., play a critical role in supporting the coral host. Typically considered a mutualism, *Symbiodinium* provide photosynthetically fixed carbon products to the coral, fulfilling a majority of the host's energetic requirements, while the coral provides a stable environment and nutrients to the symbiont. The breakdown of this symbiosis can cause coral bleaching and mortality and poses a significant threat to the future of coral reefs. Despite their critical role in sustaining valuable coral reef ecosystems, little is known about the regulation of gene expression in *Symbiodinium*. Here we evaluate the in situ transcription profiles of *Symbiodinium* in the Caribbean staghorn coral, *Acropora cervicornis*, using RNA-seq. Samples were collected at mid-day and mid-night from two regions of the coral colony, the symbiont-dense branch bases and symbiont- poor axial polyps. Samples collected from the axial tips of coral branches contained too few symbiont transcripts to detect gene expression differences between day and night. However, samples collected in branch bases show differential expression of transcripts related to translation, photosynthesis, redox homeostasis, proteolysis and apoptosis.

A Genetic Investigation on the Evolution and Taxonomy of the Genus *Nannospalax* in Turkey

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Currently there is no consensus over the details of evolutionary history and taxonomical classification of the genus *Nannospalax* in Turkey. This includes the geographical distribution of the different cytotypes, their relationships to one another, and the number of recognized species. In order to try to answer some of these questions, 896 bp segment of the mitochondrial D-loop region of 120 samples belonging to *Nannospalax xanthodon*, *Nannospalax leucodon* and *Nannospalax ehrenbergi* were amplified by the PCR method and sequenced. The relationships between species and between chromosomal forms of these species were investigated through various phylogenetic analyses. The results showed that *N. leucodon* and *N. ehrenbergi* were distinct species living in Thrace and Southeast Anatolia, respectively. Moreover, the idea that only *N. xanthodon* was distributed in the rest of Anatolia was not supported. Nine cytotpes were seen to cluster into three main groups, suggesting the presence of three different species in Turkey. *N. labaumei* includes 2n= 52S, 56W, 58 and 60 cytotpes, *N. xanthodon* contains 2n=36, 38, 40, and 52N cytotypes (western populations) and *N. nehringi* has 2n=50E, 54C and 56S cytotypes. In order to make firmer conclusions, especially with regards to if the different cytotypes are separate species and to give them proper species names, more molecular (especially nuclear), karyological and morphological studies should be performed with larger sample sizes, and also considering the potential geographical barriers between different cytotypes and species.

Evolutionary Relationships and History of Rye (Secale spp.)

Öncü Maraci, Hakan Özkan, Raşit Bilgin

Genus *Secale* belongs to the family of true grasses Poacea, which also includes wheat and barley. The genus is quite heterogeneous with annual, perennial (long or short lived) self-incompatible and self-compatible forms. Besides cultivated rye, genus *Secale* comprises weedy and wild species. There is no consensus among scientist on taxonomy of the due to the lack of diagnostic criteria, out-crossing nature of some species and the interspecific fertility. Thus, the number of species classified in the genus varies from three to 14 in different studies. According to classification system adopted by Germplasm Resources Information Network (GRIN), the taxon contains four species: *Secale cereale*, *Secale vavilovii*, *Secale sylvestre*, *Secale striticum*. Among these, *Secale cereale* and *Secale striticum* are polytypic. Moreover the origin of cultivated rye and phylogenetic relationships of genus *Secale* are still controversial. In order to gain new insights about taxonomy and evolutionary history of the genus and to understand the distribution of genetic variation within and between landrace populations and cultivars 142 different accessions of *Secale* species from different eco-geographical origins, were evaluated morphologically and molecularly. Molecular analyses included nuclear SSRs and chloroplastic and nuclear SNPs. We identified three different gene pools that are not differentiated geographically, indicating the three clades originally formed

pass across species barriers and get mixed during extensive and global geographical dispersal. Furthermore, our preliminary data confirmed that *S. sylvestre* is the first separated and most divergent species. We also observed that *S. vavilovii* is closely related to *S. cereal*e emphasizing intensive introgression between these two species.

Polygamy and Sexual Selection for Long-Life

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Humans are exceptionally long-lived primates, although it is not necessarily clear from an evolutionary perspective why this should be so. It has been suggested previously that polygynous mating practices may have contributed to enhanced selection for survival at later ages in human males, and these selective forces may have caused indirect selection for post-reproductive survival in women. This study quantifies directly the component of selection for late-life survival that is generated by polygyny in a human population. Using recently developed phenotypic selection and evolutionary demographic methods, I compare selection gradients and selection coefficients that describe the strength of selection for age-specific survival. These are measured using longevity and reproductive records from over 27,000 monogamous and polygamous families living in the Utah Territory (located in the American West) during the late 19th century. I find strong evidence for a relationship between high rates of polygamy and increased selection for long-life in males, with up to 30% of all selection for male survival in the late 50's generated by polygamy. In this population, the banning of polygamy by legal and religious edicts was closely associated with relaxed selection for long-life survival. These results suggest that extant genetic predispositions for long-life may be dividends of past selective regimes that have since been weakened by changing marriage practices.

Do Discordant Mitochondrial and Nuclear Distribution Patterns Indicate Introgression Following Secondary Contact between Anatolian Water Frog Lineages *(Pelophylax Cf. Bedriagae)* and European Water Frog Lineage *(Pelophylax Ridibundus)* in Anatolia?

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A growing number of phylogeographic studies in animals reveal discordance in the pattern of geographic distribution, degree of genetic differentiation, times of divergence, and tree topology between

mitochondrial and nuclear DNA markers. Our initial phylogeographic studies of Turkish water frogs, based on mtDNA sequences, indicated that Anatolia was exclusively inhabited by haplotypes belonging to Anatolian lineages. Although eastern Anatolia and the Black Sea region were represented by limited samples, no *ridibundus*-specific haplotypes were found except in European Turkey. In the present study, we present extended mtDNA (ND2 and ND3 genes: 1378 bp) and new nuDNA (serum albumin intron 1 + RanaCR1: 1160 bp) data sets, collected throughout Anatolia, to examine the geographical concordance between these two markers. Bayesian phylogenetic analysis of both mtDNA and nuDNA sequences indicate that the Anatolian lineage (*P.* cf. *bedriagae*) and the European lineage (*P. ridibundus*) are markedly divergent. Time estimates of their divergence, based on each marker separately and on both markers concurrently, correspond to the Messinian Salinity Crisis (MSC), about 5.0-6.0 Ma. In contrast to this well-corroborated degree of genetic differentiation, the geographic distributions of these two markers show very discordant pattern. The new nuDNA data set reveals that individuals carrying *ridibundus*-specific alleles, either in heterozygous or homozygous condition, are found not only in European Turkey but also near the Black Sea and in eastern Anatolia, even though only Anatolian- specific mtDNA haplotypes are present in Anatolia. A possible cause for this discordance is introgression following secondary contact during the latest Pleistocene or earlier Holocene, when the Black Sea was a fresh to brackish-water lake. Introgression is suggested only in central to eastern Anatolia, and only by nuDNA, not by mtDNA. It could thus be explained by sex-biased dispersal. These analyses are preliminary, however, and should be supported by additional nuDNA marker

Lizards in Space: Biogeographic Variation in Morphmetrics of *Anolis sagrei*

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In the lizard genus *Anolis*, body size, cranial and hind limb characteristics, as well as the number of subdigital lamellae, are largely plastic morphological factors that reflect a functional relationship with habitat. *Anolis sagrei* is a species that exhibits a dramatic geographic variation in phenotype across numerous Caribbean islands and mainland areas of South America. Our study aimed at understanding phenotypic distribution using *A. sagrei* as a model species. We quantified this variation by X-raying and scanning 666 specimens from 49 locations well distributed within the species' native range. We digitally measured subdigital lamellae (IV toe), and a suite of 14 cranial and hind limb traits. To account for potential influences of climate on the distribution of phenotypic characteristics, we extracted 20 climatic and spatial variables from WorldClim, and integrated them with the morphometric analyses. Our results indicate marked differences between mainland and island populations. In addition to having a significantly larger body size and greater number of lamellae, mainland *A. sagrei* have relatively larger heads and shorter hind limbs when compared to their Caribbean and Greater Antillean counterparts. The unusual morphology of one isolated monospecific island population (Swan Islands, Honduras) may suggest a colonisation event deriving from mainland populations, or the effects of ecological release. The data indicate that segregation of morphological traits within *A. sagrei* is more strongly defined by habitat (islands vs. mainland) than with spatial or climatic gradients. In the future, invasive populations will be analysed to help identify source

populations with relative ease. Our study, combined with forthcoming molecular data, will allow us to disentangle the interactions between the environmental, ecological and genetic factors that define phenotype.

Mechanisms of Testes Expression Divergence in Humans and Chimpanzees

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Although human and chimpanzee are very closely-related species, they display several conspicious phenotypic differences. One of the most stunning ones is testis size: male chimpanzees have about three times larger testes than humans. Chimpanzees are also known to produce faster sperm, in larger amounts. These species differences have been attributed to differences in mating structure. In chimpanzees, females mate with multiple males, whereas in humans, mating systems tend towards monogamy. Gorillas, which have harem systems, also have small testes and slow sperm, like humans. It was previously shown that these species differences can also be observed at the transcriptome level: humans and gorillas have similar testis expression profiles, which are distinct from those of chimpanzees. Here we investigate the mechanism of testis expression divergence among hominids. Specifically, we ask whether expression differences are driven by independent evolutionary changes across hundreds of genes, or by changes in cell type proportions and shifts in developmental timing. First, we show that human and gorilla testes have a significantly smaller proportion of post-meiotic germ cells, relative to chimpanzee. Second, we compare adult hominid testis transcriptome data, with transcriptome data from testes of 12 macaques of different ages, from birth to 31 years of age. Interestingly, we found that chimpanzee transcriptome profiles are closer to those of adult macaques, while human and gorilla profiles are both closer to those of younger macaques, implying neoteny in these species. Thus, an explanation for these distinct testis phenotypes and molecular profiles can be a simple regulatory change during developmental processes leading variation in cell type proportions among species. We are currently studying whether these changes are the result of positive selection in the chimpanzee lineage, or relaxation of selection in the human lineage.

A Novel Fixation Bias for Extended Homopolymers in the Human Genome

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Different types of mutations occur and spread in the genome at varying rates. For instance, C->T transitions at CpG sites are the most mutation in mammalian genomes. In contrast, GC-biased gene conversion causes A or T->G or C mutations to spread and fix rapidly in populations. Such fixation biases have not yet been investigated taking neighboring sequence context into account. Using human population genomic data from the 1000 Genomes Project and comparative genomic data from other primates, we investigated possible fixation biases in the human genome at the level of quintuplets: 5 bp sequences where the middle base is mutated. Unexpectedly, we found a fixation bias for mutations that extend

homopolymers (same base sequences, e.g. GGGG) across the genome. For example, since the human-chimpanzee common ancestor, the C->G mutation, AGCGG->AGGGG, has fixed in the human genome ~2.5 times more frequently than expected, relative to the symmetric "disruptive" mutation, AGGGG->AGCGG. This novel fixation bias is also observed as higher derived frequencies for homopolymer extending mutations; it can be replicated using genotyping data; and cannot be accounted for ancestral state misidentification. Meanwhile, the bias is not observed in genic regions or in CpG sites. We are currently studying possible mechanistic or selection-based explanations for this novel fixation bias.

Molecular and Morphological Phylogeny of the Genus *Orobanche* L. (Orobanchaceae) with Emphasis on Turkish Taxa ***Golshan Zare[1*], Ali Dönmez[1], Pedro Escobar Garcia[2] and Gerald Schneeweiss[2].***

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Orobanche s.l. as a large genus among the holoparasitic members of Orobanchaceae known as a taxonomically daunting group. This genus includes five genera, *Orobanche* s.s., *Phelipanche*, *Aphyllon*, *Myzorrhiza* and *Boulardia*, some of which including economically very important parasitic weeds. The main aims of this study were to investigate the phylogenetic relationships of and within *Orobanche* s.l. using molecular data and evaluate morphological character evolution and synapomorphies. This research includes 138 accessions with a broad sampling range of taxa from one of the group's diversity centers, Turkey. The phylogeny of taxa is investigated using combined nuclear ribosomal internal transcribed spacer (ITS) and plastid gene *rps*2 analyzed using Maximum parsimony, Maximum likelihood and Bayesian methods. All analyses resulted in phylogeny trees with congruent topologies. The results confirm non-monophyly of *Orobanche* s.l.and provide more evidence for disintegration into five separate genera. A lack of resolution in relationships of some taxa, especially *O. minor* and *P. ramosa* aggregations, is probably due to rapid radiation in some lineages, homoplasy or the presence of cryptic species. Evolution of inaperturate pollen and divided calyx constitutes a synapomorphy for *Orobanche* s.s., which is congruent with phylogenetic pattern within the genus.

ECOLOGY POSTER ABSTRACTS

Current Status and Threats of Elasmobranchii Species in the Seas of Turkey

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Biodiversty and its conservation are regarded as one of the major issues of enabling sustainable use of natural resources. In the Mediterranean region, elasmobranchs are characterized by their diversity (49 sharks and 36 rays). The region is known to be an important habitat for cartilaginous fish and is thought to encompass unique breeding grounds for species such as the white shark (*Carcharodon carcharias*) and thornback ray (*Raja clavata*). This review focuses on diversty, distribition and threateing status/factors of sharks and ray fishes in all seas of Turkey. The all seas of Turkey is the ideal habitat for 64 chondrichtyes species and this review included 62 native elasmobranchii species and 1 alien elasmobranchii species (*Himantura uarnak*) in the Turkey's sea belonging to 8 orders, 21 families and 36 genera. Available evidence indicates that chondrichthyans in the Turkey's seas (especially in the Mediterranean) are generally decreasing in abundance, diversity and range. Despite their evolutionary success, many elasmobranchii species are increasingly threatened with so many reasons such as human activities, environmental degradation and the conservative life history of these fishes. Critically Endangered, Endangered, Vunerable or Near Threatened status are recognized for 71% of coastal waters of Turkey. Sixteen percent (10 species) of chondrichthyan fishes of Turkey are considered Least Concern status. 21% are in Data Deficient and 2% (only one species) is Not Evaluated. Elasmobranchii species have important trophic functions in marine ecosystems. In addition, quantitatively describing the current status and threating factors are important to prevent these fishes extinction.

Orchids: Queen of Mimicry

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Mimicry is the similarity of one species to another which protects one or both. This similarity can be in appearance, behaviour, sound, scent and location. Orchidaceae is a diverse and widespread family of flowering plants with blooms that are often colourful and often fragrant, commonly known as the orchid family. They are herbaceous monocots. Along with the Asteraceae, they are one of the two largest families of flowering plants. There are between 21,950 and 26,049 species in 880 genera. Orchids can be found in almost every country in the world except Antarctica. Turkey is a rich country of terrestrial orchids and represented by 170 taxa. Terrestrial orchids have creeping, much reduced, fibrous and fleshy rhizomes or tuber like roots. Some orchids have very special ways of pollination because they use mimicry. For example, *Epidendrum ibaguense* resembles flowers of *Lantana camara* and *Asclepias curassavica*, and is pollinated by Monarch Butterflies and perhaps hummingbirds. *Cephalanthera rubra* produces no nectar, but it mimics *Campanula persicifolia* and thus deceives the leaf-cutting bee *Chelostoma fuliginosum* which visits it. The bee cannot distinguish between the colors of two flowers and pollinates both species. The Eurasian genus of *Ophrys*, the labellum is adapted to have a colour, shape and odour which attracts male

insects via mimicry of a receptive female. Pollination happens as the insect attempts to mate with flowers. All these similarities show that orchids are pollinated by pollinators deceived.

Modelling the Future Trophic State of Lake Beyşehir Considering Climate and Land Use Changes

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Lake Beyşehir that is the largest freshwater lake of Turkey was subjected to intensive anthropogenic stresses of excessive water withdrawal for irrigation, fish introduction, sewage effluents and increased agricultural pressure in the catchment during the last century. In addition to these stresses, climate change projections may also exacerbate the water quality in future. In this study, to consider the on-going processes in Lake Beyşehir catchment and their effects on lake, catchment scale model SWAT was used to predict the surface runoff and nutrient loading for the future climate projections (2031-2060) and for generated land use scenarios. Outputs of SWAT (flow and nutrient loads) and climate change projections was used as an input for lake models (PCLake, DYRESM-CAEDYM, PROTECH), which enable us to simulate future trophic structure of the Lake Beyşehir. Our results showed that future climate change in combination with generated land use scenarios will have a major impact on hydrology and nutrient loads by decreasing surface runoff up to 30% and N & P loads by %20-63 while impact of these changes on lake productivity is minor. As hydrology seems to be most affected component, future studies should focus on longer time scales (100 years or more) to determine which point in future Lake Beyşehir may no longer resist the alterations and how these extreme water level decreases affects the trophic structure of lake.

What Shapes Species Distribution? A Case Study on Spadefoot Toads (Genus *Pelobates*)

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The spadefoot toads (genus *Pelobates*) are highly specialized burrowing species, and because of their secretive behavior (e.g. nocturnal activity, weak underwater breeding call) their life histories are not well documented. Since populations living at the limits of their range are especially vulnerable to even slight climate changes, we focused our study on syntopic populations of *P. fuscus* and *P. syriacus* at the limit of their ranges (Black Sea Coast, Romania). We aim to understand the main factors limiting their distribution: life history traits, environmental conditions, biotic interactions or biogeographical barriers? Our methodology combined field surveys and experimental designs to assess population parameters, environmental plasticity and behavioral patterns. We also performed species distribution models for both

present and future climate scenarios to see if climate is a major driver in shaping their distribution. Both species have similar habitat requirements, but differ in body size and sexual dimorphism. We showed that these differences are determined by distinct patterns in growth rates before sexual maturity, and energy allocation between growth and reproduction after sexual maturity. They also exhibit different patterns of foraging behavior: *P. fuscus* is relatively sedentary whereas *P. syriacus* is a more active predator. We found significant differences in the species' response to desiccation, tolerance to salinity, and post-metamorphosis feeding rates, suggesting that *P. syriacus* is better adapted to survive in hostile environments. The present climatic models revealed a distribution which is not in equilibrium with the climate, especially over the sympatry area of the species. The range overlap is projected to expand towards the end of this century in the context of increasing drought intensity. This scenario may favor the northwards displacement of the better adapted *P. syriacus,* but further assessments are required.

Seasonal changes in microalgal flora of volcanic lakes in Turkey

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A systematic study was conducted on the microalgal flora of volcanic lakes in Turkey revealing a rich algal resource for biotechnological exploration. Present study reveals the diversity of microalgal flora of volcanic lakes, Nemrut (42° 15' 25" N 38° 31' 11" E), Aygır (42° 48' 8" N 38° 47' 31" E), Meke (37° 40' 32" N 33° 38' 36"E), Acıgöl (37° 42' 25" N 33° 39' 18" E), Narlıgöl (38° 20' 50" N 34° 29' 28" E), Gölcük (37° 41' 04" N 30° 27' 40" E), located in Middle Anatolian and South-Eastern parts of Turkey collected on January, April, July, Novemver 2013. In total, 156 microalgae species were identified. Of these, 93 species belonged to family Bacillariophyceae, 2 to Dinophyceae, 4 to Euglenophyceae, 19 to Conjugatophyceae, 31 to Chlorophyceae, 6 to Conjugatophyceae, and 31 to Cyanophyceae families. Physicochemical nature of water samples were analyzed and correlated with the total microalgal diversity. Based on the correlation coefficient data, microalgae showed positive relationships with dissolved oxygen, salinity, nutrients, and negative relationships with temperature and turbidity. The species diversity index, Species richness and species evenness were calculated and analyzed for microalgal population dynamic variation in the volcanic lakes of Turkey.

Role of Serotonin in Environmental Stress Induced Sex Determination in Daphnia

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Daphnia is a freshwater crustacean well-known for its indicative responses to environmental changes. One such response involves a switch from parthenogenesis to sexual reproduction. Non-optimal conditions including shortening of daylight duration, population crowding or food restriction lead to parthenogenetic generation of males instead of daughters, followed by sexual reproduction. However, the mechanism of environmental change-induced sex determination is not well-understood. Here we investigate how changes in the length of the light period affect sex determination. Although previous

studies have suggested methyl farnesoate, a terpenoid hormone, as the causal factor leading to the generation of males, the pathway between detection of light duration and the secretion of methyl farnesoate has remained unknown. Studies in different crustaceans have demonstrated relationships between light, serotonin and methyl farnesoate synthesis. We thus hypothesized that serotonin could be the link between photoreception and methyl farnesoate secretion. We are currently testing this hypothesis by applying selective serotonin reuptake inhibitors and multiple serotonin receptor agonists and antagonists under short and long light durations. Our results are expected to reveal a novel aspect of the ecoresponsive physiology of *Daphnia*, while illuminating the evolutionary origin of the relationship between serotonin and light.

Ecological Niche Modeling as a Baseline Tool for Evolutionary Analysis of the Melanism in Felidae

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The adaptive relevance of animal coloration has been explored and discussed for over a century. Melanism is a pigmentation phenotype that can present adaptive roles in certain ecological conditions and directly influence several biological factors such as thermoregulation, susceptibility or response to disease, camouflage, aposematism, sexual selection and reproductive success. The occurrence of melanism is rather common in the Felidae, having been documented in 13 of the 38 species, in none of them has it reached fixation, but in some cases presents very high frequencies in natural populations. We evaluate the adaptive relevance of the melanism in two great felid species and consider two alternative hypotheses: (I) melanism present throughout entire species' distribution, occurring randomly with absence of association between phenotypes and landscapes or, (II) melanism distributed according to biogeographic constraints, with evidences of demographic factors and/or natural selection. We obtained location records for 765 jaguars *Panthera onca* (696 non-melanistic / 69 melanistic) and for 623 leopards *Panthera pardus* (552 non-melanistic / 67 melanistic) and generate potential distribution models through Maxent software and environmental predictors. The frequency of melanism in natural population is about 9% in jaguars and 10% in leopards with accuracy of prediction around 94,9% and 92,6%, respectively. Our results/models reveals a nonrandom distribution across different landscape conformations, suggesting a directly influence of biomes/ecoregions with possible effect of natural selection under coat color variants in wild cats, and can be considered as an ecological tool for phenotypic conservation.

The Effect of Diet at Larval and Adult Stage on Life Span in *Drosophila melanogaster*

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Life span is the main life history trait to describe aging for many model organisms. In general, life span varies with genotype and with related environmental factors. Diet, which is a strong environmental variable for life spanthat is known to affect the longevity. We hypothesized that the effect of variable diet composition that was created by reducing yeast levels from the

optimum amount (100 g/l) will reduce the mean life span.In particular, we studied the effect of restricted yeast level on both larval and adult stage of life span with four- isofemale line selected by starvation resistance. We used three restricted yeast amounts (50 g/l, 20 g/l, 10 g/l) from optimum amount for each stage with their control groups. We measured 1000 individuals' life span for each isofemale line, male and female separately. Life spans of the different starvation resistance lines that were food restricted at larval and adult stages were analysed. To confirm the environmental stress we calculated the factor influencing the rate of mortality at all ages.The findings indicated that yeast restrictions at adult stage have higher impact on life span compared larval yeast restriction. However, restricted feeding in both larval and adult stages had a cumulative effect on life span.In general, dietary restriction that was created by reducing yeast levels from the optimum amount (100 g/l) reduces the mean life span. Additionally, stressing flies with 20 g/l and lower yeast levels leads to increase the mortality rate.Our results also indicate that inbreeding in isofemale lines can lead to dissimilar life spans because of their possibly line specific genetic background.

Changes in the Delivery of Nutrients to Coastal Ecosystems in the Anthropocene: A Sustainability Issue for the 21th Century

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Human activities affect ca. 83 % and 100 of terrestrial and ocean surface, respectively leading major, frequently irrecoverable changes in both. Among various human caused changes, nutrient enrichment of coastal ecosystems is probably the most prominent cause of concern for the sustainability of ecosystem services they provide which has been valued at 12.56 $x10^{12}$ USD annually. Our ever increasing need for food, shelter and energy is the triggering factor behind the disruption of nitrogen and phosphorus cycles which led to doubling of riverine export of nitrogen in the 20th century and significant increase in the phosphorus transport to coasts. Nutrient enrichment leads to eutrophication problem with well known consequences such as hypoxia, fish kills, loss of biodiversity and occurrence of noxious algal blooms. Changes in nutrient concentrations also influence the size-structure of phytoplankton which is crucial in determining the potential for downward transfer of carbon in the marine environment and export of organic carbon to upper trophic levels in the pelagic food webs. Nutrient stoichiometry also interacts with coastal food web dynamics in significant ways. Alterations in the ratio of N:P:Si changes the taxonomic composition of phytoplankton and their stoichiometry thus nutritional value for the consumers in upper trophic levels, producing bottleneck effects in the transfer of energy and matter at the ecosystem level. In this presentation the effects of anthropogenic alterations in the concentration and ratios of nutrients on coastal ecosystem were examined using existing data and with two selected studies; one analyzing how the change in trophic status may alter phytoplankton community size-structure even within a short distance and the other one describing the co-variation of phytoplankton and nutrient stoichiometry in a coastal lagoon along the shores of Dardanelles to provide management solutions for coastal nutrient enrichment.

Abies Taxa of Turkey; Ecological Features and Economical Uses

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Abies (Firs), a genus of Pinaceae, is reported to comprise 48 species, 7 subspecies and 24 varieties plus one nothospecies (hybrid species). It is found in mostly North and Central America, Europe, Asia, and North Africa, occurring in mountains over most of the range. Firs are most closely related to the genus Cedrus. All native species reach 10–80 m tall and 0,5–4 m trunk diameters in mature. Firs can be distinguished from other members of the pine family by incomparably attachment of their needle-like leaves and different cones. Identification of the species is based on the size and arrangement of the leaves, the size and shape of the cones, whether the bract scales of the cones are long and exserted, or short and hidden inside the cone. In Turkey, there are totally two *Abies* species and five subspecies growing naturally. These are *Abies nordmanniana* subsp. *nordmanniana* (Eastern Black Sea Fir), *A. nordmanniana* subsp. *bornmülleriana* (Uludag Fir), *A. nordmanniana* subsp. *equi-trojani* (Trojan or Kazdagi Fir), *A. cilicica* subsp. *cilicica* and *A. cilicica* subsp. *isaurica* (Taurus Firs). The wood of firs is considered unsuitable for general timber use, and is often used as pulp or for the manufacture of plywood and rough timber. Because this genus has no insect or decay resistance qualities after logging, it is generally recommended for construction purposes as indoor use only (e.g. indoor drywall framing). This wood left outside cannot be expected to last more than 12 to 18 months, depending on the type of climate it is exposed to. *Abies nordmanniana* and subspecieses are popular Christmas trees, generally considered to be the best for this purpose, with aromatic foliage that does not shed many needles on drying out.

Chitosan; Attractive Biopolymer for Removal of Heavy Metal Ions from Wastewater

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Several adsorbents have been used to remove different types of heavy metal ions from wastewater especially caused by industrial effluent. Clays, activated carbons, biopolymers, plant or lignocellulosic wastes are among the common adsorbents used. Chitosan is a type of natural biopolymer and synthesized from the deacetylation of chitin which is a polysaccharide consisting predominantly of unbranched chains of β-(1-4)-2 acetoamido-2-deoxy-D-glucose. It can be extracted from crustaceae (mostly crabs and shrimps), fungi, insects. This biopolymer represents an attractive alternative to other biomaterials because of its chemical stability, high reactivity, physico-chemical characteristics, excellent chelation behaviour and high selectivity toward pollutants. Chitosan has gained wide attention as effective adsorbents due to low cost and high contents of amino and hydroxyl functional groups which show significant adsorption potential for the removal of various heavy metal ions. The great adsorption potential of chitosan for heavy metals can be attributed to high hydrophilicity due to large number of hydroxyl groups of glucose units, a large number of functional groups, high chemical reactivity of these groups and flexible structure of the polymer chain. There are so many investigations about using chitosan for the removal of heavy metal ions. For example, removal of Cu^{+2} with using chitosan flakes has been investigated and as result of this

investigation, chitosan showed brilliant ability for Cu^{+2} adsorption with a capacity of 1.8–2.2 mmol/g dry mass. With all these informations, chitosan will be more important biopolymer for the adsorption of heavy metal ions and will increasingly use as a bioremediation agent in the future, particularly in developing countries.

Comparative Ecological Value of Sacred Groves versus Managed Forests in Terms of Bird Communities

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Sacred groves are ancient natural sites, established since at least the 15th century in Greece. They are small old-growth woodlands preserved through religion and maintained by local communities. We selected a set of eight sacred groves in Epirus region (Greece) and an associated random set of control sites of the same vegetation type (three oak woods, three evergreen woods and two pinewoods). We sampled passerines using point counts and woodpeckers with a playback acoustic method in the spring of 2013. We recorded 26 (272 ind.) and 19 (188 ind.) passerine species in sacred and control sites respectively, but no significant difference was recorded between the two types in terms of species richness and abundance (Mann Whitney test; $p>0.05$). Some species were associated with mature trees, such as *Parus montanus* and *Sitta europaea,* were found only in sacred groves. We recorded four woodpecker species in five sacred grove sites (10 ind.), and only one woodpecker individual in a control site. Sacred groves hold significantly greater woodpecker diversity than managed forests (Mann Whitney test, $p<0.05$). In conclusion, the ecological value of sacred groves seems to be high for bird species associated with mature trees, and in particular for woodpeckers. These old-growth woodlands should be maintained *per se,* as systems of special cultural and biodiversity value.

Testing New Methods to Extract Skin Toxins *in vivo* from Common Toad Tadpoles

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Previous studies investigated the behavioural, morphological and physiological aspects of the predator- induced phenotypic plasticity, but plasticity in chemical defences—which is thought to be important in amphibians—has been rarely investigated. In order to study plastic responses in chemical defence both qualitatively and quantitatively, and without killing the study subjects, non-invasive methods are needed. With such methods, one may investigate the extent of plastic responses accurately and design repeated measure experiments e. g. to examine their fitness costs. In this study, we used a hormone (norepinephrine), hormone-like substances (phenylephrine and oxymetazolin) and electro-stimulation *in vivo* to extract skin toxins from common toad (*Bufo bufo*) tadpoles and analyzed the quantity and quality of the obtained toxins and investigated the effect of these treatments on individuals' behaviour and survival. We found no significant difference in body mass between the extraction methods, but tadpoles were heavier when raised in the absence of predator cues. Activity on the 21st day was not affected by the applied

methods: treated tadpoles showed similar activity to the control individuals in both rearing environments. On the 25th day, groups in the predator cue-environment marginally differed in activity. Individuals' survival was high in all groups throughout the study (> 93 % in total). To sum it most of the applied *in vivo* toxin extraction methods had no adverse effects on the tadpoles' behavior, body mass or survival. We expect to get the results of the qualitative and quantitative analysis of the extracted toxin until March.

Effects of Past Climate Changes on the Geographic Distribution of *Quercus robur*

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Modelling the effects of past climate changes on the distribution of species allows us to understand the possible outcomes of the global climatic changes expected in near future. Ecological niche modelling (ENM) is a georeferenced approach that predicts the potential geographic distributions of species under reconstructed past and present bioclimatic conditions. This approach allowed an evaluation of climate-driven range shifts by modelling the potential distribution areas in the past, current and future under the assumption of species' habitat requirements. In this study, we conducted an ENM for the English Oak (*Quercus robur*), which distributes in Europe and Anatolia, in order to understand whether climate change affected its distribution during the late Quaternary glacial–interglacial cycles. Species' occurrence data complied from online databases and climatic variables obtained from WorldClim database. All climatic variables and occurrence data were evaluated in the maximum entropy machine learning algorithm (MAXENT) and the current and past (last glacial maximum) distribution of the English Oak were modelled. Accordingly, potential refugia for the species during the last glacial maximum were discussed in terms of ENM results. The results suggest that Anatolian Peninsula had potentially been served as one of the glacial refugia for the English Oak during the late Quaternary

EVOLUTION POSTER ABSTRACTS

Ecological and Historical Biogeography of Yellow-necked Field Mice living in and around Anatolia Using Ecological Niche Modelling and Molecular Phylogeography

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The geographic distribution and genetic structure of temperate species have been strongly influenced by the climatic oscillations of the Late Quaternary. In this study, we aimed to understand how Turkish populations of yellow-necked field mice (*Apodemus flavicollis*) have responded to global climate changes through the Late Quaternary glacial-interglacial cycles. Yellow-necked field mice are primarily woodland-dwelling small mammals and therefore distributed mainly in coastal and near-coastal areas in Turkey. In Turkey, the coastal belt retained up to about 90% of its forest cover during the Last Glacial Maximum. For this reason, we predicted that Turkish populations of yellow-necked field mice should have survived the Last Glacial Maximum in the coastal belt, supporting that Anatolia serves a glacial refugium for temperate species. We used ecological niche modelling to test this prediction. Using species occurrence data and the maximum entropy machine learning algorithm in MAXENT software, we developed an ecological niche model to predict the geographic distribution of yellow-necked field mice in Turkey under reconstructed past (the Last Glacial Maximum, 21 000 years ago) and present (1950 to 2000) bioclimatic conditions. The results demonstrated the utility of ecological niche modelling for understanding of the Late Quaternary refugial distribution of species.

Prey-predator Coevolution in Spatially Structured Environments

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Even though predator-prey coevolution has been studied theoretically and experimentally, effects of environmental changes on coevolutionary interactions remain unclear. We studied whether and how coevolutionary dynamics were affected by dispersal across spatially structured environment using a bacteria- ciliate system. In this predator-prey system quality of prey's and predator's habitats in different patches was manipulated allowing us to create different source-sink dynamics, and thus spatial heterogeneous environments. Bacterial prey and ciliates showed clear patterns of coevolution with and without spatial heterogeneity, but rates of adaptation and counter adaptation differed markedly between treatments with different dispersal and source- sink dynamics. Overall, our study suggests that changes in the abiotic environment affect coevolutionary interactions in this predator-prey system, which we aim to explore in more detail with further experiments

Differential Release of the Life History Related Genetic Variance under Dietary Restriction in *Drosophila melanogaster*

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An organism's adaptation in nature depends on lifetime strategies it can produce against changing environmental conditions. Life history traits have important roles in organism's fitness The effect of dietary restriction on heritability and the related parameters has poorly studied in context of life history traits. It is of higher importance to know the magnitude of the heritability in face of changing nutritional habits as it reflects an organism's ability to adapt to changing conditions. In our study we investigated four life history traits (developmental time, viability, fecundity and starvation resistance) with isofemale based designs. Our main aim was to show how narrow-sense heritability and related parameters of the traits changed under food stress.We measured these four life-history traits under standard and restricted conditions for 10 isofemale lines. Heritabilities were estimated for each treatment from half sibs after the basic one-way ANOVAs. Our results indicate the presence of differential release of genetic variances estimated as heritability and the related parameters per trait. In particular, additive genetic variance increased, under restriction, both for developmental time and starvation resistance. As for the fecundity, possibly as a result of restricted genetic expression under dietary restriction, additive genetic variance was decreased. Viability showed considerably lower values. Evolvability, a measure of how genetic variation reflects adaptability, increased under stressful environment for each life history trait other than viability. For heritability, we found that each trait had specific heritability values for standard and restricted conditions. We discuss all these findings with respect to the gains and losses which must be extracted from the shifts in feeding.

Global Warming and Germination Patterns in Central Anatolian Steppe (Turkey): An Experimental Approach

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Recent studies show that global warming affects phenology and distribution of many plant species. However, possible effects of the warming on seed dormancy and germination patterns of plants have been overlooked. A pronounced cold period has been seen in the Central Anatolian steppes of Anatolia (CAS) during the winter, and this can be expected to have significant impact on the germination of steppe plants. We hypothesized that germination patterns of plants in CAS should be negatively affected from shortened cold periods due to future warming. To test this hypothesis, we made a germination experiment including the seeds of 25 plant species collected from Beytepe, Ankara. Seeds were stratified at 4 °C for 1 to 5 months before they incubated in a germination cabinet at 20 °C, and the final germination percentages of treatment groups were compared to the control (untreated seeds). The probability of germination stimulation was tested by analysis of deviance (GLM) with binomial error distribution, and germination patterns of plants were further analyzed using ANOVAs as exposure period, distribution range,

phytogeographic origin and life form were considered as fixed factors. Studied species showed different germination responses to cold stratification, as one-third of species positively respond to at least one of the cold stratification periods, whereas another one-third showed negative response. The species of Irano-Turanian origin and the species that have more limited distribution range had significantly higher germination percentage after cold exposure in comparison to the control than those of unknown origin and those with wider range. The results suggest that global warming may have negative effects on the germination pattern of natural species in CAS, while that of opportunistic species might get advantage from shortened cold periods.

Rapid Identification of Two Medium-Sized Horseshoe Bats *Rhinolophus blasii* and *R. euryale* Using ISSR- PCR Method

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Distributions of Blasius's horseshoe bat, *Rhinolophus blasii* Peters, 1866, and Mediterranean horseshoe bat *R. euryale* Blasius, 1853 overlap in southeastern Europe, and they occur in sympatry in the eastern Serbia. Field identification of medium-sized horseshoe bats is sometimes difficult, especially for juvenile animals. Inter- simple sequence repeat polymerase chain reaction (ISSR-PCR) provides a quick, inexpensive and highly informative tool for species identification. Aim of this study was to test several ISSR primers in order to obtain species-specific molecular markers for *Rhinolophus blasii* and *R. euryale*. In total, 30 specimens from Serbia were analysed (15 specimens of *R. blasii* and 15 of *R. euryale*). Primers produced clear DNA profiles with reproducible band patterns and the presence of species-specific fragments. Comparing ISSR genotypes, this two species could be unequivocally distinguished. The third european medium-sized horseshoe bat, *Rhinolophus mehelyi* was not tested due to lack of samples, but it should be included in future studies. This method could be used for rapid species identification from faecal samples in roosts in order to determine composition of medium- sized horseshoe bat colonies.

Genetic Analyses on *Lynx lynx* Populations of Anatolia

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The Eurasian lynx is widely distributed in Northern Turkey while a smaller population exists in Southwestern Turkey and other areas such as Bolu, Sivas, Balıkesir and Tunceli. According to a study from 1915, Eurasian lynx in Turkey is classified within a single subspecies, *Lynx lynx dinniki*. However, the isolated lynx population of Çığlıkara Wild Life Reserve in Elmalı, Antalya, has significant phenotypical differences from the Caucasian populations. There is limited information about the lynx populations in Turkey and there is no genetic study until now. In this this study, we present a phylogenetic analysis of Northeastern and Southwestern Eurasian lynx populations in Turkey. A total of 35 scat samples of the

Eurasian lynx populations from Antalya and Caucasus have been collected and analyzed. DNA has been isolated from epithelial cells and common phylogenetic markers such as control region and cytochrome b gene of mitochondrial DNA (mtDNA) have been amplified by polymerase chain reaction (PCR) using Felidae-specific and lynx-specific primers. The presented haplotype data is not only the first genetic information about the Eurasian lynx of Anatolia, but a strong guideline for determining the conservation strategies for isolated populations.

Effects of Smoke Solutions and Nitrates on Seed Germination in Species from the Eastern Mediterranean Basin

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Soils of Mediterranean-type ecosystems are usually characterized by their low nutrient content. In these ecosystems, concentration of nitrogenous compounds in the soil (e.g., ammonium and nitrate) increase after fires. The increase of these compounds in nutrient-poor Mediterranean habitats may play an important role in the regulation of post-fire germination. The effects of fire-related cues on the germination of Mediterranean Basin plants have received more attention in recent years. However, there is limited information about the effect of nitrate on seed germination with the exception of few studies conducted in the Mediterranean Basin. In this study, we have examined the germination response of 12 eastern Mediterranean Basin species to different smoke and nitrate treatments in laboratory conditions. Smoke treatments resulted in significant increase in the germination of 4 species (*Alyssum caricum*, *Daucus carota*, *Onopordum caricum* and *Sarcopoterium spinosum*), but had negative effect on the germination of one species (*Hypericum avicularifolium*). Of the 12 species examined, 5 (*A. caricum*, *Carthamus dentatus*, *Daucus broteri*, *O. caricum* and *S. spinosum*) showed significant improvement in germination after at least one of the nitrate treatments compared to the control. In total, smoke and nitrate treatments significantly increased the germination percentage in 6 of the 12 species analyzed. Our results reveal that both smoke and nitrate have role in the stimulation of germination of Mediterranean species, and their effects are independent from each other. Our results also suggest the presence of species-specific germination response to smoke and nitrates in Mediterranean plants. More studies are still needed to clarify the role and mechanism of the nitrates in post-fire germination.

The Population Genetic Structure of *Pachygrapsus marmoratus* on Turkish Straits System, The Aegean Sea, The Black Sea and The Levantine Sea and the Role of Turkish Straits System on its Gene Flow

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Population dynamics of marine invertebrates having planktonic larval dispersal is not predictable a priori according to pelagic larval duration and geographic distances. Historical environmental factors regarding habitat, currents, sea level fluctuations together with species-specific traits and current ecological factors result in complex patterns of intraspecific genetic diversity. There is a deficit of studies about the role of Turkish Straits System (The Sea of Marmara, The Bosphorus Strait, and Dardanelles Strait) on the gene flow of marine populations. Recently, Dr. Evrim Kalkan found that Turkish Straits System acted as a semi-permeable barrier for three marine invertebrate species including *Pachygrapsus marmoratus*, behaving as a corridor from the Black Sea to the Mediterranean but as a barrier to gene flow in the opposite direction using CO1 region on mtDNA of this species. The aim of this research was to understand the population genetic structure and to infer evolutionary history of *Pachygrapsus marmoratus* (Brachyura: Grapsidae) along the coasts of Western Black Sea, Turkish Straits System, the Aegean Sea, and the Levantine Sea using 6 polymorphic microsatellite loci to combine with mtDNA analyses by Dr. Evrim Kalkan. A total of 342 specimens were collected from the upper litoral zone at a depth range of 0-0.5 m from 33 sites in total. There were eight sites from the Turkish Straits System, nine sites from the Black Sea, 13 sites from the Aegean Sea, and four sites from the Levantine Sea. Samples were analyzed at six microsatellite loci.

Integrating Phylogeny and Climatic Data to Explore Speciation in *Phoenicolacerta cyanisparsa* (Schmidtler & Bischoff, 1999) and *Phoenicolacerta laevis* (Gray, 1838)

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Variations in the climatic conditions of a region are thought to be have an important factor for speciation. Here, I combined phylogenetic information and climatic conditions among two sister species pairs within *Phoenicolacerta* genus of Lacertidae family that ranges from the west of the Amanos Mountains to its east in the south of Anatolia. In this study, I examined 26 localities data (6 for *Phoenicolacerta cyanisparsa* and 20 for *Phoenicolacerta laevis*) from known literature for the climatic conditions of two species. For phylogenetic analysis, I used 7 sequences included 1152 characters from the mitochondrial gene cyt *b* from GenBank. I found that there was a general trend of environmental divergence among sister species. Separation of two sister species clearly showed to be an allopatric speciation in both sides of the Amanos Mountains. Probably, this case arises from an barrier effect of the Amanos Mountains range. Future studies may be determined past, present and future distributions of two sister species using ecological niche modeling with many more localities data.

Transposable Element Variation and Hybrid Dysgenesis in *Drosophila simulans*

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Hybrid dysgenesis, a phenomenon manifesting in sterility and failed development of ovaries, is sometimes seen in crosses between *Drosophila* flies with different transposable element content. Specifically, offspring of crosses in which the paternal line contains a dysgenesis-causing TE--e.g, the P-element in Drosophila melanogaster-- that the maternal line lacks show DNA damage due to rampant transposition, resulting in failed ovary development, usually thought to be due to recent horizontal acquisition of a TE. The extent of hybrid dysgenesis in *Drosophila* and causal elements are still not fully understood. Here, we cross *D. simulans* flies from different geographic regions, and examine the offspring for the presence of hybrid dysgenesis. We readily observe appararent dysgenesis in these crosses, suggesting that there may be recent horizontal acquisition of a dysgenesis causing TE or TE(s) in *simulans*. We further identify potentially causal TEs from these crosses.

Determining the Replication Fidelity of Ciliate β-Family DNA Polymerases

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One of the primary sources of spontaneous mutations may be the intrinsic error rate of replication polymerases. Our lab has recently determined that the genome wide mutation rate for *Paramecium tetraurelia* is 1.94 x10-11 per site per cell division-the lowest reported for any eukaryote, and apparently a consequence of high replication fidelity. A explanation may be that the *Paramecium* replicative DNA β-polymerase is unique: we have detected changes in the amino acid sequences of all ciliate polymerases that have resulted in the switch of amino acid polarity in active sites that are otherwise highly conserved across eukaryotes. Switches in these otherwise highly conserved domains suggest a fundamental change in the mechanisms of replication fidelity in Ciliates. Rationale: Since Ciliates have a unique codon usage, we have chosen to express the *Paramecium* β - polymerases in *Tetrahymena thermophila* cells-a well-developed eukaryotic expression system. This solves the codon usage problem, and also represents the best chance of yielding native folded enzyme. Materials and Methods: In order to avoid problems with mRNA splicing between the two species, RNA was extracted from *P tetraurelia* cells, cDNAs synthesized with gene-specific primers, and these cloned into a *Tetrahymena* expression vector, which also contains affinity tags for purification. After purification, polymerases will be assayed for fidelity using deep sequencing of replication products. Conclusion: Although it remains to be seen whether low per-generation mutation rates are common to all Ciliates, the unique nuclear dimorphism that exists in ciliated protozoa suggests that this lineage is a logical target in the search for commercially useful, high- fidelity DNA polymerases. With this work, we hope to determine whether the ciliate β -polymerases are indeed the cause of the lower mutation rate in these lineages

Evolutionary Relationships of Bladder Tumors

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New genome sequencing technologies today allow the study of cancer evolution within individual tissues. In bladder cancer, a common observation was the co-occurrence of multiple tumors in a tissue, but whether these tumors are related or appear independently but synchronously, was yet unknown. Here, to address this question, we used exome sequencing from bladder tumor and normal samples from one patient. The samples included normal tissue, apex and base sections of one tumor, and the base section of another tumor. We reliably identified ~1100 single nucleotide variants (SNV) that differ among these 4 samples. Of these, 900 were shared among all tumor samples, indicating that the two tumors have a monoclonal origin. We then studied SNV patterns among these samples. First, we found that SNV frequency in the tumor samples was more than twice that of normal tissue. Second, as previously noted in the literature, TpC* mutations showed predominance in bladder tumor samples, relative to mutations found in normal tissue. TpC* mutations were particularly enriched on the shared tumor branch. Following HPV infection, TpC* mutations can accumulate due the activity of APOBEC enzymes, which are single stranded DNA/RNA editing proteins. Thus, we hypothesized that a period of APOBEC activity led to accumulation of TpC* mutations, some of which included driver mutations that led to tumor formation, and subsequent separation of the two tumors. We will further continue studying bladder cancer evolution using indel variants as well as data from other patients.

Genetic and Morphological Characterization of a Newly Found *Aphanius* Population (Cyprinodontidae) from Kaklik, Turkey

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Turkey is the hotspot for *Aphanius* species, a cyprinodont genus occurring in brackish and freshwater around the Mediterranean and in the Near East. Especially a region in the southwest of Turkey, also called the Lake District, is known for its high diversity in this taxon. To characterize a newly found *Aphanius* population in this region, we studied genetic and morphological variation in six populations. A total number of 209 specimens was included in this study, comprising the following species: *A. anatoliae* and *A. splendens*, Lake Salda, *A. sureyanus*, Lake Burdur, *A. transgrediens*, Lake Aci, *A. maeandricus*, Işıklı spring, and *A.* sp. "Kaklik cave", Kaklik. In total, four different methods were used: six microsatellite

markers, a mitochondrial marker encoding the d-loop including four out-group species, Amplified Fragment Length Polymorphism (AFLP) and geometric morphometrics for analysing photographs of each specimen. All methods show that the new population in Kaklik is distinct from its surrounding relatives with the exception of *A. maeandricus*, which is genetically related. These two species form a monophyletic mitochondrial tree with the out-group *A. chantrei*, *A. danfordii* respectively. The other methods also show a high differentiation between these species, wherefore the Kaklik population can be suggested as a new species or subspecies of *A. danfordii*.

Evolution of Gene Regulation: Do Evolutionary Forces and Physical Constraints Lead a Trade-off between Transcription Factor Binding Length and Specificity?

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A general understanding of phenotypic variation within and between populations requires a better understanding of evolutionary genetics of gene regulation. Protein-DNA interactions are crucial for gene regulation. Transcription factors (TF) activate or repress genes by binding to specific DNA regions. The fundamental question is how TFs distinguish between on-target and off-target sites in a long genome. Energetic specificity for on-target cognate sites is considered to play an important role. In this study, we focus on the interplay between binding length and specificity. By considering biophysical and evolutionary principles, we model the coevolution of a TF's specificity and TF-DNA binding length. Our modeling framework is based on the thermodynamics of protein binding and the population genetics of binding sequences.

Phenotypic Differentiation of the Genus *Mus* Based on Molar Shape

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Mus is a complex genus in the order Rodentia. Morphological and biogeographical attempts to identify *Mus* species usually fall short, if not fail. Aim of this study is to contribute to the *Mus* taxonomy by using two common but obscure species, *Mus domesticus* and *Mus macedonicus*, which are distributed in Turkey as well. These species live commensally and are transported anthropogenically. The study of geometric morphometrics is a very sensitive tool, which can be useful for separating morphologically similar species. We hypothesized that the interspecific patterns of morphological differentiation could be revealed by using an Elliptic Fourier Analysis of the first upper molar (M^1). We sampled 78 specimens from 7 localities in Marmara region. According to canonical analysis scores, *Mus domesticus* and *Mus macedonicus* populations are distinguished significantly into two separate groups. Our results show that Elliptic Fourier Analysis is a useful method to separate different species.

Mitochondrial DNA Diversity of Swordfish from the Coasts of Aegean and Mediterranean Seas in Turkey

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Swordfish (*Xiphias gladius*) is a globally and locally important food source. Studies that were carried out using different molecular markers show that global swordfish stocks can be separated into four distinct groups named as North Atlantic, South Atlantic, Mediterranean, and Indo-Pacific. Based on those studies, populations inhabiting the Mediterranean Sea are considered as a single stock. Therefore, only one conservation and management scenario is offered for the whole Mediterranean basin. However, recent studies, which used mitochondrial DNA markers, show that Mediterranean stock is not completely homogeneous. On the contrary, populations inhabiting west and east Mediterranean are genetically different and therefore it can be suggested that there are at least two swordfish stocks in Mediterranean that can be called as Eastern and Western Mediterranean stocks. Incidentally, existence of different spawning areas (Eastern and Western Mediterranean Sea) are known. In the present study, DNA is extracted from swordfish samples that were collected from the Antalya harbor of the Mediterranean Sea (n=30) and Çanakkale of Aegean Sea (n=30). Partial mitochondrial DNA (mtDNA) D-loop region (450 base pair long) sequences were obtained and these sequences were compared with those available in the literature. According to the median joining (MJ) network analysis, most of our samples are identical to those haplotypes which are observed only in the Eastern Mediterranean Sea. Thus results supports the existence of Eastern Mediterranean swordfish stock and the swordfish populations inhabiting Turkish coast of the Mediterranean and Aegean Sea belongs to Eastern Mediterranean swordfish stock .