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**Abstract Book**

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**eko**evo  
Ekoloji ve Evrimsel Biyoloji Derneği



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**5th ECOLOGY AND EVOLUTIONARY BIOLOGY SYMPOSIUM**  
**18 -20 July 2018, İzmir TURKEY**

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**ECOLOGY ORAL ABSTRACTS ..... 7**

Next-generation freshwater bioassessment in the 21 st century: Species-level resolution for non-biting midges (Diptera: Chironomidae) and implications for conservation .....	8
Cooperation and institutions: Framed field experiments with small-scale fishing communities .....	8
Metataxonomics for the Micro-plastic and other Particle Attached Habitats in the Northeastern Mediterranean Sea.....	9
Influences of climate and land use on the ecology of Mediterranean shallow lakes: a space-for-time substitution approach .....	9
UV-B stress induced changes in Asada-Halliwell pathway and the glutathione metabolism of a high altitude perennial <i>Arabidopsis thaliana</i> in comparison with its relative <i>Arabidopsis thaliana</i> .....	10
Human-Wildlife Conflict in Kastamonu: Evaluating the Perception of Game Hunters.....	10
Coevolution of social phenotypes with the context they evolve in.....	11
Cross-regional modelling of fire ignitions in Europe .....	11
Modeling vegetation dynamics in Mediterranean pine forests: Effect of fire frequency and plant abundance.....	12
Drivers of Spider (Arachnida:Araneae) Biodiversity in an ‘Olive Grove Ecosystem’ in North-Western Anatolia (Çanakkale and Balıkesir, Turkey) .....	12
Use of 3 Dimensional Geometric Morphometric for Identification of Closely Related Species of Caucasian Rock Lizards (Darevskia).....	13
An Evaluation of live-capturing methods for large carnivores in Turkey .....	13
A clinal inversion in <i>Drosophila</i> represents a life-history supergene .....	14
Reproductive ageing in male fruit flies.....	15
Adaptation to seasonal changes: A strong relationship between desiccation tolerance and seasonal cues in <i>Drosophila melanogaster</i> .....	15
Urban dishonesty in song sparrows?.....	16
Can birds beat cancer? .....	16
Detecting Density Dependence in North American Landbird Populations .....	17

**EVOLUTIONARY BIOLOGY ORAL ABSTRACTS..... 18**

Discovering prokaryotic dynamic in marine environment by using a combination of genetic analysis and numerical ecosystem models.....	19
Identification of Fish Species in Eurasian Otter ( <i>Lutra lutra</i> ) Diet Using DNA Metabarcoding of Faecal Samples .....	19
Genomic Organization and Standing Structural Variation of the MHC of the Three-spined Stickleback.....	20

Genetic structure of the bottlenose dolphin ( <i>Tursiops truncatus</i> ) in the Turkish waters based on mtDNA sequences.....	20
Radiation via hybridisation: Evolution in <i>Poecilimon bosphricus</i> species group (Orthoptera, Tettigoniidae).....	21
Natural selection via condition-dependent predation enhances the costs of male ageing on female reproductive success, exacerbating sexual conflict.....	22
The mysterious case of a single <i>Aquilegia</i> chromosome.....	22
Developmental mechanism of a major evolutionary transition in ants.....	23
Amylase copy-number analysis in different mammalian lineages reveals convergent adaptive bursts shaped by diet.....	23
Shared polymorphisms reveal additional pulses of Neanderthal introgression.....	24
Modelling the origin and expansion of Turkic speakers.....	24
Genomes from the Pontic-Caspian steppe, a closer look at the genomics behind the bronze- and iron age demography in southern Ural.....	25
Partial coincidence of microsatellite genotypes suggests a possible role of backcrosses in diversification of parthenogenetic rock lizards.....	25
Identifying patterns of rapid radiation in phylogenomics.....	26
Genetic diversity is retained in a bottlenecked Cinereous vulture population in Turkey.....	27
Domestication-driven metaorganism evolution of wheat.....	27
Identifying functionally equivalent orthologs in the context of predicting disease-causing mutations.....	28
<b>POSTER ABSTRACTS .....</b>	<b>29</b>
The investment of nuptial gift and immunity: Comparison the sexdifferences in mate searching between two species in the bush-cricket genus <i>Poecilimon</i> .....	30
Sightings of three cetacean species in the south part of the Black Sea.....	30
Analysis of body size/mass and immunity in the <i>Gryllus bimaculatus</i> (Orthoptera: Gryllidae).....	31
Information Theory in Ecology and Evolution.....	31
Polymorphisms in the Promoter Region of GULO Gene in Dogs.....	32
Analysis of Codon Differences and Glycosylation Profiles Among Mammalian and Avian Foxp2 Genes and Proteins.....	32
Altitudinal effects on evolution of globin gene clusters and host adaptation on <i>Nannospalax xanthodon</i> .....	33
Biological invasion and the conservation of endemic island species: São Tomé Archachatina giant land snails (Pulmonata: Achatinidae) .....	33

First Steps to Resolve Reticulate Speciation Process in Bisexual and Parthenogenetic lizards of genus <i>Darevskia</i> in East Anatolia and Caucasus .....	34
Testing the “unguarded X” hypothesis in <i>Drosophila melanogaster</i> : Inbreeding results in a potentially maladaptive sex-specific decline in female lifespan.....	34
First record of <i>Terpios gelatinosus</i> (orifera: Demospongiae; Bowerbank, 1866) along the coasts ofMediterranean Sea in Turkey verified byDNA barcoding .....	35
Phylogenetic and Phylogeographic resolution of the Ascidians along theTurkish Levantine Coasts .....	35
A geographical survey of mitochondrial DNA variation in greenfinch populations in Anatolia .....	36
Pilot genetic assessment of the eastern most populations of Carpathian endemic Montandon’s newt <i>Lissotriton montandoni</i> within Bibrka- Stilsko Hill ridge (Lviv region,Ukraine).....	36
Rock lizards-Gene flow and hybridization within species of 'caucasica' clade .....	37
Breeding ecology of the scops owl ( <i>Otus scops</i> ) at the metu campus (Ankara, Turkey): Preliminary findings.....	37
New insights into the maternal history of Anatolian and north Mesopotamian populations since the Neolithic.....	38
The Genome-wide analysis of spontaneous mutations in <i>Acidobacterium capsulatum</i> .....	38
Ecogeographical Variation of Rock Nuthatches .....	39
Analysis of spatial and temporal changes at surface area of Homa lagoon (İzmir Bay, Aegean Sea) using remote sensing techniques.....	39
The profile of de novo mutations in horse .....	40
Genetic and morphological variability in bisexual ( <i>Darevskia portschinskii</i> ) and unisexual ( <i>Darevskia dali</i> ) Caucasian Rock Lizards .....	40
Phylogenetic Utility of Secondary Structure of ITS2: A Snapshot from Anterastes (Orthoptera, Tettigoniidae).....	41
Gene Expression Reversals in Mouse Ageing and Its Comparison with Primates.....	41
Authentication of ancient DNA sequences when there is no reference genome .....	42
A new putative transcription termination signal which interact transcription termination factors in Ecdysozoa .....	42
Identification of differentially expressed sense and antisense transcripts in mitochondrial genes of <i>Syrista pareyysi</i> (Hymenoptera: Cephidae) .....	43
Spatially varying promoter polymorphism in <i>Dca</i> is not related to wing size cline in East European <i>Drosophila melanogaster</i> populations.....	43
Adaptation to cold tolerance in <i>Drosophila melanogaster</i> populations along latitudinal gradient in Europe.....	44

Frequency changes of phenotype-associated genetic variants between Neolithic and modern Anatolian populations .....	44
Seed iron distribution show conserved patterns among different plant lineages .....	45
Host Genetic Determinants of Xanthomonadacea abundance in <i>D. melanogaster</i> .....	45
Testing for signals of selection near fixed modern human derived sites .....	46
BROT 2.0: A functional trait database for Mediterranean Basin plants .....	46
Hospital Wastewater: a new technologies & optimal methods used for treatment of hospital wastewater before discharge into environment.....	47
Quantitative genetics of immune fuction in pond snail .....	47
A study of the changes in the forest phenology in Turkey through MODIS satellite data.....	48
Modeling spatial distribution of oriental beech ( <i>Fagus orientalis</i> ): Past, present, and future.....	49
An Ancient DNA Investigation on the Çine-Tepecik Archaeological Community: mtDNA Haplogroup Analysis.....	49
The Dilemma of species protection in action.....	49
Move Or Not To Move': A Case of Defensive Behaviours of Some Amphibians of Turkey .....	50
Species Level Molecular Identification of Bird Species Using Environmental DNA.....	50
Aiming for the moon: Maintenance of local adaptation to tidal regime .....	51
The traces of adaptive maternal effect in fluctuating temperature environments in fruitflies .....	51
Bioinformatics Processing of Double-Digest RAD-seq data in <i>Myotis capaccinii</i> around the Mediterranean Basin .....	52
Genetic variation in the six6 gene is linked to the trophic level of Atlantic salmon at sea .....	53
Intense Pyrethroid Use in Adult Mosquito Control: Possible Effects on Resistance Development and Environment.....	53

**ECOLOGY ORAL ABSTRACTS**

**Next-generation freshwater bioassessment in the 21 st century: Species-level resolution for non-biting midges (Diptera: Chironomidae) and implications for conservation**

*Bilgenur Baloğlu<sup>1\*</sup>, Esther Clews<sup>2</sup>, Rudolf Meier<sup>3</sup>*

<sup>1</sup> Department of Biological Sciences, National University of Singapore, Singapore

<sup>2</sup> Tropical Marine Science Institute, National University of Singapore, Singapore

<sup>3</sup> Lee Kong Chian Natural History Museum and Department of Biological Sciences, National University of Singapore, Singapore

Chironomid midges (Diptera) are often collected during routine water quality assessment but rarely identified to species because morphological identification requires slide mounting and the help from taxonomic experts. This is unfortunate because different species have different habitat requirements and midges could be an important bio-indicator taxon for water quality if the identification problems could be overcome. Here we test the usefulness of a new and cheap NGS-based DNA barcoding method that yields barcodes at a cost of <\$1/specimen without destroying the taxonomically important structures. We use this method to barcode >14,000 specimens from man-made aquatic habitats in Singapore. We found a surprisingly small number of species in artificial habitats (ca. 60 species of midges). In contrast, a much smaller number of barcoded specimens collected from an adjacent swamp forest yielded a much larger number of molecular operational taxonomic units (MOTUs). Despite the close proximity of the habitats, we find near-complete MOTU turnover. We predict that future bioassessment, as well as conservation programs, will benefit tremendously from comprehensive, species-level midge barcoding. It now appears realistic and cost-effective to develop species-level indices based on chironomid midge species.

**Keywords:** NGS barcoding, chironomids, freshwater bioassessment

**Cooperation and institutions: Framed field experiments with small-scale fishing communities**

*Pınar Ertör-Akyazı\**

\*Sabanci University

Economic incentives can reinforce or weaken cooperation in a resource use dilemma via framing effects when they provide cues about normatively appropriate behavior. The present study investigates framing effects of two formal institutions, a market and a fine-imposing institution, for a commons dilemma involving fishing activities, and compares them to an informal institution entailing face-to-face communication and a baseline setting representing open-access. Experimental data are collected from 240 fishers from small-scale fishing communities in Turkey via framed field experiments. The institutional context of resource use is framed as a monetary penalty (fine treatment) versus the purchase of extraction rights (market treatment) for overfishing, while keeping the economic incentives constant. Both of the formal institutions (fine and market) as well as the informal institution (communication) reduced individual extraction compared to the baseline. Yet, the fine-imposing institution reduced extraction significantly more than the market, despite providing the exact same economic incentives. These findings can have important implications for environmental policy design and sustainability research.

**Keywords:** Human behavior, Institutions, Fisheries

## Metataxonomics for the Micro-plastic and other Particle Attached Habitats in the Northeastern Mediterranean Sea

*Selin Küçükavşar<sup>1</sup>, K. Gökdağ<sup>2</sup>, AE Kıdeys<sup>3</sup>, Arzu Karahan<sup>4\*</sup>*

<sup>1,2,3,4</sup>Middle East Technical University, Institute of Marine Sciences, Erdemli, Mersin, Turkey  
Corresponding author e-mail: arzukarahan@ims.metu.edu.tr

Plastic now pollutes every corner of earth and it is one of the major environmental problems of nowadays. Beside of being directly harmful as a mimic of food sources of marine organisms, as being suitable substrate for different kind of microbes they have also indirect damage. Metataxonomics analysis using Next Generation Sequencing (NGS) technology have revealed numerous previously unrecognized microorganisms. In the present study, micro-plastic attached bacterial community of samples taken from four different depths (0, 25, 150, 200 m) from a North-eastern Mediterranean offshore station (200 m) were investigated using metataxonomics amplicon sequencing technique. Targeted marine samples were micro-plastic attached microorganisms, but because of the limited evidence it has been called as Micro-plastic and other particle attached habitats. Those samples also compared with free-living organisms in the area. About 664 Operational Taxonomic Units (OTUs-sequence variants) from 65,457 sequences were observed for all the depths. Caulobacteraceae was the most dominant order in the micro-plastic particle attached marine environment, which the members of taxa are usually known to be biofilm colonizer whereas, SAR 11 clade found to be abundant in the free-living community. Another common bacterium for marine environment was Phenyllobacterium that degrades the Chloridazon herbicide and Acinetobacter junii which was shown to have the ability to degrade biodegradable plastic. This is a first study using a culture-independent approach for identify the North-eastern Mediterranean free-living and micro-plastic particle-attached marine microorganisms.

**Keywords:** 16S rDNA, Metataxonomics, micro-plastic, particle-attached

## Influences of climate and land use on the ecology of Mediterranean shallow lakes: a space-for-time substitution approach

*Meryem Beklioğlu\**

\*Middle East Technical Univ. Limnology Lab., Biol. sciences. Dept.

Climate warming threatens the functioning and biodiversity of shallow lakes, not least lakes located in Mediterranean climatic zones that are subjected to additional stressors such as intensive land and water use. We used a space-for-time substitution approach to assess the response of trophic and community structures and biodiversity to temperature and hydrological constraints. We selected fourth-four lakes covering a wide climatic and nutrient gradients in the western Anatolian plateau of Turkey. Lakes located in the northern highlands, with the lowest agricultural activity and temperatures, had low nutrients and chlorophyll a (Chl a), low proportions of small fish, large proportions of piscivores, the dominance of large-bodied cladocerans and calanoid copepods, all of which indicate low top-down control by fish. In contrast, lowland lakes with higher temperatures and higher agricultural impact had a higher proportion of small fish and higher nutrient and Chl a concentrations with cyanobacteria dominance. The Chl a: TP ratio, omnivorous fish biomass and the fish:zooplankton biomass ratio were also higher, whereas the zooplankton:phytoplankton biomass ratio and macrophyte coverage were lower, suggesting a high top-down trophic control of fish on zooplankton. Our results indicate that climate warming in Mediterranean lakes may result in higher salinization and eutrophication with more cyanobacteria blooms and

probable loss of biodiversity if they do not completely dry out. To counteract the effects of warming, strict control of nutrients and human use of water is urgently needed.

**Keywords:** eutrophication, diversity, hydrology

### **UV-B stress induced changes in Asada-Halliwell pathway and the glutathione metabolism of a high altitude perennial *Arabis alpina* in comparison with its relative *Arabidopsis thaliana***

*Rengin Özgür Uzilday*<sup>1</sup>, *Baris Uzilday*<sup>1</sup>, *Tolga Yalçınkaya*<sup>1</sup>, *Turgut Yiğit Akyol*<sup>1</sup>, *Hasan Yıldırım*<sup>1</sup>, *İsmail Türkan*<sup>1</sup>

<sup>1</sup>Ege University, Faculty of Science, Department of Biology, Bornova, 35100, Izmir, TURKEY

UV-B (280-315 nm) stress is an important abiotic stress factor that affects plant growth and development. UV-B also contributes the climate change through the production of volatile organic compounds. *Arabis alpina* is a perennial that has been adapted to high altitudes; an environment more exposed to UV-B radiation. Phylogenetic studies suggest that Anatolia is the centre of origin for this species and *A. alpina* is also a close relative to model plant *Arabidopsis thaliana*. The aim of this study was to understand differential responses to UV-B stress in these two plant species in regards of regulation of glutathione, a low molecular weight antioxidant, which acts as a redox buffer throughout the cell. For this aim, both plant species were exposed to UV-B stress. The activities of superoxide dismutase, ascorbate peroxidase, glutathione reductase, dehydroascorbate reductase, glutathione peroxidase and glutathione S-transferase were investigated. H<sub>2</sub>O<sub>2</sub> accumulation, lipid peroxidation, and maximum efficiency of PSII (Fv/Fm) were determined in both plants. In addition, changes in levels of plastid terminal oxidase, an alternative oxidase-like protein, was determined with Western blot analysis to elucidate responses of alternative electron sinks in chloroplasts. UV-B stress decreased Fv/Fm in both species but decrease in *A. thaliana* was more prominent. *A. alpina* was able to maintain or induce activities of glutathione related enzymes. However, the activities of these enzymes decreased in *A. thaliana*. These results indicate that *A. alpina* is able to cope with the detrimental effects of UV-B by inducing its glutathione related enzymes for efficient redox regulation.

**Keywords:** *Arabis alpina*, Redox regulation, UV-B stress

### **Human-Wildlife Conflict in Kastamonu: Evaluating the Perception of Game Hunters**

*Hakan Sivri*<sup>1\*</sup>, *Gökhan Yılmaz*<sup>1</sup>, *Anıl Soyumert*<sup>1</sup>

<sup>1</sup> Kastamonu Üniversitesi

Human-wildlife conflict is one of the major problems for wildlife management in Turkey, as it takes place among the priority issues for conservation studies throughout the world. In the present study, a questionnaire survey was conducted in March-April 2018 in the province of Kastamonu to reveal the human-wildlife conflict in a region with a high richness in wildlife species. The game hunters were chosen as the target group for the survey since they have a dense interaction with the wildlife species in several aspects. Over 80 individuals who are settled at the various districts of the province filled in the questionnaires. The preliminary analysis of the surveys indicates that the wild boar (*Sus scrofa*), brown bear (*Ursus arctos*) and gray wolf (*Canis lupus*) are the species with the highest conflict with humans. Wild boar is mentioned as damaging the agricultural products by 80% of the survey respondents, while brown bear has been mentioned as 23%. For the conflict on poultry, 5% of the attendees indicate red fox in the first place, followed by stone marten (*Martes foina*) with 2% and long-legged buzzard (*Buteo rufinus*) with 1.2%. In addition to these, hunters claimed that the gray wolves

are attacking their dogs. In response to these conflict issues, the survey respondents explained that they develop solutions to frighten the animals by alternative methods such as high and sudden flashlights and buzzers or building surrounding walls for protection; or using firearms for shooting the animal for protection and to take revenge. The results reveal that human-wildlife conflict is ought to be solved both for humans and wildlife species to decrease the ongoing threats on wildlife populations and to take under control the illegal hunting for an effective conservation and management.

**Keywords:** Human-Wildlife Conflict, Wildlife conservation, Game Hunters

### Coevolution of social phenotypes with the context they evolve in

Erol Akcay\*

\*Department of Biology, University of Pennsylvania

Most phenotypes of organisms have consequences not just for their carriers, but for others as well. We have a mature theory of social evolution that tells us how selection will act on social phenotypes in a given selective context, which includes (i) the material payoffs from different phenotypes, (ii) the genetic architecture of the phenotype, (iii) the social and genetic structure of the population, and (iv) demography. In this theory, these aspects of the selective context are usually taken as fixed, yet in nature they themselves are evolving at the level of individuals, social groups, and populations. In the first part of the talk, I will review recent theoretical work that starts to address the evolution of the selective context, emphasizing cases where it lead to previously unexpected feedbacks between the selective context and social behaviors. In the second part, I will present new theoretical work on the coevolution of social structure and behaviors through the interaction of demographic processes and behavioral flexibility. In this model, natural selection has both direct (through differential reproduction) and indirect (through evolved behavioral responses) effects on the social structure that in turn feedback on the evolution of behavioral phenotypes themselves.

**Keywords:** Social evolution, coevolution, cooperation

### Cross-regional modelling of fire ignitions in Europe

İsmail Bekar<sup>1\*</sup>, Çağatay Tavşanoğlu<sup>2</sup>, Harald Vacik<sup>3</sup>, Juli G. Pausas<sup>4</sup>, Harald Bugmann<sup>1</sup>, Gunnar Petter<sup>1</sup>

<sup>1</sup> Institute of Terrestrial Ecosystems, ETH Zurich

<sup>2</sup> Department of Biology, Hacettepe University

<sup>3</sup> Institute of Silviculture, University of Natural Resources and Life Sciences (BOKU)

<sup>4</sup> Centro de Investigaciones sobre Desertificación (CIDE)

In recent years, machine learning techniques such as Maxent, commonly used in species distribution modelling, have also been successfully applied in fire ecology studies. In this study, we developed a cross-regional model of fire ignition for Europe using Maxent to improve our understanding of spatial ignition patterns. For this purpose, we modelled the fire ignition probability in four case study regions in four countries (Austria, Spain, Switzerland and Turkey) based on historical fire data, and also created a cross-regional model. We used bioclimatic (BIOCLIM), anthropogenic (e.g., land cover, human settlement, road density), and topographic variables (e.g., slope and aspect) as predictors, and evaluated model performance based on AUC values. To test the transferability of the regional models, we applied each in all other regions. Furthermore, we also investigated the effects of sample size, as well as temporal and spatial resolution. We found that all coarse resolution (1km<sup>2</sup>) regional models performed well, with AUCs varying from 0.658 (Spain) to 0.835

(Switzerland). Fine resolution (100m<sup>2</sup>) models performed slightly better, with model AUCs varying from 0.689 (Spain) to 0.856 (Switzerland). Transferability of the regional models was better than expected, and among 20 transferred models only 4 of the coarse resolution models and 5 of the fine resolution models showed AUC < 0.6. Key variables of the models showed major similarities between regions. They also did not show differences depending on the spatial resolution. The study contributes a better understanding of statistical fire ignition probability and the spatial transferability of statistical fire ignition models.

**Keywords:** Fire ecology, Statistical modelling, Maxent

### **Modeling vegetation dynamics in Mediterranean pine forests: Effect of fire frequency and plant abundance**

*Anıl Bahar<sup>1\*</sup>, Çağatay Tavşanoğlu<sup>1</sup>, Juli G. Pausas<sup>2</sup>*

<sup>1</sup> Fire Ecology and Seed Research Lab., Division of Ecology, Department of Biology, Hacettepe University, Beytepe 06800, Ankara, Turkey

<sup>2</sup> CIDE-CSIC, Ctra. Naquera Km. 4.5 (IVIA), Montcada, Valencia 46113, Spain

In recent decades, global change drivers are altering fire regime and vegetation structure across the Mediterranean Basin. Here we used a simulation model to study the effect of fire frequency on long-term vegetation dynamics of Mediterranean pine forests. Simulation scenarios were generated considering different fire frequencies and different abundance of five plant functional groups representing different growth forms and resprouting abilities: “Pinus” (seeder trees), “Quercus” (obligate resprouter trees), “Erica” (facultative resprouter shrubs), “Cistus” (seeder shrubs), and “Brachypodium” (obligate resprouter herbs). We used the spatially-explicit FATELAND model that includes several life history traits for functional groups and specific properties of fire. Specifically, we included six different fire frequencies (once in 5 to 80 years, and no fire) and 10 different classes of total plant abundances (from 0 to 100 % of the landscape) for 120 years. Pinus abundance was negatively affected by the initial abundance of Quercus and the increase in fire frequency. The effect of fire frequency on Quercus was limited, and this group dominated the final vegetation in most scenarios. The increase in fire frequency promoted Erica, Cistus, and Brachypodium abundance, but total initial plant abundance had a negative effect on these groups. A shrubland scenario (with no Pinus) resulted in similar outcomes with the woodland scenario. In the absence of Quercus, however, other functional groups had relatively more abundance values in all scenarios. Our results suggest that in addition to the fire frequency, the initial abundance of resprouter trees is a key driver of post-fire vegetation dynamics in the Mediterranean Basin.

**Keywords:** Vegetation dynamics, pine forest, fire

### **Drivers of Spider (Arachnida:Araneae) Biodiversity in an ‘Olive Grove Ecosystem’ in North-Western Anatolia (Çanakkale and Balıkesir, Turkey)**

*Mert Elverici<sup>1\*</sup>, Evrim Karaçetin<sup>2</sup>, C. Can Bilgin<sup>1</sup>, Özge Balkız<sup>3</sup>, Semiha Demirbaş Çağlayan<sup>3</sup>, Mecit Vural<sup>4</sup>*

<sup>1</sup> Middle East Technical University, Department of Biological Sciences, Ankara

<sup>2</sup> Erciyes University, Department of Environmental Engineering, Kayseri

<sup>3</sup> Nature Conservation Center, Ankara

<sup>4</sup> Gazi University, Biology Department, Ankara

Olive plantations cover vast areas on the Aegean coast of Turkey, and the southern foothills of Kaz Mountains is no exception. Olive trees dominate the terrestrial vegetation to such an extent that they form a

novel 'ecosystem'. The olive grove ecosystem is shaped by agricultural management, while impacts on biodiversity are largely unknown. We sampled spider communities living on soil surface and vegetation (understory herbaceous & tree canopy) microhabitats, alongside with various environmental variables linked to management or local habitat features in organic and conventional olive groves, as well as in relict patches of natural habitats, then used multivariate statistics to interpret associations within community composition (NMDS, CCA, RDA models) and compared diversity statistics (ANOVA, ANOSIM and permutation tests). 288 spider (morpho-) species of 14,252 adult specimens and >200 sampling units (plot based communities) were collected and standardized by sample coverage through rarefaction and extrapolation. Community composition differed by habitat type and by microhabitat. Olive groves and mixed forests had richer communities compared to maquis and pine stands. Soil surface was more species rich and diverse than vegetation. Difference between "organic" or "conventional" management types could not be distinguished well at the community level, whereas impact of soil management (tillage or herbicide use) and vegetation cover (tree/shrub vs. herb) were significant on the community. Our results may serve as evidence for a moderately strong species composition - environment relationship for spider communities.

**Keywords:** Arachnology, Community Ecology, Mediterranean

### Use of 3 Dimensional Geometric Morphometric for Identification of Closely Related Species of Caucasian Rock Lizards (*Darevskia*).

*Mariam Gabelaia*<sup>1\*</sup>, *David Tarkhnishvili*<sup>1</sup>, and *Dominique Adriaens*<sup>2</sup>

<sup>1</sup> Ilia State University

<sup>2</sup> Department of Biology, Ghent University

Geometric morphometrics has been proven to assess shape variation more efficiently than 'traditional' (based on linear measurements and scalation traits) morphometrics. In our previous paper, we used 2D, outline-based geometric morphometrics on six species from the 'rudis' and 'caucasica' clades of rock lizards' (*Darevskia*). Using an anal scale and pileus outlines, we showed that their shapes could trace the species divergence pattern and separate individual species and clades. The analysis separated the species from different clades but was unable to distinguish closely related species within the clade on the specimen level. As such, we predicted that 3D head shape data would be sufficiently discriminative to also identify more closely related species. To test this hypothesis, we compared head shapes of three closely related species of the 'rudis' clade - *D. portschinskii*, *D. valentini*, and *D. rudis*, with the latter species treated as two distinct groups (*D. r. obscura* and another form collected throughout Georgia) using 3D landmark data for geometric morphometrics. The 3D analysis did isolate the 'rudis' clade species better, now even separating individuals from populations that showed a genetic introgression pattern. The analysis also showed that *D. r. obscura* is not less distinct from the other *D. rudis* than it is from the other nominal species. For this reason, we suggest elevating the status of the subspecies *D. rudis obscura* to species level, i.e. *Darevskia obscura* Lantz & Cyren, 1936.

**Keywords:** 3D geometric morphometric, *Darevskia*, morphology

### An Evaluation of live-capturing methods for large carnivores in Turkey

*Ali Onur Sayar*<sup>1</sup>, *Alper Ertürk*<sup>\*2</sup>, *Deniz özüt*<sup>3</sup>, *Hasan Emir*<sup>4</sup>, *Taner Hatipoğlu*<sup>4</sup>, *Anıl Soyumert*<sup>2</sup> *Evren Koban*  
*Baştanlar*<sup>5,6</sup>

<sup>1</sup>Ankara University, Graduate School of Natural Applied Sciences, Department of Biology, Ankara, Turkey

<sup>2</sup>Kastamonu University, Game and Wildlife Programme, Kastamonu, TURKEY;

<sup>3</sup>Eko-Zon Public Health and Environmental Consultation, Ankara, TURKEY;

<sup>4</sup>General Directorate of Nature Conservation and National Parks, Ankara, TURKEY;

<sup>5</sup>TUBITAK Marmara Research Center GMBE, Gebze, Kocaeli, TURKEY

6Current address: Ege University, Department of Biology, İzmir, TURKEY

\*corresponding author: alionursayar@gmail.com

Large carnivores are the group of mammals, which are difficult to apply invasive research approaches including live-capture techniques due to their low population numbers and level of intelligence. However, some biological data can only be obtained by implementation of live-capture methods. Yet, the techniques applied during wild-capture studies require experience and sensitive attitudes to ensure both animal welfare and success of the study. Within this respect, the number of studies conducted on large carnivores is quite limited in Turkey, despite the need for such studies. Therefore, General Directorate of Nature Conservation and National Parks has been supporting researchers and projects to fulfill this gap in the field. Since 2011, two major projects were carried out; namely, (i) Analysis, Conservation and Management of Large Mammals in Context of National Strategies on Conservation of Biodiversity and Genetic Resources (2010-2015), and (ii) Regulation and Monitoring of Wildlife Crossings along Ankara-İstanbul Highway (2015-2018). Both projects have focused on live capturing of the cryptic large carnivores, like, striped hyena, caracal, Eurasian lynx, and others. Most importantly, both projects required a great deal of work on optimization and implementation of different methods. During these studies, we tried both common and novel live-capture methods for the target species, and we investigated the efficiency and applicability of these methods. The results suggested that the most efficient and viable techniques to be used in Turkey are; (i) the Leg-Hold EZ Grip Traps for both striped hyena and gray wolf, (ii) Aldrich Snares for brown bears, and finally, (iii) net box traps for caracal and lynx. The results also revealed that common techniques, applied in other countries, need some alterations taking the study region into account, and most of them was found to be not functional in Turkey. Furthermore, the seasonality, life history trait of the target species, quality and type of bait and finally the competency of the researcher were the most crucial elements directly affecting the capture success. As conclusion, in context of these two projects, two striped hyenas, four gray wolves, one caracal, one lynx and four brown bears were successfully live-captured. The now-how obtained in these two studies will be crucial for the success of forthcoming studies. The project was supported by the Scientific and Technological Research Council of Turkey (TUBITAK, project no: KAMAG 109G016). **Keywords:** Carnivore, live-capturing, wildlife.

**Keywords:** Carnivore, live-capturing, wildlife

### A clinal inversion in *Drosophila* represents a life-history supergene

*Esra Durmaz*<sup>\*1</sup>, *Clare Benson*<sup>2</sup>, *Martin Kapun*<sup>1</sup>, *Paul Schmidt*<sup>3</sup>, *Thomas Flatt*<sup>1</sup>

<sup>1</sup> Department of Ecology and Evolution, University of Lausanne, Lausanne, Switzerland; Department of Biology, University of Fribourg, Fribourg, Switzerland

<sup>2</sup> Department of Ecology and Evolution, University of Lausanne, Lausanne, Switzerland; School of Biological Sciences, University of Manchester, Manchester, United Kingdom

<sup>3</sup> Paul Schmidt - Department of Biology, University of Pennsylvania, Philadelphia, USA

Chromosomal inversions often contribute to local adaptation across latitudinal clines, but the underlying selective mechanisms remain poorly understood. We and others have previously shown that a clinal inversion polymorphism in *Drosophila melanogaster*, In (3R) Payne, underpins body size clines along the North American and Australian east coasts. Here we ask whether this polymorphism also contributes to clinal variation in other fitness-related traits, namely survival traits (lifespan, survival upon starvation, and survival upon cold shock). We used homokaryon lines, either carrying the inverted or standard chromosomal arrangement, isolated from populations approximating the endpoints of the North American cline (Florida, Maine), and phenotyped the flies at two growth temperatures (18°C, 25°C); in addition, we also examined the transcriptomes of the homokaryons

under these conditions. Across both temperatures, high-latitude flies from Maine lived longer and were more stress resistant than low-latitude flies from Florida, as previously observed. Interestingly, this latitudinal pattern is partly explained by the clinal distribution of the In (3R) P polymorphism, which is at ~50% frequency in Florida but absent in Maine: inverted karyotypes tended to be shorter-lived and less stress resistant than uninverted karyotypes. We also detected some interactions between karyotype and temperature on survival traits. Since In (3R) P influences body size and multiple survival traits, it can be viewed as a 'supergene', a cluster of tightly linked loci affecting multiple complex phenotypes. We discuss the phenotypic effects of In (3R) P in the light of our transcriptomic data which give us hints about the candidate genes that might underlie the observed phenotypic responses.

**Keywords:** Adaptation, Inversion, Cline

### Reproductive ageing in male fruit flies

*Irem Sepil<sup>\*1</sup>, Rebecca Dean<sup>2</sup>, Philip Charles<sup>1</sup>, Roman Fischer<sup>1</sup>, Benedikt Kessler<sup>1</sup>, Stuart Wigby<sup>1</sup>*

<sup>1</sup> University of Oxford

<sup>2</sup> University College London

Delayed fatherhood is a widespread phenomenon in developed countries. Population-based studies show that paternal age positively correlates with the likelihood of infertility. However an experimental investigation of this association and the underlying mechanisms is lacking. The ejaculate is composed of both sperm and seminal fluid. Seminal fluid contains some of the fastest evolving proteins currently known. These seminal fluid proteins play crucial roles in reproduction, such as supporting sperm function, and modifying female physiology and behavior. Reproductive deterioration in ageing males might arise from changes in the seminal fluid proteins or sperm; hence I investigate both components in my research in fruit flies. Specifically, I address the following questions: 1) Does ageing affect the composition of the seminal fluid proteins or quantity of sperm produced and transferred at mating? 2) What are the reproductive consequences of ageing in males? To address these questions I combine lab-based empirical and quantitative proteomic and fluorescent labelling methods. I quantify seminal fluid proteins and sperm in ageing males, and determine the consequences of male age for male and female fitness. I have found that the ejaculate of older males is of lower quality, which decreases their reproductive ability, and that of their partners. I have also been able to document changes in ejaculate protein composition with age, and pinpoint specific substances that are likely to be important in ageing effects. Given that some of these proteins are highly conserved, this work may have direct implications for fertility in humans and other animals.

**Keywords:** Ageing, Drosophila, Reproduction

### Adaptation to seasonal changes: A strong relationship between desiccation tolerance and seasonal cues in *Drosophila melanogaster*

*Nur Seda Coşkun<sup>\*1</sup>, Cansu Fidan Aksoy<sup>1</sup>, Ekin Demir<sup>1</sup>, Şenel Selin Yağlı<sup>1</sup>, Banu Şebnem Önder<sup>1</sup>*

<sup>1</sup>Genetic Variation and Adaptation Lab., Department of Biology, Faculty of Science, Hacettepe University, 06800, Beytepe, Ankara, Turkey

*Drosophila* populations adapt rapidly to seasonal environmental heterogeneity. This rapid adaptation provides a framework for the study of eco-evolutionary dynamics. Water presence is a major environmental stressor and shows variation among habitats. Insects are more undefended to water-related constrictions.

Therefore, desiccation tolerance is an essential physiological character of fitness for insects. Here, we investigate how populations respond to environmental changes across seasonal time. To assess change in fundamental aspects of population genetics desiccation tolerances were measured in 55 inbred lines collected from the same place, at six time points from May through October in two successive years, were treated as replicates for seasonality. Our data demonstrate a seasonal variation in desiccation tolerance. These results suggest differences in seasonal populations related to differences in environmental parameters and associated selection pressures. They also provide us more information of adaptive processes in *D. melanogaster* population faced with seasonal fluctuations

**Keywords:** Seasonal variation, desiccation tolerance, seasonal adaptation

### Urban dishonesty in song sparrows?

Çağlar Akçay<sup>\*1,2</sup>, Michelle L. Beck<sup>2,3</sup>, Kendra B. Sewall<sup>2</sup>

<sup>1</sup>Koç University

<sup>2</sup>Virginia Tech

<sup>3</sup>Rivier University

Although most signaling systems are assumed to be stable, rapid environmental change such as urbanization may generate new selection pressures, leading to changes in how signaling systems function. We tested whether urbanization affects the honesty of aggressive signaling in male song sparrows (*Melospiza melodia*). We used simulated intrusions with song playback and taxidermic models to compare rates of attack and signaling in 2 urban and 3 rural populations surrounding Blacksburg, VA. We carried out the trials in April (early spring) and May (mid-spring). Attack rates were higher in urban compared to rural habitats, and the difference was more pronounced in mid-Spring. Urban song sparrows did not reliably signal their intention to attack via soft songs and wing waves in early Spring trials but did so in mid-Spring. Thus, the signaling system showed a seasonal change in overall honesty in urban habitats. In contrast, the signaling system was reliable in rural habitats from early spring on. Selection pressures including noise, predation risk, and social stability could contribute to these differences in reliability of signaling across urban and rural populations.

**Keywords:** Urbanization, honesty, animal communication

### Can birds beat cancer?

E. Yagmur Erten<sup>\*1</sup>, Marc Tollis<sup>2</sup>, Hanna Kokko<sup>1</sup>

<sup>1</sup> University of Zurich

<sup>2</sup> Arizona State University

Growing bigger requires cell divisions. Every division is accompanied by a risk of mutations, and their accumulation can lead to cancer. Therefore, one would expect a higher cancer incidence in larger individuals. While this seems to be the case within-species, between-species it does not hold: larger animals do not have a higher cancer incidence compared to the smaller ones, which is known as “Peto’s paradox”. Evolution of better cancer defences that accompanies the size increase has been proposed as a resolution of this “paradox”. Yet, body size can also change towards the other direction through miniaturisation and a well-known example is the theropod dinosaur lineage that led to birds. What happens to the cancer defences when species shrink? Do miniaturised species have better cancer defences, evolved in their larger ancestors, compared to species with similar body size that did not shrink? Or did they lose these defences once they were redundant? We use a mathematical model that takes cancer risk as a factor in body size evolution, to see whether changes in cancer

defences will arise and get fixed in the population during the process of miniaturisation. We then relate these results to genomic data from bird species.

**Keywords:** Life history, Cancer, Coevolution

### **Detecting Density Dependence in North American Landbird Populations**

*Bilgecan Şen<sup>\*1</sup>, H. Reşit Akçakaya<sup>1</sup>*

<sup>1</sup>Department of Ecology and Evolution, Stony Brook University

Collection and analysis of mark-recapture data remain one of the few fundamental ways to estimate vital rates of many animal taxa. Monitoring Avian Productivity and Survivorship (MAPS) is one such program that spans across more than 1200 bird banding stations on North America, some of which operating since 1989. MAPS program have already published estimates of survival and recruitment rates of more than 150 bird species. One critical missing element from the models producing these estimates is density dependent factors. Without density dependence, models cannot be used to project population abundance because such attempts end with either exponential increase or decrease. We propose a hierarchical Bayesian modeling framework that can incorporate density dependent factors along with process variance of vital rates. We tested the ability of this framework to retrieve true parameter values using simulated data, and applied it to 10 MAPS species that had high numbers of individual capture histories. Negative density dependence on survival and fecundity was detected in all cases. Fecundity and survival estimates, however, are highly affected by the number of juvenile recaptures and emigration rates, respectively. Low recapture and high emigration rates lead to underestimation of density dependence and vital rates. We discuss the utility of this method in the context of parameterizing meta-population models.

**Keywords:** Mark-Recapture, Robust Design, Density Dependence

**EVOLUTIONARY BIOLOGY ORAL ABSTRACTS**

**Discovering prokaryotic dynamic in marine environment by using a combination of genetic analysis and numerical ecosystem models**

*Selin Küçükavşar<sup>\*1</sup>, Arzu Karahan<sup>1</sup>, Sinan Arkin<sup>1</sup>, Barış Salihoglu<sup>1</sup>*

<sup>1</sup>Middle East Technical University, Institute of Marine Sciences Erdemli, Mersin, Turkey

Corresponding author e-mail: [selin@ims.metu.edu.tr](mailto:selin@ims.metu.edu.tr)

Despite the many important roles, they play, bacteria are one of the least known components of the marine biogeochemical cycles. Even if they have highly diverse functional roles in the ecosystem, their representation in the marine biogeochemical models is constrained by only one functional group. In the gene-centric model approaches that uses functional gene abundance as a state variable allows for the integration of environmental genomics data and biogeochemical models. In order to determine the temporal dynamics of the species composition, the community structure, the abundances of the bacteria that play significant roles in the cycling nitrogen and phosphorus and the rates of the reactions that the bacteria perform we have used a combination of genetic analyses, biochemical measurements and numerical models in the Mediterranean. Samples (in total 65) were collected from 6 different water column depth in the oligotrophic observation station of Erdemli Time Series with monthly intervals for one year and sequenced by NGS platform using 16S rDNA Metagenomics approach. Among which, 1993 sequence variants observed, Pelagibacteraceae, Alphaproteobacteria and Flavobacteriaceae classes and *Candidatus portiera* were the highly dominantly discovered taxa. Water column stratification can be concluded as the main driving factor influencing the communities' composition. These results were further analyzed for the integration of different functional groups to numeric ecosystem model for better understanding of marine microbial reactions and carbon and nitrogen cycle in the changing marine ecosystems.

**Keywords:** 16S rDNA, amplicon sequencing, numerical models

**Identification of Fish Species in Eurasian Otter (*Lutra lutra*) Diet Using DNA Metabarcoding of Faecal Samples**

*Sevgi Kaynar<sup>\*1</sup>, Ozan Çiftçi<sup>1,2</sup>, İlhami Turan<sup>3</sup>, Emre Keskin<sup>1</sup>*

<sup>1</sup> Evolutionary Genetics Laboratory (eGL), Department of Fisheries and Aquaculture, Faculty of Agriculture, Ankara University, Turkey

<sup>2</sup>Institute of Biotechnology, Ankara University, Turkey

<sup>3</sup>West Black Sea Forestry Research Institute, Bolu, Turkey

The aim of this study is to analyze how human activities affected Eurasian Otter's nutritional behavior and test the availability of DNA metabarcoding as a tool for diet composition analysis. For this purpose, we began by studying a specific lake in Turkey inhabited by a single endemic fish species together with several non-indigenous fish species. In this preliminary study, six fresh faeces were collected throughout the perimeter of the lake area. DNA was extracted from all faecal samples using a stool DNA purification kit. For the diet analysis, hyper variable region of 12S rRNA gene was amplified using universal fish specific primers and PCR products were pooled into libraries. Then the libraries were sequenced on Illumina MiSeq platform. Raw FASTQ reads were quality-filtered using FastQC software. Further data processing and taxonomic classification through comparison with databases were performed by OBITools. Our results show that, nine fish species were identified with DNA metabarcoding of faecal samples. Species with the highest read counts were *Tinca tinca*, *Salmo trutta* and *Gobio gobio*. Therefore the results suggest that, otter's diet comprises both endemic, indigenous and non-indigenous species. However, we also obtained some false positive results through alignments from global databases (NCBI and EMBL). This alignment related bias can be prevented by building a local database

comprising all groups from macro invertebrates to mammals inhabiting Abant Lake region. As a result, DNA metabarcoding approach can be a useful emerging tool for monitoring predatory behavior of non-invasive and elusive species, like Eurasian otter, in response to changing environments.

**Keywords:** Molecular Ecology, Diet Analysis, DNA Metabarcoding

### Genomic Organization and Standing Structural Variation of the MHC of the Three-spined Stickleback

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

<sup>1</sup>MPI for Evolutionary Biology

Parasite-mediated selection has been found to be a major driver for the evolution of host genetic diversity at the nucleotide level, but less is known about its effect on structural genomic variation. The Major Histocompatibility Complex (MHC) is a genomic region essential to adaptive immunity and has many characteristics, such as high allelic variability and sequence divergence as well as potentially adaptive copy number variation (CNV) at some of its loci. Previous work revealed local adaptation of locus-specific MHC allele pools to distinct parasite communities. However, little is known about the evolutionary factors that drive this. Here, we unravel the genomic organization of the MHC class-II region of the three-spined stickleback (*Gasterosteus aculeatus*), for which we found a candidate region at one end of Chromosome VII. We used BAC-library construction and PacBio sequencing to study several CNV haplotypes of the MHC region, so as to create a reference map of the MHC class II region. Analysis of synteny revealed both homology as well as unexpected variation. The stickleback MHC class II region consists of two parts, a variable region (containing polymorphic, classical MHC loci) near the telomeric end, and an invariant region (containing a possibly non-classical monomorphic locus), closer to the centromere. We investigated phylogenetic relationships between different sequence variants in an effort to assign known ecologically relevant MHC variants to specific loci. The reference map of the MHC class-II region will facilitate characterization of natural haplotypic variation, and illuminate the importance of CNVs in local adaptation and ecological speciation.

**Keywords:** Stickleback, MHC, Genomics

### Genetic structure of the bottlenose dolphin (*Tursiops truncatus*) in the Turkish waters based on mtDNA sequences

*Arda M. Tonay*<sup>1</sup>, *Begüm Uzun*<sup>1\*</sup>, *Ayhan Dede*<sup>1</sup>, *Erdem Danyer*<sup>1</sup>, *Işıl Aytemiz Danyer*<sup>1</sup>, *Ayaka A. Öztürk*<sup>1</sup>, *Raşit Bilgin*<sup>2</sup>

<sup>1</sup> Istanbul University

<sup>2</sup> Boğaziçi University

The bottlenose dolphin is a cosmopolitan species, with an extremely wide distribution in temperate waters including the Mediterranean and the Black Sea. Black Sea population has been suggested as a subspecies *Tursiops truncatus ponticus* due to its genetic and morphological differences. In this study, mitochondrial DNA sequences of 74 bottlenose dolphin samples collected between 1999-2016 in the Turkish Black Sea coast (30 western, 1 eastern), the Turkish Straits System (TSS) (31), the Aegean Sea (7) and the Mediterranean Sea (5), revealed 15 haplotypes, 10 of which were reported for the first time. The haplotype network showed three peripheral groups (I-III). Based on haplotype frequency differences, the Black Sea dolphins were detected to be

genetically differentiated in Group-I, supporting the previous inferences that these bottlenose dolphins have been differentiated from those in the Atlantic and the Mediterranean. Moreover, Black Sea dolphins were found to be different also from the TSS when Group- II was analyzed separately. Group-III was found to comprise the individuals from Mediterranean Sea and Atlantic dominantly, and two individuals from the TSS, but none from the Black Sea, again indicative of differentiation of the latter. The Black Sea population also had low haplotype diversity levels among the populations investigated, even though its sample size was the highest, along with TSS. Its differentiation from the adjacent populations and low levels of genetic diversity indicates a conservation concern for the Black Sea population, as populations that are isolated and depauperate of genetic diversity as such might be more vulnerable to diseases, and negative changes in environmental conditions. Therefore, conservation strategies and management should be planned separately for this population. High-resolution next-generation sequencing (such as ddRAD sequencing) methods should be applied for a more complete understanding of the genetic population structure of this species, and specifically the differentiation of the Black Sea population, in a conservation perspective.

**Keywords:** Black Sea, Cetacea, Population Genetics

### **Radiation via hybridisation: Evolution in *Poecilimon bosphoricus* species group (Orthoptera, Tettigoniidae)**

*Sarp Kaya<sup>1</sup>, Uğur Karşı<sup>2</sup>, Özgül Yahyaoğlu<sup>\*2</sup>, Onur Uluar<sup>2</sup>, Battal Çiplak<sup>2</sup>*

<sup>1</sup> Mehmet Akif Ersoy University

<sup>2</sup> Akdeniz University

**Introduction:** Throughout the life on earth, populations experience many geological and climatic events that shape their evolutionary history. One of the major results of these events is the secondary contact of previously separated populations. This spatial condition could form a hybrid zone where genetically distinct populations meet and reproduce. A very few recent studies showed that hybridizing lineages rapidly radiate, as the newly gained genes has been tested in gene pool of donating population. Early genetic data from *Poecilimon bosphoricus* species group, especially those distributed around Marmara Sea indicate that there is a distinct conflict between gene trees and species trees, thus, it is a candidate model group to test assumption of radiation via hybridization. **Material and Method:** Mitochondrial cytochrome C oxidase subunits I (COI) region was amplified via PCR using appropriate primer couples. PCR amplicons were sequenced through the intake from the Macrogen Europe sequencing service. Rough sequences were processed and a data matrix was produced using appropriate programmes. Phylogenetic, phylogeographic and time estimation analyses were applied to data matrices. **Results:** Sixty-three unique haplotypes were determined from 232 sequences representing 16 species in the group. Phylogenetic analyses resulted in paraphyletic species, as a sign of frequent genetic admixture. Time estimation analyses indicated a radiation history correlated with post Messinian period. **Conclusions:** (i) COI tree does not support phenetic species, (ii) phylogroups correlate with geography, but not with phenotypic species, (iii) genetic admixture indicates frequent hybridization among species, (iv) hybridization patterns correlates with land/sea changes around Marmara Sea, and (v) all these together are in support of radiation via hybridization.

**Keywords:** Hybridisation, rapid radiation, *Poecilimon bosphoricus* group

## Natural selection via condition-dependent predation enhances the costs of male ageing on female reproductive success, exacerbating sexual conflict

*Zahida Sultanova<sup>\*1</sup>, Roberto Garcia-Roa<sup>1</sup>, Pau Carazo<sup>1</sup>*

<sup>1</sup> Ecology, Ethology and Evolution Group, Cavanilles Institute of Biodiversity and Evolutionary Biology, University of Valencia, Valencia, Spain

Recent studies suggest that, by decreasing the reproductive success of females mating with old males, male ageing can increase sexual conflict. However, the influence of natural selection on this process has been overlooked so far despite the fact that it can, via condition-dependent selective disappearance, generate a positive correlation between male age and condition, which could in turn counterbalance the costs of mating with an old partner. We used *Drosophila melanogaster* to explore the role of male/female age on reproductive behaviour, mating success and reproductive success in the presence or absence of condition-dependent selection. We mated young/old males and females subject or not to condition-dependent predation; we used climbing speed as a proxy for anti-predatory escape ability. Female age caused a decline in reproductive success irrespective of selection, but male age caused a more drastic decline in female reproductive success, and a higher increase in mating duration, under selection. Furthermore, a combined male and female age effect caused a decrease in male mating success only in the absence of selection. Altogether, we show that condition-dependent selection can exacerbate the reproductive costs of male age on females by increasing: a) male age effects on female reproductive success, b) the costs of mating with an old male (i.e. mating duration), and c) the probability of mating with old males. Our results hence not only support the notion that male ageing can magnify sexual conflict, but actually suggest this role may be more important than previously suspected.

**Keywords:** Ageing, sexual conflict, natural selection

## The mysterious case of a single *Aquilegia* chromosome

*Gökçe Aköz<sup>\*1</sup>, Daniele Filaull<sup>1</sup>, Magnus Nordborg<sup>1</sup>*

<sup>1</sup> Gregor Mendel Institute; Vienna Graduate School of Population Genetics

The genus *Aquilegia* represents a beautiful example of adaptive radiation in plants: originated in Asia, they spread both to North America and Europe. Resequencing ten worldwide *Aquilegia* species and a single outgroup species revealed the first genomic patterns of these two independent radiation events. While the split of North American *Aquilegia* is clearer and consistent with a bottleneck scenario, the relationship between European and Asian species is reticulate and thus contradicts a bifurcating speciation model. As expected from rapid speciation, a considerable proportion of derived variants is shared across all three geographic regions. This deep variant sharing gets even more extreme on chromosome four. This chromosome has nucleotide diversity almost twice that of the rest of the genome and seems more permeable to gene flow. We also know that it has a lower gene density and expression. All these results suggest that chromosome four has been under relaxed purifying selection. To get a better understanding of the unique history of chromosome four, we investigated the history of whole genome duplications in *Aquilegia*. Comparison to the grape genome reveals that unlike other *Aquilegia* chromosomes of similar size, which are all products of ancient fusion events, chromosome four appears to have reached a comparable size partly due to an expansion of repetitive DNA, partly due to numerous segmental duplications. We are now looking at population-level data to delve more deeply into the distinct path followed by this peculiar chromosome.

**Keywords:** Adaptive radiation, Aquilegia, Relaxed purifying selection

### Developmental mechanism of a major evolutionary transition in ants

*Ab. Matteen Rafiqi<sup>\*1</sup>, Arjuna Rajakumar<sup>2</sup>, Ehab Abouheif<sup>2</sup>*

<sup>1</sup> Bezmialem Vakif University Istanbul Turkey

<sup>2</sup> McGill University, Montreal Canada

Major transitions in evolution occur through integration of independently replicating units into a single, higher-level, replicating unit. Despite the importance of major transitions for understanding increases in biological complexity, the evolutionary developmental steps towards integration remain unknown. Here we use gene expression, RNAi, antibiotic treatment, and comparative phylogenetic analysis to reconstruct five evolutionary developmental steps underlying the major transition to obligate endosymbiosis between the hyper diverse genus *Camponotus* (carpenter ants) and the bacteria *Blochmannia* – *Camponotus* ensures vertical transmission through its germlasm while *Blochmannia* provides nutrition and immunity. This integration evolved through two successive rounds of duplication and divergence of a single ancestral germlasm, giving rise to three germlasms with a functional division of labor between them. *Blochmannia* induced these duplication and divergence events through its pre-adaptive relationship with the Hox genes *Ultrabithorax* and *Abdominal-A*, while *Camponotus* underwent radical alterations in its early development. We predict that the general pathway to major evolutionary transitions, including to multicellularity and eusociality, occurs by environmentally-induced duplication and divergence of pre-existing traits, allowing each duplicate to take on novel functions and divide labor.

**Keywords:** Evolution, Endosymbiosis, Development

### Amylase copy-number analysis in different mammalian lineages reveals convergent adaptive bursts shaped by diet

*Omer Gokcumen<sup>\*1</sup>*

<sup>1</sup> Department of Biological Sciences, State University of New York at Buffalo, Buffalo, NY 14260-1300, U.S.A.

The amylase gene (*AMY*), which codes for a starch-digesting enzyme in animals, underwent several gene duplications in humans, dogs, and mice, presumably along with increased starch consumption in these species. Using digital droplet PCR and genome sequence analysis, we present evidence for additional “bursts” of *AMY* copy number expansions in rats and pigs, which are also omnivorous animals consuming starch-rich diets. We also showed that all of these independent *AMY* copy number gains are accompanied by a gain in enzymatic activity of amylase in saliva. We used multi-species coalescent modeling to provide further evidence that these recurrent *AMY* gene duplication events were adaptive. The findings underscore the overall importance of gene copy-number amplification as a flexible and fast adaptive mechanism in evolution that can independently occur in different branches of the phylogeny.

**Keywords:** CNV, Anthropological Genetics, Human evolution

## Shared polymorphisms reveal additional pulses of Neanderthal introgression

*Recep Ozgur Taskent<sup>\*1</sup>, Yen-Lung Lin<sup>1</sup>, Omer Gokcumen<sup>1</sup>*

<sup>1</sup> Department of Biological Sciences, State University of New York at Buffalo, Buffalo, NY 14260-1300, U.S.A.

Humans and Neanderthals interbred in Eurasia after humans migrated out of Africa. Recent studies have shown that multiple such introgression events have happened throughout human history. However, it is not clear how many of these events have left signatures in the contemporary human gene pool. In this study, we hypothesize that multiple isolated Neanderthal populations have contributed genetic material to humans. Two recently available high-quality Neanderthal genomes (Vindija Neanderthal from Croatia and Altai Neanderthal from the Altai Mountains in Siberia) now allow us to test this hypothesis. To do this, we first investigated large deletion polymorphisms that are shared between Neanderthals and humans. These large deletion polymorphisms are unlikely to be recurrent if they share exact breakpoints. Consequently, we can argue that allele sharing between Neanderthals and humans for these deletion polymorphisms is either due to incomplete lineage sorting (ILS) or introgression. After ruling out ILS, we were able to identify three cases where one Neanderthal lineage, but not the other, putatively contributed to modern human gene pool. To verify this observation in haplotypes without deletion polymorphisms, we conducted a genome-wide search and identified 1,338 haplotypes across human genomes mapping to one Neanderthal genome but not the other. Last, we conducted population genetics analyses using only putatively introgressed haplotypes and found at least two coalescent events, indicating multiple sources of introgression. Collectively, our results suggest more than one pulse of introgression from Neanderthals to modern humans and suggest other potential sources for archaic haplotypes among extant human genomes.

**Keywords:** Admixture, Neanderthal, East Asians

## Modelling the origin and expansion of Turkic speakers

*N. Ezgi Altınışık<sup>\*1</sup>, Pavel Flegontov<sup>1</sup>, Choongwon Jeong<sup>2</sup>, Michael Frachetti<sup>3</sup>, Johannes Krause<sup>2</sup>, David Reich<sup>4</sup>*

<sup>1</sup> Department of Biology and Ecology, Faculty of Science, University of Ostrava, Czech Republic

<sup>2</sup> Department of Archaeogenetics, Max Planck Institute for the Science of Human History, Jena, Germany

<sup>3</sup> SAIE Laboratory, Department of Anthropology, Washington University in St. Louis, CB 1114, One Brookings Drive, St. Louis, MO, 63130, USA

<sup>4</sup> Department of Genetics, Harvard Medical School, Boston, USA

Turkic-speaking populations, now spread over a vast area in Asia, are highly heterogeneous genetically. The first confederation unequivocally attributed to the Turkic speakers was established by the Göktürks in the 6th c. CE. Notwithstanding written resources from neighboring sedentary societies such as Chinese, Persian, Indian and Eastern Roman, earlier history of the Turkic speakers remains debatable. In this study, we tested various admixture models for hundreds of present-day and few securely attributed ancient Turkic individuals. Firstly, we generated a PCA projection to understand genetic affinities of 133 ancient individuals with respect to present-day Tungusic, Mongolic, Turkic, Uralic, and Yeniseian-speaking group. Secondly, we modeled present-day Turkic-speaking individuals using the qpAdm tool, testing various modern Siberian and ancient West Eurasian proxies for ancestry sources. A majority of Turkic speakers in Central Asia, Siberia and further to the west share the same ancestry profile, being a mixture of Tungusic or Mongolic speakers and West Eurasian populations of Central Asia in the early 1st millennium CE. The latter are themselves modelled as a mixture of earlier West Eurasian nomads (Scythians or Sarmatians) and ancient Caucasians. For some Turkic-speaking

groups in the Urals and the Altai regions and in the Volga basin, a different admixture model fits the data: the same West Eurasian source + Uralic- or Yeniseian-related Siberians. This suggests language transfer without substantial admixture (possibly via elite dominance) happened quite frequently, and also suggests that admixture between (genetically West Eurasian) nomads occupying the Central Asian steppe at the turn of the common era and various Siberians of the forest zone happened independently on several occasions.

**Keywords:** Turkic speakers, Uralic speakers, ancient Central Asia

### **Genomes from the Pontic-Caspian steppe, a closer look at the genomics behind the bronze- and iron age demography in southern Ural.**

*Anders Götherström*<sup>\*1</sup>

<sup>1</sup>Archaeological Research Laboratory, Department of Archaeology and Classical studies, Lilla Frescativägen 7, 106 91 Stockholm University

*Lilla Frescativägen 7, 106 91 Stockholm University* The Steppe has been a breeding-ground for various mobile bronze- and iron age groups. Just keeping to the Pontic-Caspian steppe, we encounter groups such as the Srubnyas, the Andronovans, the Karasuks, the Cimerians, the Scythians, and the Sarmatians. It is, ofcourse, not always obvious what is behind these labels, and which groups are actually ethnic groups, material manifestations, regional groups, or biological groups. We have looked closer at a chronology focused in the southern Urals, but extending to the northern Black Sea area. We have sequenced genomic DNA to various depth (low- to medium coverage, 0,01-2,9X), and spanning some 2200 years. The data has been collected from Srubnyas, Cimerians, Scythians, and Sarmatians. The material presents good data, with descent preservation and relatively little contamination. We use genomic variation, shared drift, and various common types of multi-loci statistics to compare these groups with one another, and with other groups in the region. We try to find continuities and discontinuities and follow the development within one region. During this period, we find indications of all those things, continuity, discontinuity (the nomads were indeed a mobile metagroup), and also acculturation. The long chronology allows us to follow elements that increases over time (like Near Eastern parts of the genomes) and other that decreases over time. And while some groups may be more genetic distinct than others, there is always an element of gene flow.

**Keywords:**

### **Partial coincidence of microsatellite genotypes suggests a possible role of backcrosses in diversification of parthenogenetic rock lizards**

*David Tarkhnishvili<sup>1</sup>, Alexey Yanchukov<sup>\*2</sup>, Mehmet Kürşat Şahin<sup>3</sup>, Kamil Candan<sup>4</sup>, Çetin Ilgaz<sup>4</sup>, Yusuf Kumlutaş<sup>4</sup>, Sofiko Kurdadze<sup>1</sup>, Natia Barateli<sup>1</sup>, Faruk Çolak<sup>2</sup>, Marine Murtskhvaladze<sup>1</sup>*

<sup>1</sup> Ilia State University, Georgia

<sup>2</sup> Bülent Ecevit University, Turkey

<sup>3</sup> Hacettepe University, Turkey

<sup>4</sup> Dokuz Eylül University, Turkey

Most researchers interpret genotypic diversity within some forms of parthenogenetic *Darevskia* as indirect evidence of their polyclonal origin. Tarkhnishvili et al. (2017) showed that two parthenogens, both matrilineally descending from *Darevskia mixta*, share genotypes at two microsatellite loci. They concluded that a single hybrid lineage participated in the origin of both forms. At present, we analyzed ten microsatellite loci in

six out of seven parthenogens: *D. dahli*, *D. armeniaca*, *D. bendimahiensis*, *D. sapphirina*, *D. unisexualis*, and *D. uzzelli*. The two former species descend matrilineally from *D. mixta*, the others from *D. raddei*. The individuals of the former pair share modal genotypes at three loci, but show distinct genotypes at the other seven loci. *D. bendimahiensis* and *D. sapphirina* share modal genotypes at six loci, and fixed differences at three. *D. unisexualis* shares modal genotype at one locus with the latter two, and *D. uzzelli* shares modal genotype at one locus with *D. dahli*. We hypothesize that phenotypic diversity of parthenogenetic *Darevskia* developed as a result of very few initial crosses between two bisexual species, but further diversification of parthenogens resulted from (also quite rare) production of fertile individuals by the crosses between the males of clade *D. rudis* and the parthenogenetic females. Putatively fertile triploid and tetraploid hybrids are known to result from such crosses, but the continuation of clonal reproduction would require reduction of chromosomal number back to diploid. Under this hypothesis, enrichment of parthenogenetic populations with new combinations of parental alleles may be a powerful mechanism of adaptation. This study is supported by a joint TUBITAK-SRNSF grant 216Z189

**Keywords:** Parthenogenesis, Hybridization, Microsatellites

### Identifying patterns of rapid radiation in phylogenomics

*Eren Ada*<sup>\*1</sup>, *Robert Litterman*<sup>1</sup>, *Rachel Schwartz*<sup>1</sup>

<sup>1</sup> University of Rhode Island

Patterns of diversification are a major focus of biodiversity research. Many studies, ranging from those in Darwin's finches to *Heliconius* butterflies, suggest that speciation often occurs in adaptive radiations where ecological opportunity promotes rapid species and phenotypic diversification, followed by a slow-down in these rates as new species occupy available niches. Mammal and bird diversifications following the K-Pg mass extinction event have both been described as adaptive radiations. In recent years, the ability to generate phylogenies without a corresponding understanding of ecology has led to inference of rapid radiations at the base of many clades (i.e. high species diversification of species followed by a slow-down, as observed from the phylogeny). However, the approaches to identifying rapid radiations vary widely among studies and are potentially complicated by incomplete taxonomic sampling and variation in the types of available data. In this study, we investigate the role of taxonomic sampling schemes, different datasets, and statistical methodology on diversification rate estimation using Aves as a model clade. Using publicly available phylogenetic trees for birds, we examine diversification rate shifts using lineage through time (LTT) plots and the G statistic, which quantifies how internode distances vary through time compared to a null hypothesis of constant rate pure-birth diversification. To account for incomplete taxon sampling, we calculate the likelihood of the phylogenetic history under different birth-death models of diversification (pure-Birth, constant rate birth-death, density-dependent logistic, and density-dependent exponential models) using a Hidden Markov Model (HMM) approach. We use these methods to examine whole phylogenies of birds derived from various datasets, as well as subsets of these phylogenies to identify periods of rapid diversification and cases where high diversification rates have been inferred erroneously. Additionally, we compare our results using identical methods across different datasets to examine the impact of data types on these inferences.

**Keywords:** Phylogenomics, diversification, speciation

## Genetic diversity is retained in a bottlenecked Cinereous vulture population in Turkey

*Emel Çakmak<sup>\*1</sup>, Çiğdem Akın Pekşen, Cihangir Kirazlı, Elif Yamaç, Staffan Bensch, and C. Can Bilgin<sup>1</sup>*

<sup>1</sup>Middle East Technical University

Throughout the world, vulture populations have suffered threatening declines in numbers in recent years. The Cinereous Vulture *Aegypius monachus* is a highly philopatric scavenger that ranges across southern Europe and the central Asian plateau. Turkey holds the second most numerous population in the Western Palearctic but there has been no research on the genetic structure of this particular population. In this study, we used 15 polymorphic microsatellite loci to investigate levels of nuclear diversity, relatedness of individuals, and signatures of a recent bottleneck as well as estimate the effective population size. We genotyped 81 individuals from four locations: Çatacık, Tandır, Türkmenbaba, and Köroğlu. Nuclear diversity based on allelic richness and expected heterozygosity showed moderate levels of genetic diversity. We could not detect any significant differentiation between the four colonies, which suggest that the sampled individuals originated from a single panmictic population. Additionally, we observed evidence of a recent bottleneck in the Turkish populations and a low effective population size 112 (95% CI 74–201). Besides, we did not detect any sign of population expansion. In the short-term, these findings suggest that the aim should be to increase population size by providing continuous protection for individuals and habitat management by treating to the Turkish populations as a single management unit.

**Keywords:** *Aegypius monachus*, microsatellite, population structure

## Domestication-driven metaorganism evolution of wheat

*Ezgi Özkurt<sup>\*1,2</sup>, Uğur Sesiz<sup>3</sup>, Hakan Özkan<sup>3</sup>, Eva H. Stukenbrock<sup>1,2</sup>*

<sup>1</sup> Environmental Genomics, Christian-Albrechts University of Kiel, Am Botanischen Garten 1-9, 24118 Kiel

<sup>2</sup> Max Planck Institute for Evolutionary Biology, August-Thienemann-Str. 2, 24306 Plön, Germany

<sup>3</sup> Department of Field Crops, Faculty of Agriculture, University of Cukurova, 01330 Adana, Turkey.

There is evidence that the composition of microbial communities of the plant phyllosphere is maintained over different host generations. This observation suggests a conserved mechanism to assemble and maintain microbial communities in spite of changing environments. Furthermore, it points to the presence of an internal reservoir of microbes transmitted vertically from generation to generation. Here, we examine the microbial community composition of seeds of different wheat species as a source for early microbial colonization of plant seedlings. We hypothesize that vertically transmitted microbes represent tightly co-evolving endophytes possibly with beneficial effects. Furthermore, we hypothesize that domestication of wheat has impacted the ability to assemble and maintain microbial communities. To address this, we have collected seeds from *Triticum dicoccoides*, *T. boeoticum* and *T. urartu* wild wheat species and from domesticated *T. aestivum* in a region of South Turkey located in the Fertile Crescent. We characterize the microbial species by amplification and sequencing of the bacterial 16S locus and the fungal inter transcribed sequence locus (ITS) from seed derived DNA. Our preliminary data has revealed the occurrence of fungal species including species of the genera *Alternaria* and *Antrodia* genus, and bacterial species from the genera *Pseudomonas*, *Luteibacter* and *Halomonas*. Some of these microbes are associated with plant growth promotion in previous studies. To examine the in-planta occurrence and abundance of the seed-borne endophytes, we moreover germinate the wheat seeds

under sterile conditions to characterize the microbial species migrating from seeds to leaves and roots. Ultimately, this will allow us to characterize the core endophytic communities of wild and cultivated wheat species from the Fertile Crescent.

**Keywords:** microbiota, wheat, holobiont

### **Identifying functionally equivalent orthologs in the context of predicting disease-causing mutations.**

*Ogun Adebali*<sup>\*1</sup>

<sup>1</sup> Faculty of Engineering and Natural Sciences, Sabanci University

Molecular evolution provides a fundamental source of information for predicting the effects of amino acid substitutions on protein function and consequently disease. If a protein residue is under a purifying evolutionary constraint throughout millions of years, it is inferred that most substitutions in that position will disrupt the protein function and reduce the fitness of the organism. Despite the existence of a vast volume of sequence information collected across a broad spectrum of organisms, the performances of the current predictive algorithms are not at a desired level of precision. Here, we aim to improve the prediction of amino acid variant outcomes by removing the evolutionary noise introduced by paralogous proteins that were diverged and lost ancestral evolutionary constraints. As a proof of concept, we constructed the evolutionary history of NPC1 gene which causes Niemann-Pick disease type C when it loses the function. We built a phylogenetic tree of NPC1 homologs using the publicly available protein sequences and identified gene duplication and loss events. Furthermore, we discriminate between functionally equivalent and diverged NPC1 homologs. Our approach yielded a better accuracy overall compared to state-of-the-art algorithms such as PolyPhen-2 and SIFT in predicting disease-causing mutations. We anticipate our approach to be applied to other genes associated with monogenic disorders with the aim of improving diagnosis of Mendelian diseases by solely delineating protein sequences through the lens of evolution.

**Keywords:** Molecular Evolution, Protein Sequences, Disease

**POSTER ABSTRACTS**

**The investment of nuptial gift and immunity: Comparison the sex differences in mate searching between two species in the bush-cricket genus *Poecilimon***

*Hasan Sevgili*<sup>\*1</sup>, *Ebru Kiran*<sup>1</sup>

<sup>1</sup>Ordu University, Faculty of Arts and Sciences, Department of Molecular Biology and Genetic, ORDU

Both acoustic signalling and mate searching effort can be costly for both sexes. Some studies have been provided the experimental evidence that there are direct immunological costs of sexual signalling. Increased reproductive activity results in reduced immunity. This “cost” hypothesis predicts a tradeoff between immune functions and other life-history traits. During the copulation, the male bush-cricket transfers a costly spermatophore which is important nutritional sources (spermatophylax+ampulla-containing ejaculate) to the female. In this study we concentrate on how both nuptial food gift and some immune activities change in two *Poecilimon* species (*P. sureyanus*-female search and *P. inflatus*-male search) which can be an example to these two different communication/mate searching systems. While the previous theory has emphasized only the evolution of spermatophore characteristics according to the variations in mate searching protocols in the 32 *Poecilimon* taxa, we have hypothesized that in addition to this theory, some immunological activities (phenoloxidase-PO and lysozyme activities-LY) in two *Poecilimon* species may also be differentiated by male mate searching. Our results showed that species where females search produce significantly larger ampulla and more sperm than those where males search, except the edible part of nuptial gift. As predicted, in both sexes of *P. sureyanus* where females mate searching have higher PO than that of *P. inflatus*, whereas LY didn't show any significant change between species. These results indicate that physiological trade-offs are often plastic, meaning that there is no single trait to understanding of trade-offs between the immunity and sex roles in mate searching will require a more detailed analysis of the life-history traits.

**Keywords:** mate searching, nuptial gift, immunity

**Sightings of three cetacean species in the south part of the Black Sea**

*Nastassia Uluduz*<sup>\*1</sup>, *Alexey Yanchukov*<sup>1</sup>, *Mustafa Sözen*<sup>1</sup>

<sup>1</sup> Bülent Ecevit Üniversitesi

Research on cetaceans in the Black Sea has started in relatively recent times and have sporadic character. Field surveys conducted in several small regions do not reveal the general distribution of the dolphin species in the entire Black Sea. A pilot study started in the winter season from December 2017 and still continuous. Sightings of cetaceans were recorded during coastal observations, at two observation points separated by 30 km, in the southern Black Sea near Zonguldak (Turkey). Environmental conditions, coordinates of observation points, cetacean presence and their number, behavior of animals were documented in each standardized shore watch. Over 20 days of surveys 165 specimen of all three species of cetaceans inhabiting the Black Sea were observed. The Bottlenose Dolphin (*Tursiops truncatus ponticus*) was recorded in 7 observations, the Short-beaked Common Dolphin (*Delphinus delphis ponticus*) in 3 observations, and Harbour Porpoise (*Phocoena phocoena relicta*) in 7 observations. Our study will provide the first systematic record of dolphin distribution in the south central part of the Black Sea, and will be essential for development of conservation program of their populations.

**Keywords:** cetaceans, sightings, South Black Sea region

**Analysis of body size/mass and immunity in the *Gryllus bimaculatus* (Orthoptera: Gryllidae)**

*Hasan Sevgili*<sup>1</sup>, *Dilek Arslan*<sup>\*1</sup>

<sup>1</sup> Ordu University, Faculty of Arts & Sciences, Department of Molecular Biology and Genetic, Ordu, 52200, TURKEY.

\* Corresponding author: [hsevgili@gmail.com](mailto:hsevgili@gmail.com)

Body size and mass are perhaps the most conspicuous feature of an organism, in particular, orthopteroid insects display some of the most striking variation in size among the insects. Because these features influence nearly all aspects of biology and are important implications for the insect's competitive ability and mating success. Life-history theory assumes that there should be some trade-offs that are to be expected between life-history traits such as body growth and immune function. In this study, we described the maturation of the innate immune system of the Mediterranean Field Cricket, *Gryllus bimaculatus* during the last nymphal stage, during early (3 days) and late adulthood (25 days) for three generations under laboratory conditions. We examined how variation in body size/mass affect the immune functions by following three successive generations. There were positive relationships between body mass and development time (day), phenoloxidase activity (PO) and body size for each generations. We found that a negative relationship between body mass and cuticle melanisation (darkness). There was a positive relationship between PO and body mass in all developmental stages and for both sexes. Both lytic activity and encapsulation ability were independent of the body mass/size. We found a negative relationship between total cuticle melanisation and development time for each age groups. In general, body size (not body mass) had an effect on total cuticle melanisation. Thus, in this system, the results have implications for understanding how body size/mass influences immune functions with different generations and age groups in *G. bimaculatus*. In addition, this study is supported by TUBITAK project, No: 215Z455.

**Keywords:** Body size and mass, innate immunity, *Gryllus bimaculatus*

**Information Theory in Ecology and Evolution**

*Yekbun Adiguzel*<sup>\*1</sup>

<sup>1</sup> Altinbas University

Information Theory is inherently related to the diversity and variation in every type of populations, and sub-populations. However, the concept and its broad applicability is currently not widely known in some communities of interest, to the best of our knowledge. Therefore, (i) here it is aimed to introduce the concept with various relevant examples of applications in ecology and evolution. The (ii) materials and methods of this study will include the review of the recent work in the literature, including examples from our own previous and ongoing studies. As a result, (iii) it is believed that a basal level of understanding would be attained, and the attention could be drawn to the concept, to stimulate further research and application of information theory in various new fields of ecology and evolution. It is (iv) concluded that this introductory review with examples from our own work can be of importance, considering the numerous applications of the theory in a substantially wide part of the community, and potential of its immediate influence and use in distinct studies.

**Keywords:** Information Theory, Ecology, Evolution

## Polymorphisms in the Promoter Region of GULO Gene in Dogs

*Roja Fidel Acar<sup>\*1</sup>, Cemal Ün<sup>1</sup>*

<sup>1</sup>Ege University, Faculty of Science, Department of Biology 35100 Bornova/İzmir

L-ascorbic acid, originally called Vitamin C, is an important vitamin for the health of mammals. GULO encodes for a catalytic enzyme in the terminal step of the biosynthesis of vitamin C. Despite its importance both in human and other primates, an accumulated mutation in the last 40 million years silenced it. And again, in teleost fishes, passeriformes bird species, guinea-pigs and some of the fruit bats GULO is pseudogene while it is still functional all other animals and plants. In dogs, GULO gene which is active is mapped to chromosome 25. The purpose of this study is to detect polymorphisms in the promoter regions of the GULO gene in dogs and to provide a baseline data for further research towards identification of the effects of polymorphisms on this gene's activities. Thus, blood sample from 50 stray dogs was collected to isolate genomic DNA. Further the relevant region of the DNA amplified with polymerase chain reaction (PCR) technique using primers specifically designed for the promoter region of GULO and sequenced. MEGA 7 was used for alignment and identification of polymorphism. After analysis, GULO gene promoter polymorphism at 9 different positions were detected. From this result is possible to conclude that the defined polymorphisms could affect GULO gene expression. However, further study is required to identify the genuine effect of the polymorphism on its activity for this particular gene.

**Keywords:** GULO gene, Promoter region, Polymorphisms

## Analysis of Codon Differences and Glycosylation Profiles Among Mammalian and Avian Foxp2 Genes and Proteins

*Ahmet Efe Köseoğlu<sup>\*1</sup>, Cemal Ün*

FoxP2 is an important transcription factor expressed during the embryonic development of many organs such as brain, heart, lung; and controls the regulation of various genes related to embryogenesis. FOXP2 gene, the first gene detected related with speech and language was first identified in a family suffering from speech impairment after discovering a mutation at 7q31 chromosomal location. FoxP2 is a glycoprotein and undergoes glycosylation after translation. Glycosylation is the attachment process of sugar subunits (glycans) to proteins, basically has two types: N- linked and O- linked glycosylations producing N- linked and O- linked glycans on glycoproteins. The aim of this study was detection of FoxP2 gene codon differences and FoxP2 protein glycosylation profiles (N- and O-) in different mammalian and avian organisms. 13 different species (two individuals from each species) were selected and 26 FoxP2 gene sequences retrieved from NCBI. The gene sequences were aligned, trimmed into ORFs and compared by using MEGA 6.06 to detect codon differences. Also, a phylogenetic tree was reconstructed based on these sequences. 26 FoxP2 protein sequences were analyzed by NetNGlyc 1.0 and NetOGlyc 4.0 Servers to determine glycosylation profiles. The results revealed species/lineage specific codon differences and conserved glycosylation profiles. The information obtained from the phylogenetic tree reconstructed based on FoxP2 gene sequences was interpreted to understand conserved codon differences and glycosylation profiles among mammalian and avian FoxP2 genes and proteins.

**Keywords:** FoxP2, Codon differences, Glycosylation profiles

**Altitudinal effects on evolution of globin gene clusters and host adaptation on *Nannospalax xanthodon***

*Halil Mert Solak*<sup>\*1</sup>, *Alexey Yanchukov*<sup>1</sup>, *Jamie Winternitz*<sup>2</sup>, *Faruk Çolak*<sup>1</sup>, *Ferhat Matur*<sup>3</sup>

<sup>1</sup> Department of Biology, Faculty of Arts and Science, Bülent Ecevit University, Zonguldak, Turkey

<sup>2</sup> Department of Animal Behavior, Bielefeld University, Bielefeld, Germany

<sup>3</sup> Department of Biology, Faculty of Arts and Science, Dokuz Eylül University, İzmir, Turkey

Altitudinal differences cause many different adaptations in the physiology of organisms and are detectable at the level of DNA primary sequence. Simple mutations in the globin genes of mammals often cause significant improvement of the Oxygen binding function that allows populations to quickly adapt to new environments across different altitudes. Therefore, the altitude-related genetic adaptations are indeed often observed among recently diverged animal groups or even within the same species. The genes responsible for the mammalian immune system are also known to display exceptional genetic diversity. The complexity and/or success of immune system is especially affected by the abundance of parasites that shaped the evolution of their vertebrate hosts. However, immune defense is costly to maintain and deploy, and the optimal investment into immune defense should depend on the risk of infection. Altitude is a natural environmental gradient that is predicted to affect parasite abundance. In light of these ideas we are going to test the hypotheses that the evolution of parasite resistance and the evolution of globin gene clusters is affected by the altitude. We will examine the genetic diversity of two different gene clusters – Major Histocompatibility Complex (MHC) and  $\alpha$ - and  $\beta$ - globin gene clusters – and will measure the immune responses of the Turkish, or Nering's mole rat *Nannospalax xanthodon* (cytotype  $2n = 58$ ) to test for influences of altitude, by collecting approximately 20 animals from several localities in the Central Taurus mountains at elevations from 1030 to 3000 m a.s.l.

**Keywords:** spalax, immune, globine

**Biological invasion and the conservation of endemic island species: São Tomé Archachatina giant land snails (Pulmonata: Achatinidae)**

*Panisi, Martina*<sup>\*1,2</sup>, *de Lima, Ricardo F*<sup>1,2,3</sup>, *Oquiongo, Gabriel*<sup>3</sup>, *Palmeirim, Jorge*<sup>1,2</sup>, *Soares, Filipa*<sup>1,2</sup>, *Sampaio, A. S.*

1 Centre for Ecology, Evolution and Environmental Changes (Ce3C), Faculdade de Ciências, Universidade de Lisboa, Campo Grande 016, 1749-016 Lisboa, Portugal.

2 Departamento de Biologia Animal, Faculdade de Ciências, Universidade de Lisboa, Campo Grande 016, 1749-016 Lisboa, Portugal.

3 Associação Monte Pico, Monte Café, São Tomé, São Tomé e Príncipe.

The biodiversity loss crisis is severely affecting invertebrates worldwide. Island terrestrial molluscs are among the most vulnerable taxa, being particularly affected by habitat destruction and introduced species. The Gulf of Guinea Giant Land Snail *Archachatina bicarinata*, endemic to the islands of São Tomé and Príncipe, has suffered a severe population decline in the last decades. One of the most likely causes for the demise of this endemic species is the introduction of the West African Giant Land Snail *Archachatina marginata*, which in just half a century spread across much of the island. Through transect sampling, species distribution modelling and interviews to local human population, we aim to understand possible interactions between the exotic and native giant land snails in São Tomé Island. We found a strong temporal and spatial segregation between the two species. The reports of local inhabitants seem to match written accounts in that the contraction of the endemic giant snail's distribution coincided and is linked to the expansion of the introduced. Nowadays, the distribution of the two species in São Tomé is almost complementary, and they use very distinct habitats. Our results

represent the first systematic report on the distribution and habitat preferences of the endemic snail in São Tomé Island, providing further indications that the introduced snail is behaving as an invasive and seems to be linked to its dramatic decline. The situation of this endemic species requires immediate conservation action and that its conservation status on the IUCN Red List is upgraded.

**Keywords:** habitat degradation, ecological modelling, spatial segregation

### First Steps to Resolve Reticulate Speciation Process in Bisexual and Parthenogenetic lizards of genus *Darevskia* in East Anatolia and Caucacus

*Meriç Erdolu*<sup>\*1</sup>, *Natia Barateli*<sup>2</sup>, *Mari Murtskhvaladze*<sup>2</sup>, *Mehmet Kürşat Şahin*<sup>3</sup>, *Yusuf Kumlutaş*<sup>4</sup>, *Çetin Ilgaz*<sup>4</sup>,  
*Ferhat Matur*<sup>4</sup>, *Kamil Candan*<sup>4</sup>, *Faruk Çolak*<sup>5</sup>, *David Tarkhnishvili*<sup>2</sup>, *Alexey Yanchukov*<sup>5</sup>

<sup>1</sup> Middle East Technical University, Biology Department, Ankara, Turkey

<sup>2</sup> Iliia State University, Biology Department, Tbilisi, Georgia

<sup>3</sup> Hacettepe University, Biology Department, Ankara, Turkey

<sup>4</sup> Dokuz Eylül University, Biology Department, İzmir, Turkey

<sup>5</sup> Bülent Ecevit University, Biology Department, Zonguldak, Turkey

*Darevskia* genus is a specific biological system where both bisexual and parthenogenetic unisexual species live together. These lizard species live in East Anatolia, Georgia, Armenia and Azerbaijan. For this study, we will use samples from East Anatolia and Georgia. The parthenogenetic species in *Darevskia* system are produced by hybridization of bisexual species and seven unisexual species are currently originated from only four parental bisexual species because same parental pairs are able to produce different daughter unisexual species. In many studies about parthenogenetic species in *Darevskia* genus show that although these species reproduce clonally, they can preserve heterozygosity. Three hypotheses currently exist to explain that: 1) accumulation of random mutations in clonal lineages, with limited effect recombination; 2) multiple past hybridization events; 3) backcross gene flow from one parental (paternal) species to its daughter parthenogenetic species. To test these hypotheses, for the first time, we will investigate the population genetic structure of six parthenogenetic species and four parental bisexual species. After a preliminary population survey with microsatellite markers, we will do large-scale genotyping of several hundred individuals, representing all species, using high-resolution genomic ddRAD markers. We start by looking at the existing shotgun sequencing data for three partheogenetic species: *Darevskia dahli*, *D. portschinski*, *D. armeniaca* and their bisexual parents *D. valentini* and *D. mixta*. After the data quality check and trimming processing, we are going to identify homologous loci using the software STACKS. Later the same procedure will be applied to the ddRAD data. In addition, this study is supported by the joint TUBITAK-SRNSF project \*216Z189.

**Keywords:** Parthenogenesis, Reticulate Speciation, Genetic Diversity

### Testing the “unguarded X” hypothesis in *Drosophila melanogaster*: Inbreeding results in a potentially maladaptive sex-specific decline in female lifespan

*Zahida Sultanova*<sup>\*1</sup>, *Muhammed Andic*<sup>1,2</sup>, *Pau Carazo*<sup>1</sup>

<sup>1</sup> Ecology, Ethology and Evolution Group, Cavanilles Institute of Biodiversity and Evolutionary Biology, University of Valencia, Valencia, Spain

<sup>2</sup> Department of Biotechnology, Faculty of Science, Necmettin Erbakan University, Konya, Turkey.

Sex differences in ageing and lifespan is widely observed across the tree of life. A possible explanation for this phenomenon is the 'unguarded X' hypothesis (UXh), which suggests that sex differences in lifespan may

be partly due to the expression of recessive mutations in the unguarded sex chromosomes of the heterogametic sex (X or Z chromosomes). According to the UXh, inbreeding is predicted to decrease the lifespan of the homogametic sex more than the heterogametic sex, as the expression of recessive deleterious mutations in the X (or Z) chromosome will only increase in the former. In this study, we tested this central prediction of UXh by exploring the effects of inbreeding on lifespan (across three different social environments) and fitness in male and female *Drosophila melanogaster*. We found that inbreeding resulted in a greater reduction of female than male lifespan. Crucially, this sex-specific lifespan effect was consistent across the social environments and was not counterbalanced by inbreeding effects on fitness, indicating that it was potentially maladaptative. Our results are consistent with the UXh and suggest that it might have a crucial contribution to sex-specific ageing; however, other processes such as sex-specific gene expression patterns and sexually antagonistic recessive genes could at least partly explain the results obtained here. Hence, we suggest that more attention should be paid to the potential role of sex chromosomes in the evolution of sex-specific lifespan.

**Keywords:** sex-specific ageing, unguarded x hypothesis, fitness

### **First record of *Terpios gelatinosus* (orifera: Demospongiae; Bowerbank, 1866) along the coasts of Mediterranean Sea in Turkey verified by DNA barcoding**

*Esra Öztürk*<sup>\*1</sup>, *Berivan Temiz*<sup>1</sup>, *Arzu Karahan*<sup>1</sup>

<sup>1</sup>Middle East Technical University, Institute of Marine Sciences, Erdemli, Mersin, Turkey

Hibernal activity tends to increase year by year, especially in steppe and forest openness microhabitats. The most preferred refuges are the sunny ones while comparing to shadows in each microhabitat. When foraging activity takes into account, major microhabitat preferences change due to seasonal ambient dynamics. For example, in the beginning of spring, they are very active in forest openness; whilst in the fall the steppes and meadows. Furthermore, the most suitable microhabitat for mating activity, which has only been recorded in spring, was the forest openness. As a result, it is clear that some irregular temperature values in the first months of the years, especially in 2018, may cause an “early spring effect” during its hibernal activity period. Additionally, microhabitat preferences change through the seasons due to ectothermic strategy.

**Keywords:** artificial refuges, seasonal activity, reptile

### **Phylogenetic and Phylogeographic resolution of the Ascidiaceae along the Turkish Levantine Coasts**

*Berivan Temiz*<sup>\*1</sup>, *Esra Öztürk*<sup>1</sup>, *Arzu Karahan*<sup>1</sup>

<sup>1</sup>Middle East Technical University, Institute of Marine Sciences, Erdemli, Mersin, Turkey

Tunicates are primitive chordate and unlike the other chordates they have whole body regeneration potential. They are used as a model organism for stem cell study in many laboratories. The ‘Stem Cell’ technology is one of the most innovative and essential application in biomedicine and thus, identification of the organism is the most basic step to able to use organisms in biotechnological studies.

Botryllus and Botrylloides are in the botryllid ascidiaceae genera most of which originated from Mediterranean Sea and these invasive colonial tunicates are globally distributed in almost all of the seas with 30 and 18-recorded species respectively. Due to low interspecific variation and high intraspecific diversity with respect to their colours, structural organization and zooid adaptation, identification of tunicates that only based

on morphologic features have some limitations. Molecular tools are necessary to get over these ambiguities and classify them into the right taxa. In the Levantine coasts, only two species of tunicates are recorded to date, which are *Botryllus schlosseri* and *Botrylloides leachii*. Nevertheless, our observation indicates the existence of at least 10 different botryllid ascidian morphs along the Mediterranean coasts of Turkey. In this study, we aim to determine the biodiversity of botryllid ascidians along the North-eastern Mediterranean Sea's 8 different stations between Hatay and Antalya regions and also North Cyprus using mitochondrial and nuclear DNA markers (COI, 28S, 18S and H3). In addition, we targeted to monitor variation of transient sampling residing at the Kızkalesi, Hatay and Alanya region populations. So far about 100 colonies have been collected from Hatay, Antalya and Mersin regions. DNA isolation for all the regions has been completed. With a preliminary work high sequence quality has been obtained from three samples by using the four different primers. The next step of the project will be to complete all samples' PCR and sequencing steps to perform bioinformatics analysis for the elucidation of species/population compositions and interaction.

**Keywords:** Botryllid ascidians, Molecular Markers, Mediterranean

### A geographical survey of mitochondrial DNA variation in greenfinch populations in Anatolia

*Utku Perktas<sup>1</sup>, Banu Şebnem Önder<sup>1</sup>, Can Elverici<sup>\*1</sup>, Eylem Usatabaş<sup>1</sup>*

<sup>1</sup> Hacettepe University, Faculty of Science, Department of Biology

One of the fundamental goals of phylogeographical studies should be to achieve a wide-ranging geographical sampling of any investigated group. In this study, we conducted the mitochondrial DNA phylogeography for the greenfinch (*Chloris chloris*), including populations from Anatolia, in order to evaluate its genetic structure. At the same time, we tested published sub-species limits (Roselaar, 1994) within the species, which currently includes 3 recognized subspecies based on morphological characters. We based our study on haplotypes for the mitochondrial gene NADH dehydrogenase subunit 2 (ND2) and subunit 3 (ND3). Most haplotypes were obtained from fresh tissues. We also discussed gene flow pattern through isolation-by-distance. Results were further discussed with the biogeographic history of Anatolia.

**Keywords:** Anatolia, birds, gene flow, phylogeography, population genetics, species limits, ND2, ND3.

### Pilot genetic assessment of the eastern most populations of Carpathian endemic Montandon's newt *Lissotriton montandoni* within Bibrka- Stilsko Hill ridge (Lviv region,Ukraine)

*Anastasia Osiyeva<sup>\*1</sup>, Ostap Reshetylo<sup>1</sup>, Alexey Yanchukov<sup>2</sup>*

<sup>1</sup> Lviv Franko National University of Ukraine, Faculty of Biology, Lviv, Ukraine

<sup>2</sup> Department of Biology Faculty of Arts and Sciences, .Bulent Ecevit University, Zonguldak, Turkey

The smooth newt (*Lissotriton vulgaris*) is a widely distributed amphibian in the lowland East and Central Europe, while the closely related Montandon's newt (*L. montandoni*) is only found in the Carpathian Mountains. Despite the fact that these two species have distinct geographical ranges, there is a wide introgression of both nuclear and mitochondrial genes between them, to the extent that the entire mtDNA of *L. montandoni* has been completely replaced by the one of mtDNA haplotypes of *L. vulgaris*, at least among the populations samples until now (Babik et al. 2005). The previous sampling of *L. montandoni* mtDNA haplotypes did not include the area of Bibrka-Stilsko Hill ridge (Lviv region, Ukraine). The population of *L. montandoni* in this area is isolated from the main range of the species by the wide valley of river Dniester, and is surrounded by the populations of *L. vulgaris*. The extent of the mtDNA introgression from *L. vulgaris* to *L. montandoni* has not been studied in

this area. To establish the precise distribution pattern of the two species in this area, we have first conducted the extensive mapping of their respective habitats in 2016-17, taking into account the orographic and vegetation characteristics of the landscape. Next in 2018, we plan to collect newt specimens in several localities in the Bibrka-Stilsko ridge, the Dniester river valley, and the nearest part of the Carpathian mountains. Two gene fragments of mtDNA, ND2 and ND4, according to Babik et al. 2005, will be amplified and sequenced in order to establish which particular Lissotriton mtDNA haplotype occurs in the area. We then plan to resolve the phylogenetic relationship of our samples in respect to the published mtDNA sequences from a wider area in Central Europe. The Bibrka-Stilsko hill region represents the eastern most margin of *L. montandoni* range, therefore it is important to establish the genetic composition of this endemic and vulnerable Carpathian species in the area, in order to develop conservation strategy in the future.

**Keywords:** Montandon's and smooth newts, mtDNA haplotypes, gene introgression

### Rock lizards-Gene flow and hybridization within species of 'caucasica' clade

*Sofiko Kurdadze*<sup>\*1</sup>

It is hypothesized that a narrow-ranged rock lizard, *Darevskia mixta*, has a hybrid origin. Specifically, Darevsky (1967) suggested that this is a hybrid between a rock-dwelling lizard *D. parvula* and ground-dwelling *D. derjugini*. Indeed, the latter species and *D. mixta* belong to the same mitochondrial clade, are commonly found in the same habitat, and are morphologically similar. The aim of the present research was to find the evidence if there is natural hybridization between *D. mixta* and *D. derjugini*. Previous study performed at Ilia State University revealed few *D. derjugini* individuals carrying mitochondrial haplotypes of *D. mixta*. The current research included ca. 150 individuals of both species from throughout their ranges, including the entire area of the range overlap. The genotypes of the studied individuals were scored for ten microsatellite loci: Du161, Du183, Du255, Du231, Du363, Du215, Du47, Du418, Du323, and Du218. The genotypes were analyzed using software Structure and Arlequin. The results of the analysis did reveal two individuals that could suspiciously be next-generation hybrids or backcrosses, however further study is required for confirming this hypothesis. Simultaneously, the studied samples of *D. derjugini* suggested substantial geographic differentiation of this lizard species.

**Keywords:** Hybridization, *D. mixta*, *D. derjugini*

### Breeding ecology of the scops owl ( *Otus scops* ) at the metu campus (Ankara, Turkey): Preliminary findings

*Elif Göçer*<sup>\*1,3</sup>, *Mustafa Sözen*<sup>1</sup>, *C. Can Bilgin*<sup>2</sup>, *David H. Johnson*<sup>3</sup>

<sup>1</sup> Bülent Ecevit University, Graduate School of Natural and Applied Sciences, Department of Biology, 67100 Zonguldak, Turkey.

<sup>2</sup> Middle East Technical University, Department of Biology, 06800 Ankara, Turkey

<sup>3</sup> Global Owl Project, 6504 Carriage Drive, Alexandria, Virginia 22310 USA

Nest boxes are a practical method to support and study the ecology of many cavity-dependent species. In this project, we used wooden nest boxes to study Scops Owls around Ankara, Turkey. In February 2017, we placed 40 nest boxes on trees at the Middle East Technical University (METU) northern campus and 30 nest boxes around Eymir Lake. We have monitored them and collected reproductive parameters during visits at 5-10 day intervals. A total of 11 nest boxes were used by owls; there were a total of 41 eggs from 11 nests (average

3.72 per nest) and 31 hatchlings from 10 nests (average 3.1 per nest). Hatching started during the third week of May at Eymir Lake and the first week of June at the campus. A total of 17 young fledged from 10 nests (average 1.7 fledged young per nest attempt). Predation occurred at two nests, and the eggs at one nest did not hatch. Our study provides the first ever data on the breeding ecology of this species in Turkey.

**Keywords:** Scops owl, nest boxes, breeding ecology

### **New insights into the maternal history of Anatolian and north Mesopotamian populations since the Neolithic**

*Reyhan Yaka<sup>\*1</sup>, İnci Togan<sup>1</sup>, Mehmet Somel<sup>1</sup>*

<sup>1</sup>Department of Biological Sciences, Middle East Technical University, Ankara, Turkey

Recently we reported the ancient mitochondrial DNA (mtDNA) profiles from the Late Iron Age Çemialo Sırtı excavation site in Batman, southeast Turkey, including Hypervariable Region I (HVRI) sequences from 12 individuals. A comparative analysis of this data with ancient and modern-day west Eurasian populations of the last 10,000 years, using coalescent simulations under various population sizes, revealed maternal continuity in the region from Neolithic Period to present-day (Yaka et al., 2018). In the present study, we examine the maternal continuity hypothesis further by including recently-produced mtDNA datasets from Anatolia and neighboring populations. Our approach uses  $F_{st}$  and diversity calculations using complete mtDNA and also HVRI sequences from different periods, and comparing the observed data with genetic simulations to test population continuity and migration in this region.

**Keywords:** ancient DNA, Anatolia, coalescent simulation

### **The Genome-wide analysis of spontaneous mutations in *Acidobacterium capsulatum***

*Sibel Kucukyildirim<sup>\*1</sup>, Samuel F. Miller<sup>2</sup>, Hongan Long<sup>3</sup>, Michael Lynch<sup>2</sup>*

<sup>1</sup>Biology Department, Hacettepe University, Ankara, TURKEY

<sup>2</sup>Biodesign Center for Mechanisms of Evolution, Arizona State University, Tempe, AZ, USA

<sup>3</sup>Institute of Evolution and Marine Biodiversity, KLMME, Ocean University of China, Qingdao, CHINA

Analyses of spontaneous mutation has shown that total genome-wide mutation rates are remarkably similar for most of prokaryotic organisms. However, this estimation is mainly based on organisms which grow best around neutral pH values (5.5-7.5). In particular, whole genome mutation rate has not been determined for an acidophilic organism. Here, we determined the genome-wide measurement of spontaneous mutations in the acidophilic *Acidobacterium capsulatum* using a direct and unbiased method: mutation-accumulation experiments and whole-genome sequencing. Whole-genome sequencing of 70 mutation accumulation lines of *A. capsulatum* after an average of ~2900 cell divisions yielded a base-substitution mutation rate of  $5 \times 10^{-4}$  per genome per generation, which is lowest compare to the consensus value of mesophilic prokaryotic organisms with DNA genomes.

**Keywords:** Mutation rate, Mutation spectrum, Whole genome sequencing

## Ecogeographical Variation of Rock Nuthatches

*Can Elverici<sup>\*1</sup>, Utku Perktas<sup>1</sup>*

<sup>1</sup>Hacettepe University, Faculty of Science, Department of Biology

To investigate whether any significant geographic variation exists, morphological characters of Rock Nuthatches (*Sitta neumayer* and *Sitta tephronota*) were tested using traditional and multivariate statistical techniques. For this, we measured various external morphological characters (bill, wing, tarsus, tail, nostril lengths) collected throughout the species' distribution range, and we used traditional statistical approach to test each character variation, then we derived body size components using principal component analysis. Preliminary results indicated that significant geographic variation in morphological characters occur throughout species' distribution range, and further discussion will be made using ecogeographical hypotheses (e.g. Bergmann's rule) for both species.

**Keywords:** Geographic variation, morphology, ecogeographical rules, multivariate statistics, birds

## Analysis of spatial and temporal changes at surface area of Homa lagoon (İzmir Bay, Aegean Sea) using remote sensing techniques

*Meriç Halide Boyar<sup>\*1</sup>, Uğur Sunlu<sup>2</sup>*

<sup>1</sup>Ege University, Center for Environmental Studies 35100 Bornova-İzmir/Turkey

<sup>2</sup>Ege University, Department of Aquaculture 35100 Bornova-İzmir/Turkey

Lagoons are affected by physical, chemical and biological factors. Homa Lagoon is the only one standing in the İzmir Bay. It was taken to the protection status in 1982 and group 'A' is in wetland status. The wetland area is the protection and reproduction area of bird populations, and the conservation of biological reserves is the RAMSAR region since 1998. In this thesis, it is aimed to determine the current state of the surface area of the lake and to determine the changes occurring in the surface area of the lake from past years to the day by using remote sensing methods. Eight selected Landsat 5 TM and Landsat 8 OLI images were used from 1984 to 2017. These images were geometrically corrected and made to fit the study by making field crossings. The images were classified and changes in the surface of the lake were analysed with the normalized vegetation index (NDVI). In the direction of the analyses, it is seen that the Kırdeniz Lagoon feeding the Homa Lagoon completely disappeared and the Homa Lagoon was experiencing a relatively less shrinkage in line with the conservation work done in the region. The amount of these changes is important in terms of watershed management, sustainable development. This study will be pioneer on it with using remote sensing in this area and it will form the basis for modelling studies.

**Keywords:** Homa Lagoon, Remote Sensing, Temporal and Spatial Change

### The profile of de novo mutations in horse

*Elif Bozlak<sup>\*1</sup>, Aybar Can Acar<sup>1</sup>, Mehmet Somel<sup>2</sup>, Barbara Wallner<sup>3</sup>*

<sup>1</sup> METU / Informatics Institute

<sup>2</sup> Mehmet Somel - METU / Biology Department

<sup>3</sup> Barbara Wallner - Universtiy of Veterinary Medicine, Vienna

Accumulation of germ line mutations have key role in understanding the evolutionary history of populations. Next generation sequencing technologies today allow precise determination of de novo mutation events, which are defined as mutations that arise in the germline of an individual's parents or in the fertilized egg at an early stage. These can be inferred from analyzing genomes of trios (two parents and an offspring), where a variant is identified in the offspring, but neither of the parents carry this variant. In this project, whole genome next generation sequencing data from three horse trios from three different Austrian horse breeds (Haflinger, Noriker, and Lipizzaner) were analyzed to determine germline de novo variants detected only in the offspring. After quality control based trimming, and alignment to the horse reference genome, SNP calling was made by GATK algorithm. We then predicted de novo variants using a custom Python code developed for this study. de novo variant predictions for the Lipizzan trio were further compared with validation data from Sanger experiments to optimize the filtering steps. Finally, for each trio (Lipizzan, Noriker Haflinger) we predicted 50-60 de novo mutations in the offspring, corresponding to a mutation rate of  $2.25 \times 10^{-8}$  per generation. This de novo mutation rate is comparable to what has been described for other mammalian species, including human.

**Keywords:** de novo mutation, population genetics, horse genome

### Genetic and morphological variability in bisexual (*Darevskia portschinskii*) and unisexual (*Darevskia dali*) Caucasian Rock Lizards

*Natia Barateli<sup>\*1</sup>, David Tarkhnishvili<sup>1</sup>, Giorgi Iankoshvili<sup>1</sup> and Marine Murtskvaladze<sup>1</sup>*

<sup>1</sup> Ilia State University

We compared morphology and genetics of bisexual lizard *Darevskia portschinskii* and unisexual (Obligatory Parthenogenetic) lizard *Darevskia dali*. The aim of the study was to compare the variability of genetic and morphological traits of unisexual and bisexual lizards from the same geographic locations and to evaluate inheritance of the morphological traits. We compared microsatellite genotypes and scalation traits of unisexual and bisexual lizards in three geographic areas, where they coexist. Based on the obtained data, we described the heritability of individual morphological traits. Genetic variations were higher in sexually breeding *D. portschinskii* than in parthenogenetic *D. dali*. The most of the studied morphological traits were also more variable in *D. portschinskii* that suggests a high degree of their heritability. However, there were several morphological characters whose variations depended on a geographic setting but was not correlated with a genetic diversity. After comparing morphological, genetic and geographical distances, we concluded that 1) genetic differences are not determined by distance, 2) differences in some morphological characters correlate with distance, which can be connected with (a) their heritability that cannot be recorded using the analysis of microsatellite diversity (b) ecological / climatic differences between different areas where the samples were collected.

**Keywords:** Darevskia rock lizards, morphology, population genetics

### Phylogenetic Utility of Secondary Structure of ITS2: A Snapshot from Anterastes (Orthoptera, Tettigoniidae)

*Onur Uluar<sup>\*1</sup>, Sarp Kaya<sup>2</sup>, Battal Çiplak<sup>1</sup>*

<sup>1</sup> Akdeniz University

<sup>2</sup> Mehmet Akif Ersoy University

Last two decades witnessed a revolution in using DNA sequences in phylogeny estimation. The general practice is using direct linear base sequences. But, some markers such as ribosomal gene internal transcribed spacer 2 (ITS2) allow to benefit also from secondary structure in producing characters and estimating phylogeny. In the present study we aimed to compare phylogenetic utilities of linear DNA and secondary structure of ITS2 using sequences from tettigoniid genus *Anterastes* (Orthoptera, Tettigoniidae). Sequences of the ITS2 regions were obtained from 144 specimens of *Anterastes* representing 15 species. A data matrix was produced from the linear sequences. The secondary structures of the same sequences were predicted by using MFOLD. Then sequence-structural alignment dataset of ITS2 produced from the same matrix. Both matrices were analysed under the maximum likelihood (ML) algorithm and phylogenetic trees were compared. 53 unique haplotypes were detected from the data matrices of linear sequences. The ML analysis of linear matrix and secondary structure resulted in to a poorly resolved phylogenetic tree. ITS2 gene is highly conserved and includes poor phylogenetic information both in *Anterastes* and contrary to some other tettigoniids. The secondary structure does not improve phylogenetic utility of ITS2 in *Anterastes*. These results constitute a conflict with several other lineages such as fungi, plants and corals.

**Keywords:** ITS2, Secondary structure, Orthoptera

### Gene Expression Reversals in Mouse Ageing and Its Comparison with Primates

*Hamit İzgi<sup>\*1</sup>, Ece Kocabıyık, Philipp Khaitovich, Ding Ding Han, Mehmet Somel*

Ageing, characterized by the progressive loss of functions in an organism, has not been fully understood at the molecular level. In previous studies of brain transcriptome age-series, we showed that the majority of genes' expression levels in ageing reverse back to levels observed in postnatal development. In other words, genes up-regulated during development tend to be down-regulated during ageing, and vice versa. This result was interpreted as indication that cellular identity loss due to stochastic damage accumulation in neurons. Here we study whether such gene expression reversals are also observed in other, shorter lived mammalian taxa, and in other tissues, using *Mus musculus* as a model. We generated an RNA-sequencing time-series dataset of 63 mouse samples, representing the full lifespan of the mouse from postnatal day 2 to day 905, and comprising 4 different tissues (cortex, liver, lung and skeletal muscle). We find that more than 50% of the genes shows reversal pattern in all tissues studied in the mouse. This supports the idea that expression reversals, and possibly loss of cellular identity, are a general phenomenon in mammalian ageing, and not restricted to neuronal tissue in long-lived mammals.

**Keywords:** ageing, transcriptome, gene expression reversal

### Authentication of ancient DNA sequences when there is no reference genome

*Emrah Kırdök<sup>\*1</sup>, Andres Aravena<sup>2</sup>, Macha Nikolski<sup>2</sup>*

DNA sequences recovered from archeological remains (aDNA) provides us with clues to understand ancient times. To make valid conclusions, we need to know if these sequences originated from the archeological source. If there is a reference genome, alignment-based methods offer a fair way to authenticate DNA sequences based on nucleotide transitions that are specific to aDNA fragments. However, most of the times it is not possible to align every DNA sequence to a reference genome. Thus, a significant proportion of aDNA reads cannot be authenticated using alignment methods. We think that machine learning approaches can complement alignment-based methods in this authentication task when there is no reference genome. In this study, we used a set of machine learning algorithms to build models that can authenticate aDNA sequences without a reference genome. To train these machine learning models, we simulated a dataset that contains ancient and modern DNA sequences. Using classification and regression tree approach, we classified correctly at least 90% of simulated DNA sequences. Furthermore, we extended this approach using experimental aDNA datasets obtained from human sources. We used alignment-based methods (e.g., pmd-tools) to separate human reads into ancient and modern DNA. Our preliminary results show that the method classifies correctly half of the real aDNA sequences. Moreover, we did not observe any false positive classifications. In conclusion, further improvement of this method can allow us to authenticate aDNA sequences without a reference genome.

**Keywords:** aDNA, authentication, machine learning

### A new putative transcription termination signal which interact transcription termination factors in Ecdysozoa

*Merve Nur Aydemir<sup>\*1</sup>, Habeş Bilal Aydemir, Mahir Budak, E. Mahir Korkmaz, Hasan H. Başibüyük*

DmTTF (Drosophila melanogaster mitochondrial transcription termination factor), unlike known insect mitochondrial transcription proteins, recognises two similar sequences lie between two gene clusters that are transcribed in opposite directions. The recognition sites are the intergenic regions found between tRNA-Glu/tRNA-Phe and tRNA-Ser (UCN)/ND1, respectively. The characterization of hymenopteran mitogenome data obtained from NCBI indicates that transcription polarity is steadily conserved in the intergenic region between ND4L and ND6 genes. This conserved region is also found at the same location when the data of Ecdysozoa mitogenomes were characterised from the Genbank. A conserved sequence motif was detected in ND4L / ND6 gene cluster when the strand change is reflected to primary sequence data,. This motif consists of a 'WHWGHTW' sequence and it is a reverse complementary of previously described DmTTF binding sequence. The structural and functional similarity is additionally observed throughout the Ecdysozoa. These results support a hypothesis that this conserved sequence motif could be a functional new mitochondrial transcription signal, and a new molecular synapomorphy for the Ecdysozoa superphylum. Acknowledgements: The study is supported by The Scientific and Technological Research Council of Turkey (TÜBİTAK) via a research project with grant number 117Z020.

**Keywords:** mitochondrial transcription, mTERF, transcription signal

**Identification of differentially expressed sense and antisense transcripts in mitochondrial genes of *Syrista pareyssi* (Hymenoptera: Cephidae)**

*Habeş Bilal Aydemir*<sup>\*1</sup>, *Merve Nur Aydemir*, *Sevcan Yangin*, *Mahir Budak*, *E. Mahir Korkmaz*, *Hasan H. Başibüyük*

Mitochondria are known to be the energy production center of cells through oxidation-reduction reactions. Mitogenome usually fixes 37 genes in bilateral animals: 13 protein-coding genes, 2 ribosomal RNA genes, and 22 transfer RNA genes. Mitogenomic transcription is controlled by molecular mechanisms that are different from its nuclear counterparts. Transcription of insect mitogenomes starts from three promoters and generates five polycistronic units. The differential expression levels are expected between these polycistronic units, but, it is important to find the differences among mRNA levels of the genes located in the same transcription unit. This can be resulted from the function of the ncRNAs in regulation of transcription and translation. Here, we investigated to identify the differentially expressed sense and antisense transcripts in mitochondrial genes of *Syrista pareyssi* (Hymenoptera: Cephidae). Total RNA was extracted from one specimen stored in RNAlater solution. The cDNAs generated from this purified RNA sample were quantified on the Biorad CFX Connect Real-Time PCR detection system for eight different gene regions using gene specific primers. The mitogenome of *S. pareyssi* (KX907847) was investigated by NCBI ORF Finder to find whether the expressed antisense transcripts are translated to protein or they are ncRNAs. We found that (i) each mitochondrial gene exhibits differences in their expression levels; (ii) the genes of Coxs and rRNA are also significantly expressed in their corresponding antisense chains. These preliminary results suggest that lncRNAs are expressed by insect mitogenomes and they are probably functional in their mitochondrial transcription stage. Acknowledgements: The study is supported by Scientific Research Project Fund of Cumhuriyet University (CUBAP) via a research project with grant number F-459.

**Keywords:** mitochondrial gene expression, ncRNAs, *Syrista pareyssi*,

**Spatially varying promoter polymorphism in *Dca* is not related to wing size cline in East European *Drosophila melanogaster* populations**

*Cansu Fidan Aksoy*<sup>\*1</sup>, *Bengisu Sezen Subaşı*<sup>1</sup>, *Alper Orhan*<sup>1</sup>, *Iryna Kozeretka*<sup>2</sup>, *Elena Pasyukova*<sup>3</sup>, *Banu Şebnem Önder*

<sup>1</sup> Genetic Variation and Adaptation Lab., Department of Biology, Faculty of Science, Hacettepe University, 06800, Beytepe, Ankara, Turkey

<sup>2</sup> National Taras Shevchenko University of Kyiv, Kyiv, Ukraine

<sup>3</sup> Institute of Molecular Genetics of RAS, Moscow, Russian Federation

*Drosophila melanogaster* is a cosmopolitan species that spread over temperate regions. It is a widely used model organism to study the evolutionary dynamics associated with genetic and environmental heterogeneity in a broad geographical distribution area. In *D. melanogaster*, many characters are known that exhibit a latitudinal cline. These clines are widely interpreted as an adaptive result of spatially varying selection. Also, body size is a well-known character for strong latitudinal cline. Clinal variation in traits often reflects local adaptation and give an opportunity to link candidate genes to adaptive variation in traits. There is a hypothesis that revealed the gene *Dca* accounts to the wing size variation and therefore is a candidate gene for climatic adaptation. To test this hypothesis, we measure the variation of wing size in 210 inbred lines of *D. melanogaster*, which were collected from three different latitudes including Turkey, Ukraine, and Russia; and genotype the inbred lines for the promoter region of *Dca*. We found a spatially varying promoter polymorphism in *Dca* and wing size cline while *Dca* polymorphism was not associated with wing size variations. Our results show that the

Dca polymorphism does not seem to play the crucial role in wing size in European populations of *D. melanogaster*.

**Keywords:** latitudinal cline, wing size, Dca polymorphism

### **Adaptation to cold tolerance in *Drosophila melanogaster* populations along latitudinal gradient in Europe**

*Esin Dural<sup>1</sup>, Ezgi Çobanoğlu<sup>1</sup>, Seda Demirel<sup>1</sup>, Nazlıhan Gürbüz<sup>1</sup>, Betül Çelik<sup>1</sup>, Buse Kuzu<sup>1</sup>, Sinem Özcan<sup>1</sup>, Nazlı Karol<sup>1</sup>, Başak Dalkıran<sup>1</sup>, Şenel Selin Yağlı<sup>1</sup>, Ekin Demir<sup>1</sup>, Nur Seda Coşkun<sup>1</sup>, Cansu Fidan Aksoy<sup>1</sup>, Banu Şebnem Önder<sup>\*1</sup>*

<sup>1</sup> Genetic Variation and Adaptation Lab., Department of Biology, Faculty of Science, Hacettepe University, 06800, Beytepe, Ankara, Turkey

Thermal tolerance is a critical determinant of species distribution range and organismal adaptation to environments. Most insects display spatial pattern in cold tolerance that closely matches local adaptation. Adaptation to cold climates and its genetic basis is one of the leading concerns of evolutionary biology. Following the end of the last ice age, *Drosophila melanogaster* has spread from its ancestral range in subtropical Africa and is now a cosmopolitan species. *D. melanogaster*, displays adaptability to very different climates, spreading to almost all of the earth, except in extreme arid and entirely frozen regions. Understanding the response of *D. melanogaster* to the cold environmental temperature is of high importance to understand the ecological adaptability of this animal and hence its evolutionary adaptation. To investigate this we measure cold-tolerance in three distinct geographic populations, which latitudes stretch from 40° to 57°. We conducted an experiment to test mortality after cold shock between -1 °C and -7 °C in 9 inbred lines. We find an increase in cold tolerance with latitude. Our data suggest that as *D. melanogaster* expanded from warm ancestral environments, it may have evolved greater cold tolerance. In addition the ability to study cold tolerance evolution in a parallel framework will enhance this classic study system for climate adaptation.

**Keywords:** *Drosophila melanogaster*, local adaptation, thermal tolerance

### **Frequency changes of phenotype-associated genetic variants between Neolithic and modern Anatolian populations**

*Erinç Yurtman<sup>\*1</sup>, Evrim Fer<sup>2</sup>*

<sup>1</sup> Department of Biological Sciences, Middle East Technical University, Ankara, Turkey

<sup>2</sup> Informatics Institute Department of Bioinformatics, Middle East Technical University, Ankara, Turkey

The Neolithic Transition, which is the transition to sedentism and food production, changed human populations' genetic and phenotypic traits as a result of novel selection pressures that arose from altered living habits and conditions, and changing interaction patterns among individuals. Here, we study the frequency changes of alleles associated with specific phenotypic traits between Neolithic Period and modern-day Anatolian populations. Combining imputed ancient genome sequences with modern-day genome-wide polymorphism data, we study the driving forces behind allele frequency changes in time, including gene flow, genetic drift, as well as positive and negative selection. To test for natural selection, we use both genome-outlier approaches as well as coalescent simulations that include gene flow from neighboring early Holocene populations. We particularly focus on loci associated with diet-related metabolism, blood types and observable phenotypic traits such as skin, hair and eye colors. Finally, we discuss our results in the context of the transition to farming and sedentism.

**Keywords:** Neolithic, Phenotypic traits, Fst analysis

### Seed iron distribution show conserved patterns among different plant lineages

*Seckin Eroglu<sup>\*1</sup>, Nur Karaca<sup>2</sup>, Bahattin Tanyolac<sup>2</sup>*

<sup>1</sup> Izmir University of Economics

<sup>2</sup> Ege University

In Arabidopsis embryo, Fe accumulates in endodermal cell layer and it is strictly dependent on the presence of a vacuolar Fe influxer, VIT1(VACUOLAR IRON TRANSPORTER1). In the subcellular level, Arabidopsis stores Fe in vacuoles, most probably associated with phytate; contrasting to legumes which store most of the Fe reserves in ferritin cages inside plastids. For legumes, endodermal cell layer is not particularly reported as a Fe hotspot, which raises the question that how well VIT1-dependent Fe enrichment seen in Arabidopsis is conserved among plants. In order to investigate the similarity and differences in seed iron storage among different plant lineages, seeds from more than 30 species that belong to several different orders were embedded in resin, cut and cross sections were obtained. Using Perls/DAB staining, Fe distribution in tissue and subcellular level was investigated. In parallel, an independent Arabidopsis T-DNA screening approach was taken to identify a mutant which shows a phenotype in seed Fe localization. Perls/DAB staining of the sections and bioinformatics analysis showed that VIT1-dependent iron enrichment around the endodermal veins is largely conserved among dicots. Even in legumes, where massive Fe stores are distributed homogeneously and obscure small Fe enrichments, careful examination revealed endodermal cells are Fe enriched. Understanding Fe distribution patterns and underlying genetic factors inside the seeds may contribute developing plant seeds that contain higher levels of bioavailable Fe.

**Keywords:** Iron, seed, vit1

### Host Genetic Determinants of Xanthomonadacea abundance in *D. melanogaster*

*Efe Sezgin<sup>\*1</sup>*

<sup>1</sup> Izmir Institute of Technology

Microbiota is the collection of all microorganisms that are in a symbiotic relationship with their host, and they have a profound effect on the health and survival of their host. The gastrointestinal (digestive) system in *Drosophila* has the richest microbiota ecosystem on that organism and shows individual and population level diversity. The effect of host genetics on the microbiota diversity is not well understood. We aimed to identify the host genetic factors that influence the abundance of a common bacteria in *D. melanogaster* microbiota, Xanthomonadacea. Xanthomonadacea abundance data was obtained by next generation sequencing of the bacterial ribosomal gene from 100 inbred lines from *Drosophila* Genetic Reference Panel (DGRP), whose genome sequence is available. Whole genome wide association was conducted to identify host genetic factors that were associated with the Xanthomonadacea abundance. Results showed that genes coding for DNA binding factor (Sox21b), glucose metabolism control (Ca-beta), immune response/polysaccharide binding (CG42339), and immunity response against fungi (Lmpt) were significantly associated with Xanthomonadacea abundance even after a strict multiple test Bonferroni correction. We conclude that *D. melanogaster* can be a model system for studying host – microbiota interactions.

**Keywords:** Microbiota, *Drosophila*, host genetics

### Testing for signals of selection near fixed modern human derived sites

*Arev Pelin Sümer*<sup>\*1</sup>, *Stéphane Peyrégne*<sup>2</sup>, *Kay Prüfer*<sup>2</sup>

<sup>1</sup> Middle East Technical University, Department of Biological Sciences, Ankara, Turkey

<sup>2</sup> Max Planck Institute for Evolutionary Anthropology, Department of Evolutionary Genetics, Leipzig, Germany

Corresponding authors: [arev.sumer@metu.edu.tr](mailto:arev.sumer@metu.edu.tr), [stephane\\_peyregne@eva.mpg.de](mailto:stephane_peyregne@eva.mpg.de), [pruefer@eva.mpg.de](mailto:pruefer@eva.mpg.de)

Some of the observable phenotypic and hypothesized behavioral differences between modern and ancient humans may have been driven by positive selection since both groups of humans parted. Peyrégne et al. (2017) used a hidden Markov model approach to infer regions in the human genome that were shaped by such events of positive selection. This model yields candidate regions enriched for regulatory functions. To further investigate how selection may have affected classes of genomic regions differently, we focused here on fixed derived changes in modern humans, i.e. positions where present-day Africans carry an allele that is not observed in the genomes of two Neandertals, a Denisovan and great apes. These alleles must have increased faster in frequency than many other alleles, and variants that conveyed an advantage for modern human carriers in the past are expected to be enriched among them. The positions at which these variants reside were classified according to the class of genomic region (UTRs, coding, regulatory, intergenic, etc) and further annotated with the probability for positive selection from Peyrégne et al. (2017). Comparing the average probability for selection at fixed positions of different genomic classes to the average probabilities of putatively neutral variants from intergenic regions, we found that coding and 5' UTR variants show an enrichment. This signal fades with increasing distance from the fixed variant. We caution that these signals could be driven by negative selection and further investigation will be needed to characterize how past episodes of positive selection shaped present-day human variation.

**Keywords:** selection, genomes, sweeps

### BROT 2.0: A functional trait database for Mediterranean Basin plants

*Çağatay Tavşanoğlu*<sup>\*1</sup>, *Juli G. Pausas*<sup>2</sup>

<sup>1</sup> Department of Biology, Hacettepe University, Ankara, Turkey

<sup>2</sup> Centro de Investigaciones sobre Desertificación, CSIC, Valencia, Spain

Plant trait databases are becoming a key research tool for testing hypothesis regarding the ecology and evolution of species, communities, and ecosystems. Here, we present a database of functional traits for vascular plant species of the Mediterranean Basin (BROT 2.0). In total, we compiled functional trait data from 624 sources, of which 448 are articles published in peer-reviewed journals between 1893 and early 2018, plus some field and experimental observations. The database includes 25,764 individual records of 44 traits from 2,457 plant taxa distributed in 119 taxonomic families. The plant functional traits considered include 22 general vegetative traits (e.g. growth form, specific leaf area, and root depth), 15 regeneration traits (e.g. resprouting capacity after disturbance, heat-stimulated germination, and age at maturity of sapling), and 7 sexual reproductive traits (e.g. dispersal mode, fruit type, and seed dry mass). Data records are geographically distributed throughout the Mediterranean Basin, but some parts of the basin (e.g. the southern rim) are poorly represented, reflecting the lower number of available studies in this area. All records are fully referenced and, in many cases, include geographic coordinates. The database is structured to include different levels of accuracy of trait information for each entry. BROT 2.0 should facilitate testing hypotheses on plant functional ecology within the Mediterranean Basin, and comparing this region with other ecosystems worldwide. The BROT 2.0 database and its trait definitions can be used as a template for creating similar trait databases in other regions of the world.

**Keywords:** database, plant functional traits, the Mediterranean Basin

### **Hospital Wastewater: a new technologies & optimal methods used for treatment of hospital wastewater before discharge into environment**

*Shadmaan Tariq Sadiq<sup>\*1</sup>, İhsan Yaşa<sup>1</sup>*

School of Natural Sciences, Faculty of Science, Ege University, 35040 Izmir, Turkey.

Rescent study aim is : -study the effects of hospital wastewater on the Environment. -Minimizing the dangerous ingredients of hospital wastewater. -Treatment of the hospital wastewater with optimal method. Nowadays there are more interest in environmental pollutants due to much of pollution sources Such as hospital wastewater hww , urban wastewater and industrial water. This problem has a huge effect on environment and human health due to releasing of the toxic substances, pharmaceutical, pathogens as well as to heavy metals without any treatment. Researchers are trying to discover some effective treatments methods for HWW, which is meet the requirements to remove the contaminants, Hospital wastewater release to an aquatic environment large amount of microorganisms, toxic chemicals, organic and heavy metals. This study revealed some new techniques useful for HWW treatment like fungal treatment technology, biological oxidation, Moving Bed Biofilm Reactors, membrane bioreactor, Nano-graphene oxide magnetite, thermal plasma reactors, and electro-oxidation and electro-Fenton. In future work these aspects need more attention and will be the subject of another continuing study. A study by Pauwels et al (2006) was achieved to measure the performance quality between conventional activated sludge (CAS) and the MBR system. They performed equally well in terms of Total Ammonium Nitrogen (TAN) removal and Ethinylestradiol (EE2) removal. The conventional activated sludge system and MBR typically reduced bacterial groups for about 1 log unit and 3 log units respectively. Among these microorganism's coliforms fecal were reduced for 1.4 log units in the conventional activated sludge system while in the MBR 3.6 log removal. COD efficiency elimination was 88% in CAS whereas MBR 93%. Another study by Chamam et al (2017) revealed the MBR have a better global efficiency compared to CAS. Where the study carried out under a similar biological conditions. In general, wastewater can be treated by conventional methods. One of the novel methods is Advanced Oxidation Processes (AOPs). It used to remove and destroyed the pathogens from wastewater. The most combinations are used to give effective treatment: 1. 1- Photo-Fenton processes combined with TiO<sub>2</sub>. 2-UV/O<sub>3</sub>/H<sub>2</sub>O<sub>2</sub>. 3- wet air oxidation or other non-photochemical AOP 4-Combinations with PAOPs with ultrasound 4. 5- Combination of AOPs with conventional methods, mostly biological oxidation, is very much studied at present. after deep study we found that the Advanced oxidation processes (AOPs) one of the most effective method in contrast to other methods because of its ability to destroyed dangerous elements in wastewater, an electro-Fenton one of the electrochemical advanced oxidation processes, it is an environmental-friendly and effective process for the elimination of risky pollutants. The only concern that reduces an efficiency methods are costs and energy consumption. Moreover, a combination of EAOPs with biological treatment is best solution. In this combination the removal efficiency increase while minimizing costs.

**Keywords:** Hospital wastewater, Eco toxicity, Wastewater treatment

### **Quantitative genetics of immune fuction in pond snail**

*Cansu Cetin<sup>\*1</sup>, Coen M. Adema<sup>2</sup>, Philine Feulner<sup>3</sup>, Otto Seppala<sup>1</sup>*

<sup>1</sup>EAWAG, Institute of Aquatic Ecology & ETH-Zürich, Institute of Integrative Biology,Switzerland/ETH Zurich

<sup>2</sup>Center for Evolutionary and Theoretical Immunology, Department of Biology, University of New Mexico, Albuquerque, NM 87131, USA

<sup>3</sup>Department of Fish Ecology and Evolution, Center for Ecology, Evolution and Biogeochemistry, EAWAG, Switzerland

Parasites pose serious threats to organisms by decreasing their fitness. Hence, understanding evolutionary potential of defence against parasites is very important. Since many immunological traits are not very specific to certain parasites, they are predicted to evolve via selection on additive genetic variance. Quantitative genetics is a useful tool to understand evolutionary potential of phenotypic immune traits under natural conditions. High-marker density genotyping allows for estimating genetic relatedness of individuals and thus makes it possible to calculate quantitative genetic parameters of wild populations. Freshwater snail *Lymnaea stagnalis* (Gastropoda, Mollusca) is an important model organism in ecological immunity because the methods to quantify its immune defense traits have been quantified. Main aims of this research are 1) To calculate additive genetic variance and covariance of phenotypic immune traits in *L. stagnalis* under field conditions 2) To learn about genetic architecture of those traits e.g. how many genes contribute to phenotypic variation and find out genomic regions responsible for these variations 3) To determine quantitative genetic parameters of a wider range of immune traits based on transcriptomic data. First, heritability of immune traits of a field population will be estimated by using RAD-seq data and genetic architecture of the traits will be determined. Then, detailed genetic variance components (e.g. additive genetic variance, dominance variance, parental effects) of wider range of immune traits including gene expression will be calculated by using diallel cross breeding design. This will provide a general understanding of snail immune function and its evolutionary potential.

**Keywords:** quantitative genetics, immune defense traits, next-generation sequencing

### **A study of the changes in the forest phenology in Turkey through MODIS satellite data**

*Yetkin İpek<sup>1</sup> and H. Nüzhet Dalfes<sup>1</sup>*

<sup>1</sup> ITU Eurasia Institute of Earth Sciences, Istanbul, Turkey

The Start of Growing Season (SGS) marks the time of year where a type of plant starts its growing season; therefore, forming green leaves. The End of Growing Season (EGS) is the opposite, where plants end their growing seasons and start defoliation. The difference in green leaf changes are much more dramatic in deciduous forests than coniferous forests, all plants show annual differences after SGS and EGS. As all plants undergo SGS and EGS, they look for environmental cues in order to keep up with their annual cycles. To detect variations in SGS and EGS, MODIS imagery was used. MODIS satellites have a polar orbit and capture images in 7 spectral bands daily. To detect the SGS and EGS from MODIS satellite data by comparing the surface reflectance in red versus green through the GRVI index. The threshold for the detection of SGS and EGS is set to  $GRVI = 0$ . If  $GRVI > 0$ , then it is currently the growing season; if  $GRVI < 0$  then it is the senescence season. Yearly GRVI estimates are analyzed to detect the SGS and EGS by catching GRVI zero crossing. We tried to detect the yearly shifts of SGS and EGS and see if there is any correlation with the GDDs. For these measurements, daily MODIS Terra MOD09GA V006 products were downloaded for the period 2007-2017, then analyzed through an R script using RASTER package. Later, the refined data were compared annually and among regions with different vegetation to look for the correlation mentioned above.

**Keywords:** phenology, MODIS, climate

### Modeling spatial distribution of oriental beech (*Fagus orientalis*): Past, present, and future

*A. Dilşad Dağtekin<sup>\*1</sup>, Evrim A. Şahan<sup>1</sup>, Nesibe Köse<sup>2</sup>, H. Nüzhet Dalfes<sup>1</sup>*

<sup>1</sup>Eurasia Institute of Earth Sciences, Istanbul Technical University, 34469, Istanbul/Turkey.

<sup>2</sup>Forest Botany Department, Faculty of Forestry, Istanbul University, 34473, Istanbul/Turkey.

Climate change is impacting forest biomes more severely than ever, even with the ~1°C temperature warming so far. Their geographical distributions are linked to warming temperatures and decreasing precipitation. Forest species try to adapt to this change by forcing these constraints. Recent warming not only impacted the survival rates of most tree species, also increased risks in their handling of extreme events. *Fagus orientalis* is a temperate, deciduous, broad-leaved species, which covers a wide range from the eastern Balkans through northern Turkey, Caucasus, Crimea and northern Iran, extending to the Amanos Mountains in the South, with a large elevational distribution from sea level to 2100 m. Several studies indicate that *F. orientalis* species are disturbed by changing climate due to increasing temperature and decreasing precipitation. Because of its importance in forestry, industry and ecosystem, *Fagus* sp. were the focus of interest in this study. We conducted species distribution model simulations with different algorithms (chosen from BIOMOD2) and with climate information for the present, past and future from WordClim 1.4. Our present-day classifications fitted well the distributional data obtained from the General Directorate of Forestry and EUFORGEN project. These models were used to ‘predict’ distributions through climate changes spanning Last Glacial Maximum, Mid-Holocene, 2050 and 2070 (as simulated with MIROC-ESM and CCSM4). We observed that *F. orientalis* distribution is predicted to shift toward the northeast from its present distribution, where colder and wetter regions are available according to future climatic conditions.

**Keywords:** sdm, *fagus*, climate change

### An Ancient DNA Investigation on the Çine-Tepecik Archaeological Community: mtDNA Haplogroup Analysis

*Sevgi Yorulmaz, Füsün Özer, Ali Metin Büyükkarakaya, Mehmet Somel*

Mitochondrial DNA analysis of ancient ten individuals from Çine Tepecik, Aydın. Here we report the genetic analysis of ten individuals unearthed from the Çine Tepecik excavation site at Aydın, in southwest Anatolia, dating to BC ~ 5000-2000. After ancient DNA extraction using bone and teeth samples, we attempted to amplify mitochondrial DNA (mtDNA) Hypervariable region I and Hypervariable region II (HVRI-HVRII). We obtained positive results for 10 individuals’ samples, which were then sequenced using the Sanger method. We determined major haplogroups. We further analysed the data by treating Çine Tepecik individuals as a single population, and calculating *Fst* between this group and modern and ancient human populations from West Eurasia. To our knowledge, this is the first ancient DNA study from a southwest Anatolian site.

**Keywords:** aDNA, mtDNA, Southwest Anatolia

### The Dilemma of species protection in action

*Semiha Demirbaş Çağlayan<sup>\*1</sup>, Can Bilgin<sup>2</sup>*

<sup>1</sup>Middle East Technical University, Department of Earth System Science

<sup>2</sup>Middle East Technical University, Department of Biology

Species action plans (SAPs) can be effective tools in nature conservation. These guideline documents inform the status and threats of species and their habitats, and they identify and prioritize actions to enhance the species populations. They both disseminate and make use of useful relevant information by involving local stakeholders, natural resource managers, conservationists and decision makers. The Turkish Ministry of Forestry and Water Affairs aims to complete 100 SAPs between 2013 and 2023. Until mid 2018, 41 SAPs were concluded successfully and the final reports are available online. SAPs were conducted so far was evaluated considering the taxonomic groups and selection procedures followed. The effectiveness of 41 SAPs were analyzed by analyzing presence, appropriateness or accuracy of elements expected to be a part of SAP documents, with a particular emphasis on monitoring plans. Overall, the species selection process does not appear to be based on clearly defined criteria or a transparent process. Rare plants in steppe ecosystems are the most studied species group. Among 41 SAPs, only two SAPs present well-articulated objectives and indicator support. Moreover, only half of the SAPs evaluated based on a detailed a monitoring activity. SAPs can be instrumental in species conservation since they are approved by government authorities. However, this well-intentioned attempt may not serve its purpose if they do not follow well-defined standards, or if they fail to be based on all available research and expertise.

**Keywords:** Species Action Plans, Biodiversity Monitoring, Turkey

### **Move Or Not To Move': A Case of Defensive Behaviours of Some Amphibians of Turkey**

*Batuhan Yaman Yakın<sup>\*1</sup>, Ulvi Kerem Günay<sup>1</sup>, Birgül Afsar<sup>2</sup>, Cemal Varol Tok<sup>1</sup>*

<sup>1</sup> Graduate School of Natural and Applied Sciences, Çanakkale Onsekiz Mart University, 17100, Çanakkale, Turkey.

<sup>2</sup> Department of Biology, Faculty of Arts and Sciences, Celal Bayar University, 45000, Manisa, Turkey.

Here, we reviewed the literature and personal data on defensive behaviours of some amphibian species from Turkey. According to the recent studies, there are 35 amphibian (18 urodela, 17 anura) species in Turkey (Baran et al., 2012; Yaşar, 2018). Many vertebrates show a large variety of defensive behaviour to be protected from the predators, such as “run for life”, “counter-attack”, “chemical defense”, and become “immobile”. “Immobility” and “chemical defense” can be an option for amphibians. “Pretend dead”, “not to move”, “mimicry”, and show the 'threatening' body coloration are the most seen defensive behaviours for amphibians. This behaviours are mostly seen on terrestrial amphibians, because of the higher risk of becoming a prey and the possibility of facing a predator than the aquatic species. During the fieldworks “head down defensive posture” is seen almost all of the Lycian salamanders. Also “unkenreflex” and “showing the threatening ventral coloration” is observed in *Ommatotriton vittatus* juveniles which are semi- aquatic species (Yakın and Tok 2018). “Eye protecting” behaviour is observed both a terrestrail and excavator toad, *Pelobates syriacus* and *Rana macrocnemis* which is a mountain frog. On the other hand “a chemical defensive behaviour” was observed in the tadpoles of *Bufo bufo* (Bókony et al., 2016). A total “unkenreflex” also reported for both *Bombina bombina* and *B. variegata* (Bajger et al., 1980). We are of the opinion that, behavioural data about this species could be use to find out the evolution and history of defensive behaviours which are still not unveiled completely.

**Keywords:** Amphibia, immobility, defensive behaviour

### **Species Level Molecular Identification of Bird Species Using Environmental DNA**

*Ayşegül Er<sup>\*1</sup>, Esra Mine Ünal<sup>1</sup>, Emre Keskin<sup>1</sup>*

<sup>1</sup> Evolutionary Genetics Laboratory (eGL), Ankara University, Turkey

In this study, we designed different experimental conditions to test the effect of time on degradation of DNA to be used in species level molecular identification of bird species from faecal samples. As the eDNA method has never been used to identify bird species from faecal samples dropped into aquatic environment such as ponds and lakes; we used 16 aquariums filled with 5 litres of water. Four different aquarium set-ups were inoculated with bird faecal samples and kept at different time periods (1,3,8,25 days). Fresh, fresh homogeneous, frozen and frozen homogeneous faecal samples were used as a part of experimental design. Water samples were filtrated using a manifold set-up through cellulose nitrate filters with a 0.22 µm pore size and DNA extractions were conducted using a modified eDNA extraction protocol. Extracted template DNA's were then amplified using bird specific barcoding primers Bird F1/Bird R1 and L5216/ H6313, and sequenced. Sequences were analysed using local (eGL Bird) and universal reference databases (GenBank and BOLD). According to our results we performed species level molecular identification from only 1, 3 and 8 days samples. We have successfully identified *Melopsittacus undulates* and *Columba livia* using faecal samples with both primers. Primer set L5216/ H6313 amplified bacterial sequences after 3 days samples. Primer set Bird F1/Bird R1 resulted with only bird sequences. These results show that bird species can be detected by eDNA method using faecal samples up to 8 days. More detailed studies could be designed to detect rare, migrating and endangered bird species.

**Keywords:** Environmental DNA, Bird Species, Molecular Identification

### **Aiming for the moon: Maintenance of local adaptation to tidal regime**

*Runa Kvamme Ekrem<sup>\*1</sup>, Hanna Kokko<sup>1</sup>, Tobias Kaiser<sup>2</sup>, Matthias Galipaud<sup>1</sup>*

<sup>1</sup> University of Zürich

<sup>2</sup> Max Planck Institute for Evolutionary Biology, Plön

For organisms living in a temporally fluctuating environment, timing important life history events to favorable periods may be crucial for their existence. Biological clocks allow organisms to track predictable fluctuations in their environment. Additionally, biological clocks may allow for synchronized reproduction. Geographical variation in the phase of an environmental cycle at a given time, and polymorphism within populations, may cause temporal isolation in reproductive timing among individuals, and allow sympatric speciation to occur. However, if individuals following different cycles overlap temporally for a proportion of their reproductive period, interbreeding may produce maladapted emergence times and inhibit adaptation to environmental fluctuations. *Clunio marinus* is a marine midge living in the intertidal zone. Their adult life span is limited to only a couple of hours during the lowest low tides, occurring on spring tide days. Emerging outside of these time periods result in a lack of exposed substrates for oviposition. Therefore, *C. marinus* is highly reliant on correct timing of adult emergence. Within sites, different genotypes follow distinctive cycles, in which emergence times occasionally overlap temporally, and along the coast populations are adapted to their site-specific tidal regime. However, up to now, there has been a lack of understanding how these genotypes interact. I aim to develop a population dynamics models with varying degree of reproductive timing overlap and gene flow among populations in order to explain the coexistence of different strategies within a site, and the maintenance of local adaptation along an environmental gradient.

**Keywords:** Coexistence, Local adaptation, Biological clocks

### **The traces of adaptive maternal effect in fluctuating temperature environments in fruitflies**

*Pinar Kohlmeier<sup>\*1</sup>, Mario Santos Mira<sup>1</sup>, Ido Pen<sup>1</sup>, J. Christophe Billeter<sup>1</sup>, Ton Groothuis<sup>1</sup>*

<sup>1</sup> University of Groningen

Temperature is one of the most important factors with large influence on biological processes. When out of optimum range, it may cause stress, lead to significant decrease of fitness and ultimately cause population extinction. Rapid changes in temperature from one generation to the next force organisms to adjust their phenotype as rapidly as possible. Besides individual experience, one source of adaptation in changing environments are maternal effects on offspring phenotype based on maternal experience of temperature, which is known as anticipatory or adaptive maternal effects. Although theoretical work has shown that such maternal effects can play a role in influencing evolutionary dynamics of offspring by influencing their fitness, there is a lack of empirical work supporting these models. In *Drosophila melanogaster*, maternal effects on temperature-related traits are known but their adaptive value is still under debate. To uncover the adaptive value of maternal effects, we use a match-mismatch split-brood design. In this design, we split the brood of the mothers who are exposed to hot or cold temperatures. Half the eggs of each mother is allocated to both matched and unmatched temperatures relative to the maternal ambient temperature. We then quantify the effects on offspring survival until adulthood. We repeated this experiment six times. There was considerable variation between experiments in the survival difference between matched and unmatched offspring. Matched offspring of cold mothers consistently survived better than unmatched offspring of cold mothers, although the magnitude of the effect varied considerably between experiments, but offspring survival of hot mothers was less consistent. Moreover, there was a strong maternal environmental effect on offspring survival, regardless of offspring treatment, explaining about two thirds of variation in offspring survival. Thus, the experiments provide only weak support for adaptive anticipatory maternal effects.

**Keywords:** Maternal effect, split brood design, *Drosophila melanogaster*

### **Bioinformatics Processing of Double-Digest RAD-seq data in *Myotis capaccinii* around the Mediterranean Basin**

*Ahmad Al Ajami<sup>1</sup>, Elizabeth Hemond<sup>1</sup>, Kübra Karaman<sup>2,3</sup>, Raşit Bilgin<sup>\*3</sup>*

<sup>1</sup> Bahçeşehir University, Faculty of Engineering and Natural Sciences, Molecular Biology and Genetics Department, Çırağan Cad. No: 4, 34353, Beşiktaş Istanbul, Turkey

<sup>2</sup> Istanbul University, Faculty of Science, Department of Biology 34134 Vezneciler Istanbul, Turkey

<sup>3</sup> Institute of Environmental Sciences, Boğaziçi University, 34342, Bebek, Istanbul, Turkey

Double digest restriction-site associated DNA sequencing (ddRAD-seq) -based phylogenetic and population genetic studies are becoming more common, due to the vast amount of data collected using this method. However, the large quantity of SNP data produced requires processing to filter out uninformative and misleading data prior to downstream analyses. Studies comparing the sensitivity and effectiveness of different ddRAD-seq data analysis pipelines have mainly focused on how different parameters affect the number of loci generated or genetic variants detected, without evaluating their effects on the results of population genetic analyses. This study explores the effects of two parameters used to filter loci, minor allele frequency (MAF) and percent of individuals, on population genetic inferences of the long-fingered bat, *Myotis capaccinii*, around the Mediterranean basin. The ddRAD-seq data, produced by Illumina sequencing, were assembled using the de novo approach, and a range of datasets were produced based on filtration of SNP loci by MAF (0, 0.1, 0.2, 0.3, 0.4, 0.5) and percent of individuals (0%, 25%, 50%, 75%). The results show that: 1) datasets containing only loci with data for at least 50-75 % of individuals in each population show more consistency in determining population genetic parameters, regardless of the MAF, and 2) datasets containing loci with 0 and 0.5 MAF thresholds give results inconsistent with those produced by datasets applying intermediate interval MAF thresholds (0.1, 0.2, 0.3, 0.4). We also present the response of some individual population genetics parameters such as observed heterozygosity, observed homozygosity, nucleotide diversity, FST, and FIS to different filters.

Overall, the results suggest using loci with a MAF threshold in the interval 0.2-0.4 and a minimum of 50-75% of individuals in a population to calculate different summary statistics.

**Keywords:**

**Genetic variation in the six6 gene is linked to the trophic level of Atlantic salmon at sea**

*Tutku Aykanat<sup>1</sup>, Martin A. Svenning<sup>2</sup>, Craig R. Primmer<sup>1</sup>*

<sup>1</sup> University of Helsinki, Organismal & Evolutionary Biology Research Programme, Helsinki, Finland.

<sup>2</sup> Norwegian Institute for Nature Research (NINA), Arctic Ecology Department, Fram Centre, Tromsø, Norway.

The time Atlantic salmon (*Salmo salar*) spent at sea before maturation has profound effect on reproductive output of fish, and inherently related to survival. The trait variation within and among populations is linked to a major effect locus by the *vgll3* gene, however, ecological drivers of this association are yet to be resolved. Here, using genetic information and stomach content data from more than 2000 adult fish, captured at sea on their return migration, we quantified the genetic variation in the *vgll3* gene as a function trophic level, and feeding success. We showed that, irrespective of sea age at maturity, fish with late maturing allele (L) preys on larger fish species (i.e. haddock and herring) and have heavier stomach content, compared to fish with early maturing allele (E) that preys on smaller fish species (i.e. capelin and sand-eel). We demonstrated that genetic variation in the *vgll3* gene may modulate age at maturity via a regulation in feeding preference across trophic levels. Our results further points out bottom-up effect in the ocean food webs as a potential modifier of age structure in salmon.

**Keywords:** evolutionary ecology, age-at-maturity, life-history variation

**Intense Pyrethroid Use in Adult Mosquito Control: Possible Effects on Resistance Development and Environment**

*Onur Guntay<sup>\*1</sup>, Savas Izzetoglu<sup>1</sup>, Mehmet Salih Yikilmaz<sup>1</sup>*

<sup>1</sup> Ege University

Mosquitoes are considered one of the most important species in public health control programs due to it being a nuisance among other health-related problems. Pyrethroids are widely used for both adult mosquito controls and agricultural pest management in Izmir, Turkey as part of integrated pest management. However, long-term and frequent use of insecticides against adult mosquitoes causes increased numbers of resistant individuals and populations. In this study, we collected *Culex pipiens*, the most common mosquito species in Turkey, from three locations and examined status of susceptibility to four different pyrethroids (deltamethrin, permethrin,  $\alpha$ -cypermethrin and cyfluthrin). To achieve this, adult susceptibility bioassays were performed using with WHO insecticide-impregnated papers (0,05% deltamethrin, 0,75% permethrin, 0,05%  $\alpha$ -cypermethrin, 0,15% cyfluthrin). From each site, 150 females mosquitoes aged 3-5 days old were used and all treatments were replicated three times. No susceptibility was observed in any of three populations (mortalities <63%) to four pyrethroids. The results confirm that adult mosquitoes develop resistance against pyrethroids. Primary reason for this resistance is that mosquito control programmes have been done often with adults besides larvae for many years. The success rate of the adult control is low and this leads to the selection of the resistant individuals in the

population. Most importantly, these pyrethroids cause serious environmental problems such as contamination of soil and water sources.

***Keywords:***