

**EEBST
2022**



**8th Ecology and
Evolutionary Biology
Symposium, Turkey**

7th - 9th September 2022



**Symposium Programme
&
Abstract Book**



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Ecology and Evolutionary Biology Society



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METU**

8th Ecology and Evolutionary Biology Symposium
7-9 September 2022, Ankara, Turkey

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THE ORGANIZING AND SCIENTIFIC COMMITTEES

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SYMPOSIUM PROGRAMME

WEDNESDAY, SEPT. 7TH 2022

09:00-09:30	Registration	
09:30-09:45	Welcome from the Organizing Committee and EkoEvo President	
	Session 1: Ecology I	
09:45-10:00	İsmail Bekar	Integrating burnt area as a complementary performance measure for daily fire danger
10:00-10:15	Vildan Acar	Using functional diversity components to describe phytoplankton community assembly processes in Turkish shallow lakes
10:15-10:30	Nur Bikem Kesici	An assesment on the coastal ecosystem of the North Aegean Sea through cryptobenthic fishes
10:30-10:45	Alper Ertürk	Applying random encounter model for wild boar population densities in northwestern Anatolia to track zoonotic disease risk at European level
10:45-11:15	Coffee Break	
11:15-11:30	İbrahim Kaan Özgencil	Factors driving the breeding microhabitat preferences of two endangered ducks in a shallow lake as revealed by a multidisciplinary approach
11:30-11:45	Zeynep Ersoy	Future-proofing environmental DNA and trait-based predictions of food webs
11:45-12:00	Nurbahar Usta Baykal	A comparison of recruitment networks in woody plant communities in Mediterranean ecosystems of western Anatolia
12:00-13:30	Break for Lunch	

13:30-14:30	Keynote Speaker <u>Invertebrate Conservation in the XXI Century</u> Pedro Cardoso Finnish Museum of Natural History University of Helsinki
	Session 2: Population Genetics
14:30-14:45	Sibel Öncel Directed laboratory evolution to induce DMI-fungicide resistance in fungal pathogen
14:45-15:00	Kanat Gürün MAXENT modelling and mitochondrial DNA phylogeography of the long-fingered bat (<i>Myotis capaccinii</i>)
15:00-15:15	Ortaç Çetintaç The complex phylogeographic history and speciation in subterranean blind mole rats (<i>Spalax</i> and <i>Nannospalax</i> sp.)
15:15-15:45	Coffee Break
15:45-16:00	Meriç Erdolu Multiple parental individuals contributed to common gene pool of the hybridogenic parthenogenetic lizards <i>Darevskia bendimahiensis</i> and <i>D. sapphirina</i>
16:00-16:15	Elif Kaplan Evolutionary genetics of Behcet's disease
16:15-16:30	E. Yağmur Erten Body size relates to the level of cancer suppression across non-human primates
16:30-18:00	Poster Session

THURSDAY, SEPT. 8TH 2022

09:00-09:30	Registration	
	Session 3: Bioinformatics	
09:30-09:45	Ogün Adebali	Phylogeny-based inferences in protein function
09:45-10:00	Ecem Su Koçkaya	In silico discovery of epitopes of gag and env proteins for the development of a multi- epitope vaccine candidate against Maedi Visna Virus using reverse vaccinology approach
10:00-10:15	Fatma Rabia Fidan	SWAMPy - Simulating SARS-CoV-2 wastewater amplicon metagenomes in Python
10:15-10:30	Malavi Sengupta	Genomic basis of saltwater adaptation in <i>Alburnus tarichi</i>
10:30-10:45	Arzu Karahan	The connection between Sea of Marmara biodiversity and mucilage occurrence incidence
10:45-11:15	Coffee Break	
11:15-12:00	Poster Session	
12:00-13:30	Break for Lunch	
13:30-14:30	Keynote Speaker <u>From the Stone Age to Today: Disease, Epidemics and the Emergence of Genetic Variants for Chronic Inflammatory Diseases</u> Ben Krause-Kyora Institute of Clinical Molecular Biology University of Kiel	
	Session 4: Microbial Evolution	
14:30-14:45	Baran Taylan Fidanoğlu	Temperature dependent infection risk of plant diseases: <i>Peach-Monilinia</i> spp. pathosystem as a model

14:45-15:00	Ezgi Özkurt	LotuS2: An ultrafast and highly accurate tool for amplicon sequencing analysis
15:00-15:15	Yekbun Adıgüzel	In silico study on HLA affinity-based changes related to Omicron 21K and Omicron 21L have implications for host-pathogen coevolution
15:15-15:45	Coffee Break	
15:45-16:00	Özgür Yüksel	Game theoretical analysis of cooperation and cheating among lipase producing <i>Yarrowia lipolytica</i> sub-cultures
16:00-16:15	Murat Tuğrul	Understanding individual heterogeneity in ageing from stochastic gene expression dynamics in <i>E. coli</i>
16:15-18:00	Extraordinary General Meeting of the EkoEvo Society, Turkey	

FRIDAY, SEPT. 9TH 2022

09:00-09:30	Registration	
	Session 5: Ancient DNA	
09:30-09:45	Funda Özdemir Değirmenci	Best practices for DNA extraction from charred seeds: The Kaymakçı archaeological case
09:45-10:00	İdil Taç	The effect of Neolithization on complex diseases in Anatolia: preliminary results
10:00-10:15	Fatma Küçük Baloğlu	Determination of DNA preservation in human bones from Anatolian Neolithic by a pre-screening method based on FTIR spectroscopy
10:15-10:30	Mustafa Özkan	Speciation status, complex population history and extinction mechanisms of European wild ass
10:30-11:00	Coffee Break	
11:00-12:00	Panel: <i>Brain Drain in Academia & Monopolization in Academic Publishing</i> Ezgi Özkurt, Mehmet Somel <i>Civil Society and Academy Cooperation in Nature Conservation</i> Yıldıray Lise	
12:00-13:30	Break for Lunch	
13:30-14:30	Keynote Speaker <u><i>Why Theoreticians Love Their 'what if?' Scenarios</i></u> Hanna Kokko University of Zurich	
	Session 6: Ecology II	
14:30-14:45	Evrin Karaçetin	Discovering the migration route of the painted lady butterfly
14:45-15:00	Alaettin Kaya	Geomorphometric shape variations of <i>Nannaospalax ehrenbergi</i> cytotypes in Asia Minor

15:00-15:15	Sarah Syedia Hasnain	Maternal thermal environment mediates <i>Daphnia magna</i> grazing response to thermal stress
15:15-15:45	Coffee Break	
15:45-16:00	Alper Yelimlieş	Do common chaffinch vocalizations differ between urban and rural habitats?
16:00-16:15	Bilgecan Şen	Spatio-temporal predictability of population dynamics: A case study with the Adélie penguin
16:15-16:30	Bikram Pandey	Precipitation and potential evapotranspiration determines the distribution patterns of threatened plant species in Sichuan province of China
16:30-18:00	Awards and Closing Ceremony	

ABSTRACT OF ORAL PRESENTATIONS
ECOLOGY SESSION

Keynote address : Invertebrate Conservation in the XXI Century

Pedro Cardoso

Laboratory for Integrative Biodiversity Research (LIBRe), Finnish Museum of Natural History Luomus, University of Helsinki, Finland

Insect population declines and extinctions recently made the headlines worldwide. Other invertebrates follow the same worrying trends, and yet, beyond pollinators, they are still largely ignored in public policies and research agendas that could help abate threats on them. Habitat loss, degradation, and fragmentation, use of polluting and harmful substances, the spread of invasive species, global climate change, direct overexploitation, and co-extinction of species dependent on other species, all contribute to the current trends.

Nevertheless, we still miss information on most taxa. Most species are undescribed (the Linnean shortfall); the distribution of described species is mostly unknown (the Wallacean shortfall); the abundance of species and their changes in space and time are unknown (the Prestonian shortfall); and species ways of life and sensitivities to habitat change are largely unknown (the Hutchinsonian shortfall). These shortfalls require innovative methods to be minimized.

Many methods are being developed in taxonomy, with the rapid description of species mostly based on barcoding becoming more frequent. Automated morphological descriptions feeding into ontological frameworks are however keeping pace and the two approaches combined might lead to a future of mostly automated integrative taxonomy. Species distributions are being inferred from fast and efficient sampling methods and statistical frameworks that, together with global spatial data on threats, help fill gaps from scarce occurrence data. Population abundance trends are increasingly derived from computer vision or sound identification methods that reach unparalleled amounts of data for some taxa. Finally, the automated acquisition of functional traits from text and images allows us to have important additional data to understand how species behave when faced with varied threats.

All these different sources of data are rapidly allowing us to fill the gaps. I will overview many of the methods being developed, and how they integrate to quantify, understand and ultimately stop invertebrate declines and extinctions.

Contact: cardosopmb@gmail.com

Integrating burnt area as a complementary performance measure for daily fire danger assessment: a large-scale test

İsmail Bekar¹, Gianni Boris Pezzatti², Marco Conedera², Juli G. Pausas³, Sylvain Dupire³, Harald Bugmann¹

¹ETH Zürich

²Swiss Federal Institute for Forest, Snow and Landscape Research - WSL

³Centro de Investigaciones sobre Desertificación

⁴University of Grenoble Alpes

Fire weather indices are often used for studying the relationship between fire weather and the probability of fire occurrence. However, the relationship between fire weather indices and burned area at a daily resolution is scarcely studied. CLARE is a newly developed metric that takes burned area into account when assessing fire danger. We evaluated CLARE performance in 11 regions with a broad range of environmental conditions. We also assessed the impact of (i) different groups of input variables, (ii) model complexity, and (iii) the modeling approach on the performance of CLARE. We found that models that achieve a high AUC for predicting fire occurrence may fail to show a high performance when predicting burned area. Using a multi-variable modeling approach is likely to provide higher CLARE performance than using single-variable fire weather index models, especially among models that have high AUC values. Moreover, using this approach led to better multi-variable meteorological model performance than single-variable fire weather models for some regions. This may be particularly valuable for regions where the calculation of fire weather indices is not possible due to lacking weather data. Finally, the differences between the modeling approaches were mainly related to the region or groups of environmental variables. Overall, our results highlight that including burned area in the fire danger assessment process is feasible across a wide range of environmental conditions and provides valuable insights from a scientific as well as a practical point of view.

Keywords: forest fire, fire danger, burned area, fire weather index, modeling

Contact: ibekar@ethz.ch

Using functional diversity components to describe phytoplankton community assembly processes in Turkish shallow lakes

Vildan Acar¹, Sarah Hasnain¹, Şeyda Erdoğan, İbrahim Kaan Özgencil¹, Erik Jeppesen, Meryem Beklioğlu¹

¹Middle East Technical University

The recent increase in biodiversity loss due to various anthropogenic effects makes it crucial to understand the relationship between biodiversity and ecosystem functioning (BEF) for the conservation and preservation of ecosystems. Classically, BEF studies use species diversity as a measure of biodiversity, but functional diversity has been shown in some cases to better explain and predict ecosystem-level processes. In this study, we investigated the role of dispersal, environmental filtering, and limiting similarity in the assembly of phytoplankton communities from 44 Turkish lakes. Dispersal integrates both local and regional diversity patterns, while environmental filtering and limiting similarity

affect local community structure. At the local level, species' traits are expected to converge as a result of environmental filtering or diverge due to limiting similarity. We initially found that dispersal limitation was not of importance for the phytoplankton community assembly in our study lakes. We found that some functional traits were affected only by environmental filtering (i.e. unicellularity, silica demand, etc.) or limiting similarity (i.e. toxin production, mixotrophy) or while both processes acted simultaneously on other traits (i.e. sexual reproduction). Also, the effects of different assembly processes varied along different environmental gradients such as total nitrogen and salinity.

Keywords: assembly, functional diversity, functional traits, phytoplankton

Contact: vildanacr@gmail.com

An Assessment on the Coastal Ecosystem of the North Aegean Sea through Cryptobenthic Fishes

Nur Bikem Kesici

Istanbul University

Cryptobenthic fishes inhabiting in the coastal zones, such as combtooth (Blennidae) and threefin blennies (Tripterygiidae) and gobies (Gobiidae) are valuable elements of the coastal biodiversity. Due to the site fidelity, life strategies and habitat preferences, they offer us an opportunity to measure the impact of any positive or negative changes in the ecosystem. The determined area of this study includes parts of the Aegean Turkish coastline located north of 40 degrees latitude. The cryptobenthic fish populations are observed and sampled in 40 different stations along the rocky coasts of Saros Bay and Gökçeada. We intend to introduce a new method, by standardizing the obtained data with both space and time. Three habitat characteristics are recorded in order to reveal the ecological characters of cryptobenthic fish communities; substrate type, biocover and depth. Substrates to be studied are categorized according to the EUNIS habitat types. Tide pools, estuaries, coralligenous habitats, corals, phanerogams and harbours are determined as some of the important habitats. In addition, regions that are exposed to negative effects such as pollution or habitat degradation and regions that are considered to be inherent, will be evaluated separately. Overall, the aim of the study is to find the answer to the question of whether these species are an ecological marker that shows the health of their ecosystem. Up to date 12 dives were conducted; a total of 166 individuals of 19 cryptobenthic fish species were observed. Density of the cryptobenthic fishes were estimated as 11.4 (ind. per hour) in May and June of 2021 (while intense mucilage formation was observed) and 17.8 (ind. per hour) in July and August of 2021. The overall results seems to indicate that the anthropogenic effects are destructive for the target species.

Keywords: cryptobenthic fish, ecological marker, coastal ecology, visual census, SCUBA

Contact: nbkesici@gmail.com

Applying random encounter model for wild boar population densities in northwestern Anatolia to track zoonotic disease risk at European level

Alper Ertürk¹, Anıl Soyumert¹, Massimo Scandura², Marco Apollonio², Ezio Ferroglio², Stefania Zanet², Oliver Keuling³, Tomasz Podgórski⁴, Graham Smith⁵, Jim Casaer⁶, Patrick Jansen⁷, Joaquin Vicente⁸

¹Hunting and Wildlife Program, Kastamonu University, Kastamonu

²Dept. Veterinary Medicine, University of Sassari, Sassari

³Institute for Terrestrial and Aquatic Wildlife Research, University of Veterinary Medicine Hannover, Hannover

⁴Mammal Research Institute, Polish Academy of Sciences, Białowieża

⁵Czech University of Life Sciences, Prague

⁶Research Institute of Nature and Forest, INBO

⁷Department of Environmental Sciences, Wageningen University

⁸National Institute on Wildlife Research (IREC), University of Castilla-La Mancha and Consejo Superior de Investigaciones Científicas, Ciudad Real

Sustainable and effective management based on scientific foundations for wild populations are important in terms of wildlife conservation in human dominated landscapes. Coexistence of wild animals, humans and livestock arises several side effects such as zoonotic diseases, which are generally omitted in most of the countries including Turkey. In the natural and semi-natural areas human activities coincide with wildlife that risks both local people and also the livestock therefore, it becomes a public issue. Despite the monitoring and management actions by the government there is still a huge gap in disease control, and this creates a risk factor for both human dimensions and wildlife itself. The ENETWILD Project (<https://enetwild.com>), which is funded by The European Food Safety Authority (EFSA) aims to analyse risks of diseases shared between wildlife, livestock and humans since 2017. Camera-trapping surveys were conducted in 2021 concurrently with 19 regions throughout Europe within the network of European Observatory of Wildlife (EOW; <https://wildlifeobservatory.org>) through the project ENETWILD. Being the first focused species in the project, wild boar (*Sus scrofa*) population density has been estimated by applying Random Encounter Model (REM) in northwestern Anatolia. The outcomes of the study showed that the density of wild boar population is 5.75 ± 2.40 (SE) indv/km² in the study area, which has human settlements and forestry activities with no artificial feeding for wild animals. The progress of the study indicates that Random Encounter Model is an applicable tool for collaboration among different organisations to obtain standard results for wildlife populations.

Keywords: Camera trapping, Random Encounter Model (REM), population density, wildlife ecology, zoonotic diseases

Contact: erturk@kastamonu.edu.tr

Factors driving the breeding microhabitat preferences of two endangered ducks in a shallow lake as revealed by a multidisciplinary approach

İbrahim Kaan Özgencil¹, Deniz Mercan², Gencer Yaprak¹, Gülümser Genç³, Dilan Melisa Özsoy³, Alaz Uslu⁴, Melisa Soyuluer¹, Mustafa Korkmaz¹, Berkay Gülen⁵, Metehan Arıkan⁵, Esra Mine Ünal⁵, Emre Keskin⁵, Sedef Alkan³, Defne Budak¹, Şeyma Gül¹, Hilal Kiran¹, Feride Avcı¹, Nur Filiz¹, Gülce Yalçın¹, Meryem Beklioğlu¹

¹Middle East Technical University

²Eskişehir Osmangazi University

³Hacettepe University

⁴Bolu Abant İzzet Baysal University

⁵Ankara University

Shallow lakes are crucial habitats for breeding waterbirds including diving ducks, some of which are globally endangered. Understanding factors affecting breeding habitat preferences of these endangered species can allow for more efficient management and conservation planning. In this study, we investigated breeding microhabitat preferences of two globally endangered omnivorous diving ducks: White-headed Duck (*Oxyura leucocephala*) and Common Pochard (*Aythya ferina*) at Lake Mogan, a shallow lake in central Turkey. We used waterbird surveys, water clarity measurements, submerged macrophyte surveys, environmental DNA, satellite imagery, supervised image classification, and generalized linear models to figure out the factors that may be driving the microhabitat preferences of

the two breeding endangered diving ducks, which seem to utilize only some of the visually suitable sites in the lake. We found that higher abundances of the study species were found in areas with (i) high macrophyte submerged macrophyte coverage (ii) high water clarity (iii) high benthic macroinvertebrate food abundance (iv) lower fish biomass (v) high reed percentage and (vi) high reedline complexity. Strength of some of the dependence relationships varied over time with the effects getting stronger towards the end of the breeding season. Our results indicate that the two endangered duck species utilize refuges with certain ecological features, which constitute a small fraction of the lake's surface area. These findings can be used to guide the management and conservation efforts aiming at preserving such refuge areas and thus the study species.

Keywords: Diving ducks, Environmental DNA, Microhabitat preference, Remote sensing, Shallow lakes

Contact: kaanozgencil@gmail.com

A comparison of recruitment networks in woody plant communities in Mediterranean ecosystems of western Anatolia

Nurbahar Usta Baykal¹, İrem Tüfekçioğlu¹, Kahraman İpekdağ², Cihan Ünal Değirmenci¹, Pınar Kütüküt¹, Çağatay Tavşanoğlu¹

¹Hacettepe University

²Kırşehir Ahi Evran University

Plant-plant interactions are considered one of the main drivers of the species assembly in ecological communities. These interactions include intra- and inter-specific competition, facilitation, and mutualism. Studying facilitation networks has been a common approach to understanding facilitation processes in plant communities, but recruitment networks (RNs), a relatively recent approach, provide better data for understanding plant-plant interactions in an ecological community. Revealing RNs in plant communities improves our knowledge on not only facilitation interactions, but also competitive ones in the studied community. We studied plant recruitment networks in four vegetation types in the Mediterranean ecosystems of western Anatolia, Turkey. Fieldwork includes low- and high-altitude Mediterranean woody vegetation, namely high-altitude mixed pine-fir and pure fir forests (Kazdağı National Park, NW Turkey) and low-altitude Mediterranean pine forest and shrublands (Datça area, SW Turkey). Using the line transect methodology, we collected data on the recruits of woody species and their nurse plants by recording the canopy plants in which saplings were found underneath. We also recorded the frequency of saplings under open canopy gaps and estimated the cover of each woody species. We tested whether recruitment systems differ between low- and high-altitude Mediterranean ecosystems and among specific vegetation types. The results provide the first detailed information on plant-plant interaction systems of the studied vegetations in Turkey and allow us to define competitor and facilitator species in these plant communities. Results suggest the existence of a diversity of plant-plant interactions in Mediterranean woody communities and that the altitude is one of the drivers of this diversity.

Keywords: Plant-plant interactions, facilitation, plant community, Mediterranean forests and shrublands, recruitment

Contact: ustanurbahar@gmail.com

Discovering the migration route of the Painted Lady butterfly, *Vanessa cardui*, in Türkiye, through citizen science

Evrin Karaçetin

Erciyes University, Department of Environmental Engineering, Kayseri, 38039, Turkey

Painted lady, *Vanessa cardui*, is a cosmopolitan continuously brooded butterfly species which migrates each year between Africa and Europe. Its migration route in Europe is well defined with spring flights being northward and summer/autumn flights being southward. However, the route of the migration through Türkiye is yet to be discovered. In certain years number of migrating butterflies can be so enormous that migration gets public attention. For identifying the route of the butterfly, citizen science is the most effective tool, where public is asked to share their observations including the coordinates, and the direction of the flight. This paper combines the data from the high number migration years of 2009, 2017 spring data and 2022 summer data when hundreds of observations were shared with the author. Although the data is scattered and more observations are still needed, it shows that the butterfly flies from east to west in spring and west to east in summer which is different from European migration route. This paper fills an important gap in the migration route of the painted lady, and it stresses the importance of citizen science, which is not only a tool for collecting data, but also a very effective method for increasing public awareness for observing and conserving nature. Acknowledgements: The author individually thanks to the data contributors.

Keywords: *Vanessa cardui*, butterfly migration, citizen science, painted lady, route

Contact: ekaracetin@erciyes.edu.tr

Geomorphometric Shape Variations of *Nannaospalax ehrenbergi* Cytotypes in Asia Minor

Alaettin Kaya*¹, Yüksel Coşkun², Gökhan Yürümez³

¹University of Dicle, Veterinary Medicine Faculty, Basic Science Department, Diyarbakır, Turkey

²University of Dicle, Science Faculty, Biology Department, Diyarbakır, Turkey

³University of Batman, Science and Art Faculty, Biology Department, Batman, Turkey

Seven cytotypes of *N. ehrenbergi* were investigated by a landmark-based geometric morphometric method to reveal the shape and size differences. Geometric morphometric (GM) is an impressive approach to obtain information about the shape attributes. 59 of them belong the *N. ehrenbergi* in seven chromosomal groups, the other four samples belong *N. munzuri* as out group. Cranium and mandible images of the samples were taken by digital camera and images were analysed by geometric morphometric procedure. Landmarks were collected with the tpsDig 2.3 program. Analysis were performed by MorphoJ and PAST softwares. According to the Procrustes ANOVA, the size and shape of the cranium were significant for cytotypes and for sexes. The size and shape of mandible were significant for cytotypes, the size of mandible has difference for sexes, but the shape has not differences. The first three Principal components explains 46,7 percent of the total variation on cranium and 51,6 percent of the total variation on mandible. In CVA, according to permutation p values based on Mahalanobis and Procrustes distances for the cranium and mandible, all cytotypes significantly differed, only the permutation p values for the cranium and mandible depending on Procrustes distance between 48 and 52b cytotypes were not significant. Confusion matrix for cranium %80,9 correctly classified all samples and for mandible %98,4 correctly classified all samples.

Keywords: Spalacidae, Blind mole rat, 2D Geometric morphometry, Türkiye.

Contact: altkaya21@gmail.com

Maternal thermal environment mediates *Daphnia magna* grazing response to thermal stress

Sarah S Hasnain¹, Kemal Ali Ger², Lucia Cabrera-Lammana³, Meryem Beklioğlu¹

¹Middle East Technical University

²Universidade Federal do Rio Grande do Norte

³Radboud University

Ectotherms, constituting the vast majority of living organisms, rely on environmental temperatures to regulate metabolic processes. Increasing temperatures as a result of global climate change is expected to exert a strong selective pressure on these organisms. For *Daphnia*, the maternal environment has been shown to mediate the physiological response of offspring to abiotic stressors. We conducted a reciprocal transplant experiment to assess if differences in the maternal thermal environment affected the grazing response of *Daphnia magna* to thermal stress. *Daphnia magna* were reared for two generations at either 18°C or 24°C. Offspring from the second generation were exposed to either 18°C or 24°C for a period of 12 hours and an assay was conducted to measure algal clearance rates. Our results show that *Daphnia* from mothers reared at 24°C had higher clearance rates, and reduced nitrogen and phosphorus excretion when exposed to higher temperatures than those whose mothers were reared at 18°C. These results suggest that the maternal thermal environment plays a critical role in determining *Daphnia* physiological response to thermal stress.

Keywords: Temperature, Maternal effect, Grazing rate, Excretion rates, Ectotherm, Transgenerational plasticity

Contact: sarah.s.hasnain@gmail.com

Do common chaffinch vocalizations differ between urban and rural habitats?

Alper Yelimliş¹, Berkay Atalas², Çağla Önsal¹, Çağlar Akçay^{1,3}

¹Department of Psychology, Koç University, İstanbul, Turkey

²Department of Biological Sciences, Middle East Technical University, Ankara, Turkey

³School of Biological Sciences, Anglia Ruskin University, Cambridge, UK

Anthropogenic noise interrupts acoustic communication between animals by masking their vocalizations. Accumulating evidence shows that some urban living animals are able to overcome this interruption using various strategies. Here we compared acoustic parameters of songs and rain calls of common chaffinches (*Fringilla coelebs*) recorded in rural and urban parts of İstanbul, Turkey. We expected that vocalizations recorded from urban chaffinches would have higher minimum frequencies, narrower bandwidths, and longer durations, which would allow them to transmit better in low-frequency anthropogenic noise. We found that trilled parts of the songs and rain calls did not differ in any of the acoustic parameters between habitats. Terminal flourish phrases of the songs, on the other hand, had lower minimum frequencies and broader bandwidths in urban territories, contrary to our predictions. We discuss this finding in relation to its potential adaptive significance.

Keywords: Urbanization, Anthropogenic Noise, Communication, Birdsong, Common Chaffinch

Contact: ayelimlies17@ku.edu.tr

Spatio-temporal predictability of population dynamics: A case study with the Adélie penguin

Bilgecan Şen¹, Christian Che-Castaldo¹, Kristen Krumhardt², Laura Landrum², Marika Holland², Michelle LaRue³, Matthew Long², Stephanie Jenouvrier⁴, Heather Lynch¹

¹Stony Brook University

²National Center for Atmospheric Research

³University of Canterbury

⁴Woods Hole Oceanographic Institution

Ecological predictions are fundamental for informing conservation management decisions in response to environmental change. To be useful in this regard, ecological models must be transferable in one or more dimensions, where transferability is the successful projection of responses outside of the model data bounds. While much is known as to what makes spatially-oriented models more transferable, there is no general consensus as to the temporal transferability of ecological time series models. As a case study, we use a suite of environmental covariates to predict population growth rates of Adélie penguins from abundance time series collected at 23 long-term study sites around Antarctica in order to determine what factors affect temporal transferability of ecological models. We show that weighted permutation entropy (WPE), a model free intrinsic predictability measure recently introduced to ecology, is highly correlated with the predictive performance of our models. This suggests that intrinsic predictability is not only useful for detecting potential forecast performance prior to modeling, but also for separating sites whose dynamics are largely stochastic from those responding to systemic drivers or other regulatory mechanisms. We argue that the low intrinsic predictability of some colonies could be caused by stochastic demographic events that do not have consistent temporal patterns.

Keywords: forecasting, population dynamics, Adélie penguin, Antarctica, intrinsic predictability, weighted permutation entropy, transferability

Contact: bilgecan.sen@gmail.com

Precipitation and potential evapotranspiration determines the distribution patterns of threatened plant species in Sichuan province of China

Jiangong Li^{1,2}, Bikram Pandey^{3,4,5}, Mohammed A. Dakhil⁶, Manita Khanal⁷ and Kaiwen Pan³

¹ Key Laboratory of Forest Ecology in Tibet Plateau (Tibet Agricultural and Animal Husbandry University), Ministry of Education, Nyingchi, Tibet 860000, People's Republic of China.

² National Forest Ecosystem Observation & Research Station of Nyingchi Tibet, Nyingchi, Tibet 860000, People's Republic of China.

³ CAS Key Laboratory of Mountain Ecological Restoration and Bio-resource Utilization and Ecological Restoration Biodiversity Conservation Key Laboratory of Sichuan Province, Chengdu Institute of Biology, Chinese Academy of Sciences, Chengdu, 610041, Sichuan, China.

⁴ University of Chinese Academy of Sciences, Beijing, China.

⁵ Uniglobe College, Kathmandu, Nepal

⁶ Botany and Microbiology Department, Faculty of Science, Helwan University, Cairo 11790, Egypt

⁷ Institute of Forestry, Tribhuvan University, Pokhara, 33700, Nepal

A fundamental aspect of ecologists is to determine the large-scale gradients in species richness. The threatened plants are priority of such studies because of narrow distribution and confined to specific habitat. Studying the distributions pattern of threatened plants can be crucial for identifying global conservation prioritization. In this study, we investigated the richness pattern of threatened plant species along spatial and elevation gradients in Sichuan province of China, considering climatic, habitat-heterogeneity, geometric constrains and human-induced factors. We analyzed the species richness pattern and linked the predictor variables, including temperature (TEMP), precipitation (PPT), potential evapotranspiration (PET), habitat-heterogeneity (HHAT), and disturbances (DIST), to species richness.

This was done using geographical distribution data of threatened species compiled at a spatial resolution of 20 Km × 20 Km. We used generalized linear models (GLMs) and structural equation modelling (SEM) to determine the individual and combine effect of each variable on species richness pattern. The result showed a total of 137 threatened plant species distributed between 200 and 4800 m a.s.l. The central region of the province harbors the highest species diversity. PPT and PET profoundly explained the richness pattern. However, the result underscores the role of disturbance that explains the least variations in the richness patterns of threatened plants. We concluded that the distribution of threatened species was highly influenced by climatic variables rather than human disturbance. These conclusions can be helpful to determine the richness pattern of threatened plant species in other mountainous regions of the world, considering the impact of climate change.

Keywords: disturbances, species richness, potential evapotranspiration, diversity-climate relationship, statistical modeling

Contact: bikram_pandey4@yahoo.com

POPULATION GENETICS SESSION

Directed Laboratory Evolution to Induce DMI-Fungicide Resistance in Fungal Pathogen *Monilinia fructicola* and Highlighting the Role of a Transposable Element

Muhammed Raşit Durak², Kübra Arslan², Baran Taylan Fidanoğlu¹, Sibel Öncel², Hilal Özkılınc²

¹Canakkale Onsekiz Mart University, School of Graduate Studies, MSc Program in Molecular Biology and Genetics, Canakkale/Turkey

²Canakkale Onsekiz Mart University, Dept. of Molecular Biology and Genetics, Canakkale

Fungicides are widely used control methods against to fungal pathogens. DMI group fungicides, also known as the azoles, among the fungicide groups with many different mechanisms of action, block the biosynthesis of ergosterol which causes the cell membrane structure to deteriorate. In in vitro fungicide tests, we determined that the population of the fungal pathogen *M. fructicola*, which is a cause of brown rot in peach, was sensitive to Propiconazole (Prop) and Difenconazole (Dif) from DMIs. Therefore, the question of whether resistance develops in these sensitive isolates was wondered and an experimental evolution procedure was directed to selected *M. fructicola* isolates. The transfers were made every 10 days for Prop and 5 days for Dif in the media where the IC₅₀ dose determined for each fungicide was applied. After 10 transfers, resistance phenotype, with over 50% relative growth value in comparison to its control, to Prop was detected. Furthermore, the genomes of an evolved lab-isolate and an ancestral isolate were comparatively analyzed. It was determined that a nested TE element (defined as Class II/DNA element and Class I/Retrotransposon element) in the 223 bp upstream region of CYP51 gene, which is associated with azole resistance response, was found in the resistant lab-isolate but not in the highly susceptible ancestral isolate. This TE is expected to increase the expression level of CYP51 and is currently under investigation. Although it has the same mechanism of action, the resistance response to Dif has not yet occurred and the experimental evolution process is continuing.

Keywords: Transposable Elements, Fungicide Resistance, Experimental Evolution

Contact: sibeloncel.mbg@gmail.com

MAXENT modelling and mitochondrial DNA phylogeography of the long-fingered bat (*Myotis capaccinii*)

Gürün K^{1,2*}, Karaman K.^{1,3}, Çoraman E.^{1,4}, Furman, A.¹, Viglino A.⁵, Caniglia R.⁵, Juste J.⁶, Puechmaillie S.^{7,8}, Papadatou E.⁹, Benda P.^{10,11}, Ibanez C.⁶, Russo D.¹², Bilgin R.¹

¹Institute of Environmental Sciences, Boğaziçi University, 34342 Bebek, İstanbul, Turkey.

²Department of Biological Sciences, Middle East Technical University, 06800, Ankara, Turkey

³Department of Biology, Faculty of Science, Istanbul University, Istanbul, Turkey

⁴Eurasia Earth Sciences Institute, Istanbul Technical University, Maslak, İstanbul Turkey.

⁵Unit for Conservation Genetics (BIO-CGE), Italian Institute for Environmental Protection and Research (ISPRA), Via Cà Fornacetta 9, 40064 Ozzano dell'Emilia (BO), Italy.

⁶Doñana Biological Station (CSIC), Avda. Américo Vespucio 26, Isla de la Cartuja, Seville 41092, Spain.

⁷School of Biology and Environmental Science, University College Dublin, Belfield, Dublin 4, Ireland.

⁸ISEM, Univ Montpellier, CNRS, EPHE, IRD, Montpellier, France.

⁹ARUP, 3 Piccadilly Place, Manchester M1 3BN, UK.

¹⁰Department of Zoology, National Museum (Natural History), Václavské nám. 68, 115 79 Praha 1, Czech Republic.

¹¹Department of Zoology, Faculty of Sciences, Charles University, Viničná 7, 128 44 Praha 2, Czech Republic.

¹²Wildlife Research Unit, Dipartimento di Agraria, Università degli Studi di Napoli Federico II, via Università, 100, 80055 Portici (Napoli), Italy

The long-fingered bat, *Myotis capaccinii* is a bat species with a wide distribution spanning Northern Africa in the south, the eastern parts of the Iberian Peninsula in the west and Mesopotamia in the east, with a contact zone between mitochondrial clades in southeastern Europe. In this study, a large number of genetic samples collected from the whole distribution range of the species were

analyzed to build on previous studies, and investigate the phylogeography of the species, confirming and fine tuning the split zones among the existing mitochondrial clades. We found that the species is characterized by three mitochondrial clades, which we describe as B, C1 and C2. The divergence time of clades B and C, as well as that of clades C1 and C2 were estimated using three different approaches, and were dated to around 350K years and 120K years before present, respectively. Species distribution modelling was used to determine suitable areas for the three mitochondrial clades, for both the present and the last glacial maximum (or for both the present and the year 2070). Results indicate a serious threat for the future conservation of *M. capaccinii* due to predicted climate change and the resulting loss of suitable habitats. Thus, the specific habitat requirements and the narrow overlap of current and possible future ranges of *M. capaccinii* clearly suggest priority conservation strategies for this vulnerable bat species.

Keywords: species distribution modelling, phylogeography, glacial refugia, mitochondrial clades, temporal distributions, *Myotis capaccinii*

Contact: kanatgurun@yahoo.com

The complex phylogeographic history and speciation in subterranean Blind Mole Rats (*Spalax* and *Nannospalax* sp.)

Ortaç Çetintaç¹, Halil Mert Solak¹, İbrahim Raşit Bilgin², Faruk Çolak¹, Mikhail Rusin³, Nedko Nedyalkov⁴, Mustafa Sözen¹, Ferhat Matur⁵, Alexey (Oleksiy) Yanchukov¹

¹Zonguldak Bülent Ecevit University

²Boğaziçi University

³Kyiv Zoo

⁴Bulgarian Academy of Sciences

⁵Dokuz Eylül University

The blind mole rats (BMR - *Spalax* and *Nannospalax* sp.) are long-lived, solitary subterranean rodents characterized by slow dispersal found over a large distribution area from Egypt to the Caspian. We have sampled the (i) six out of seven *Spalax* species and (ii) majority of known *Nannospalax* populations, with Anatolia particularly well-represented, and constructed their most detailed, up-to-date, molecular phylogeny based on partial mtDNA sequences. The most basal lineages within *Spalax* have surprisingly disconnected geographic ranges respectively in the Carpathian and the North Caucasus, with more recently diverged groups found in Ukraine. The genus *Nannospalax* includes two species complexes (*N. ehrenbergi* and *xanthodon+leucodon*) with more >70 chromosomal races (CFs) combined, but the phylogenetic relationship among cytogenetically diverse parapatric populations is still not clear. The *xanthodon+leucodon* complex includes two highly diverged groups, which correspond neither to the current taxonomical division nor to the underlying geography: i.e. one major branch combines populations from as far as the Aegean island(s) and the mountains of the South Caucasus, while the other includes populations centered around Central Anatolia and the Taurus mountains. We combine our mtDNA results with the recently published microsatellite, behavioral and morphological data, and hypothesize on the complex phylogeographic history and the major speciation events within the Spalacinae subfamily. As we are still in the process of obtaining and analyzing the genome-wide ddRAD-seq marker data, we will soon be able to gain better insight into the speciation process in this fascinating animal group.

Keywords: Phylogeography, Cytochrome b, *Nannospalax xanthodon*

Contact: ortacetintas@gmail.com

Multiple parental individuals contributed to common gene pool of the hybridogenic parthenogenetic lizards *Darevskia bendimahiensis* and *D. Sapphirina*

Meriç Erdolu¹, Mehmet Somel¹, David Tarkhnishvili², Mehmet Kürşat Şahin³, and Alexey Yanchukov⁴

¹Middle East Technical University, Faculty of Science, Department of Biology, Ankara, Türkiye

²Iliia State University, Tbilisi, Georgia

³Karamanoglu Mehmetbey University, Karaman, Türkiye

⁴Zonguldak Bülent Ecevit University, Zonguldak, Türkiye

The rock lizards *Darevskia* includes dozens of sexually reproducing species and seven diploid parthenogenetic species that evolved via hybridization between the bisexuals. A fundamental question is how often such hybridization events occur in nature, which can be addressed by examining the genetic diversity of the present-day parthenogenetic populations. In this study, we genotyped 18 individuals from parthenogenetic taxa *D. bendimahiensis* and *D. sapphirina*, endemic to eastern Türkiye, and 42 from their parental taxa *D. raddei vanensis* and *D. valentini*, at 277725 autosomal ddRAD-seq loci. First, we show that *D. bendimahiensis* and *D. sapphirina* are not reciprocally monophyletic, but represent a genetically uniform group which could theoretically have descended from a single ancestral F1 genotype / one pair of parental individuals. To investigate this further, we focused on loci with 3 alleles per locus in the hybrid populations. The third allele in hybrids could have appeared by mutation within a parthenogenetic lineage, or inherited from additional parental genotypes. We found that (i) such third alleles' frequencies in the parthenogens are correlated with those in the parental populations; whereas the same alleles' frequencies were uncorrelated between the two parents, and (ii) some loci contained three alleles with >1 nucleotide difference from each other. This appears compatible with >2 different parental haplotypes present in the parthenogenetic population. Further, we found that the third alleles, when unambiguously assigned to the maternal or paternal parent, are more frequent on the paternal side. We conclude that *D. bendimahiensis* and *D. sapphirina* likely emerged from multiple hybridization events.

Keywords: Hybridization, Parthenogenesis, *Darevskia* lizards, RAD-seq, Reticulate evolution

Contact: mr.erdolu@gmail.com

Evolutionary Genetics of Behcet's Disease

Elif Kaplan¹ and Efe Sezgin¹

¹Izmir Institute of Technology

Behcet's Disease (BD) is an auto-immune/autoinflammatory complex disease which causes inflammation of the blood vessels. The underlying cause for BD is unknown. The highest prevalence is seen in populations along the ancient silk road, raising the possibility that it may have its origins along these historic trade routes. The genetic makeup that increases BD susceptibility in modern populations might have been advantageous for certain environmental stress factors such as resistance to infections and pathogens. Such advantage is expected to leave signs of selection on the genes associated with BD. Our aim is to find out the nature of this selection by comparing the ancient DNA variation with the contemporary modern human variation. In our previous studies, we have observed a possible recent selection on HLA-B as suggested in previous reports, but recent selection signature was not unique to HLA-B, 14 other BD associated genes also showed recent selection including other MHC loci such as HLA-G, and other genes such as KCKN9 and NOD2 showed even a stronger selection than HLA-B. Therefore, we hypothesized that we can independently test and compare the recent selection suggestion by comparing the allele frequencies of BD associated alleles in ancient and modern populations. Recent selection might have increased BD associated allele frequencies in modern day

populations compared to ancient populations, through adaptation to or selection from environmental factors. We will also support our hypothesis by comparing the genomic variation in contemporary Asian populations with the European populations- which have a lower risk for Behcet's Disease.

Keywords: Behcet's Disease, Selection, Population Genetics, Ancient DNA Variation, Bioinformatics.

Contact: elifkaplan404@gmail.com

Body size relates to the level of cancer suppression across non-human primates

E. Yağmur Erten¹, Amy Boddy², Hanna Kokko³

¹University of Jyväskylä

²University of California, Santa Barbara

³University of Zurich

Virtually all multicellular organisms are susceptible to cancer due to oncogenic mutations that can occur during cell divisions. Although larger species typically require more cell divisions to reach and maintain their body size than smaller ones, cancer incidence across species does not increase with body size (Peto's paradox). Selection for stronger cancer suppression can explain how large species are not more cancer-prone than smaller species. Here, we take advantage of a high-resolution cancer database and use a maximum likelihood modelling approach to study whether body size relates to the level of cancer suppression in non-human primates. We conceptualize cancer defences as the number of mutational hits until cancer and the rate at which these hits occur, with more mutational hits and lower rate implying more robust cancer defences. To estimate these parameters, we fit 10 multistage cancer models to the cancer incidence data. Our models differ in how cancer defences relate to body size, species differences, and sex differences and we compare them with an information-theoretic approach. Our results suggest that larger species have lower rate of oncogenesis than smaller species, suggesting stronger cancer suppression. Interestingly, most of our best-supported models indicate a higher rate of oncogenesis in females than males. Overall, our approach lends support to the hypothesis that stronger cancer suppression could resolve Peto's paradox. Considering life history as a factor that influences the evolution of cancer suppression could lead to a better understanding of the diverse cancer defence mechanisms found in nature.

Keywords: life history, cancer, body size evolution, Peto's paradox, comparative oncology

Contact: erten.yagmur@evobio.eu

BIOINFORMATICS SESSION

Keynote address: From the Stone Age to today - disease, epidemics and the emergence of genetic variants for chronic inflammatory diseases

Ben Krause-Kyora

Institute of Clinical Molecular Biology, University of Kiel

Contact : b.krause-kyora@ikmb.uni-kiel.de

Phylogeny-based inferences in protein function

Ogün Adebali

Sabancı University

Evolutionary conservation is a fundamental resource for predicting the substitutability of amino acids and the loss of function in proteins. However, using multiple sequence alignment alone—without considering the evolutionary relationships among sequences—results in the redundant counting of evolutionarily related alteration events as if they were independent. We developed a new method, PHACT, that predicts the pathogenicity of missense mutations directly from the phylogenetic tree of proteins. PHACT travels through the nodes of the phylogenetic tree and evaluates the deleteriousness of a substitution based on the probability differences of ancestral amino acids between neighboring nodes in the tree. Moreover, PHACT assigns weights to each node in the tree based on their distance to the query organism. For each potential amino acid substitution, the algorithm generates a score that calculates the effect of substitution on protein function. The experiments demonstrated that our method outperformed the widely used pathogenicity prediction tools (i.e., SIFT and PolyPhen-2) and achieved a better predictive performance than other conventional statistical approaches presented in dbNSFP. Moreover, we aim to develop machine-learning models to achieve better predictive performance so clinicians can use our tool in practice. In parallel, we develop different phylogeny-based algorithms with similar methodologies to infer coevolving amino acids, which might contribute to understanding the proteins' molecular functioning. Finally, we aim to distinguish the pathogenic loss-of-function and gain-of-function mutations. Here we employ a similar strategy that benefits from phylogenetics and ancestral reconstruction.

Keywords: Phylogenetics, pathogenicity prediction, missense mutations, co-evolution, Loss-of-function, Gain-of-function

Contact: oadebali@sabanciuniv.edu

In silico discovery of epitopes of gag and env proteins for the development of a multi-epitope vaccine candidate against Maedi Visna Virus using reverse vaccinology approach

Ecem Su Koçkaya¹ , Hüseyin Can¹ , Yalçın Yaman² , Cemal Ün¹

¹ Ege University Faculty of Science Department of Biology Molecular Biology Section, İzmir, Turkey

² Department of Breeding and Genetics, Bandırma Sheep Breeding Research Institute, Bandırma, Balıkesir, Turkey

Maedi Visna Virus (MVV) causes a chronic viral disease in sheep. Since there is no specific therapeutic drug that targets MVV, development of a vaccine against the MVV is inevitable. This study aimed to analyze the gag and env proteins as vaccine candidate proteins and to identify epitopes in these proteins. In addition, it was aimed to construct a multi-epitope vaccine candidate. According to the obtained results, the gag protein was detected to be more conserved and had a higher antigenicity value. Also, the number of alpha helix in the secondary structure was higher and transmembrane helices were not detected. Although many B cell and MHC-I/II epitopes were predicted, only 19 of them were detected to have the properties of antigenic, non-allergenic, non-toxic, soluble, and non-hemolytic. Of these epitopes, five were remarkable due to having the highest antigenicity value. However, the final multi-epitope vaccine was constructed with 19 epitopes. A strong affinity was shown between the final multi-epitope vaccine and TLR-2/4. In conclusion, the gag protein was a better antigen. However, both proteins had epitopes with high antigenicity value. Also, the final multi-epitope vaccine construct had a potential to be used as a peptide vaccine due to its immuno-informatics results.

Keywords: MVV, B cell epitopes, MHC-I/II epitopes, immuno-informatics, peptide-based vaccine

Contact: esukockaya@gmail.com

SWAMPy - Simulating SARS-CoV-2 Wastewater Amplicon Metagenomes in Python

Fatma Rabia Fidan¹, Will Boulton², Nicola De Maio³, Nick Goldman³

¹Middle East Technical University, Department Of Biological Sciences, Ankara, Turkey

²University of East Anglia

³EMBL - EBI

Wastewater surveillance and sequencing have been essential tools for dealing with the SARS-CoV-2 pandemic as they proved useful in tracking variants and their prevalence in an unbiased manner. It has been shown that wastewater surveillance correlates with clinically reported case numbers and it is possible to detect an emerging variant from wastewater samples earlier than its detection at hospital clinics. This data is critical for public healthcare decisions like policies regarding the measures taken against variants of concern. Since such surveillance has important consequences, it is also vital to test and validate the surveillance methodologies and software packages, which in turn creates a need for a realistic SARS-CoV-2 wastewater sequencing data simulator. Existing sequencing simulators fail to cover all of the specialised set of characteristics we observe in this type of data. We set out to create a simulator, namely SWAMPy, that accounts for the essential characteristics of the data that were not covered by the existing simulators such as PCR and other library preparation errors, RNA degradation, differential variant abundance in the wastewater and primer set-specific amplicon abundance. SWAMPy is publicly available at <https://github.com/goldman-gp-ebi/sars-cov-2-metagenomic-simulator> under GNU general public license.

Keywords: simulation, SARS-CoV-2, wastewater, sequencing

Contact: f.rabiafidan@gmail.com

Genomic Basis of Saltwater Adaptation in *Alburnus tarichi*

Malavi Sengupta¹, Vahap Eldem², Ayca Arslan Ergul¹, Mehmet Somel³, Can Alkan¹

¹Bilkent University

²University of Istanbul

³Middle East Technical University

Osmoregulation is the maintenance of fluid balance and the regulation of the concentration of electrolytes in the bodily fluids of an organism. For freshwater fish, this involves maintaining a higher concentration of solutes in bodily fluids, and vice-versa for marine fish. Anadromous fish have to do both, at different stages of their life cycle. One such fish is the Pearl Mullet, *Alburnus tarichi*, which is found in Lake Van, a highly saline and alkaline (pH 9.7-9.8) lake in Turkey. Being endemic, *A. tarichi* is of immense ecological and socio-economic importance, but how it evolved to adapt to Lake Van remains to be understood. The aim of this project is to understand the genomic basis of osmoregulation in highly saline and alkaline conditions. Gene variants that confer a selective advantage are subject to positive selection, and become fixed in the population over time. So, positively-selected genes in the *A. tarichi* lineage were sought. For this, single copy orthologs (SCO's) were found for 4 species, *Danio rerio*, *Cyprinus carpio*, *Sinocyclocheilus grahami*, and *Alburnus tarichi*. Then, the four DNA sequences in each SCO cluster were aligned and analysed using CODEML, giving us 30 positively-selected genes. Then, GO annotations for these genes, and positively-selected sites within them were found. Then, *Alburnus sellal* was added to this analysis to find sites specific to saltwater adaptation. Further studies in this direction will lead us to the genomic basis of adaptation to a highly alkaline environment, and help us understand *A. tarichi*'s unique ecological position and physiology.

Keywords: *Alburnus tarichi*, adaptation, osmoregulation, conservation, Lake Van

Contact: malavi@unam.bilkent.edu.tr

The connection between Sea of Marmara biodiversity and mucilage occurrence incidence

Arzu Karahan¹, Selin Deliceirmak², Mertcan Esti¹, Evrim Kalkan Tezcan¹, Esra Öztürk¹, Hasan Örek¹

¹Middle East Technical University, Institute of Marine Sciences, 33731, Erdemli, Mersin, Turkey

²Near East University, Faculty of Arts and Sciences, Department of Molecular Biology and Genetics, Nicosia, Turkish Republic of Northern Cyprus

Mucilage shapes because of the sudden death of certain bacteria and/or phytoplankton right after their bloom. During the processes, they do not sink and decay quickly; as a result, polysaccharides are produced, and the hydrocarbons increase in the seawater. Mucilage is also formed by the benthic filamentous macroalgae besides the pelagic species in the water column. The mucus-like structure negatively affects the organisms by either accumulating on the soft and hard bottom of the seabed or by directly covering the organisms. This study aims to determine the taxa responsible for mucilage formation in the Sea of Marmara using 16S amplicon sequencing and metabarcoding techniques (18S and ITS) and to understand their possible effects on the Sea of Marmara ecosystem. Within this scope, the prokaryotic (archaea and bacteria) and eukaryotic diversity in 30 mucilage samples taken from 23 stations representing a large part of the Sea of Marmara are studied using the Next Generation Sequencing technique. In the study, the prokaryotic and eukaryotic diversity of the mucilage in the Çınarcık Pit and İzmit Bay stations has been revealed by now. Bioinformatic analysis of the other 28 samples is ongoing. Interpreting the genetic data with the physical and chemical parameters, those collected from the mucilage sampling stations within this study scope and the other stations representing the whole Sea of Marmara are essential to reveal the environmental triggers that cause mucilage formation or formation induced by mucilage.

Keywords: Mucilage, Sea of Marmara, 16S, 18S, ITS, metabarcoding

Contact: arzucar@metu.edu.tr

Speciation status, complex population history and extinction mechanisms of European Wild Ass

Mustafa Özkan¹, Kanat Gürün¹, Eren Yüncü¹, Kivılcım Başak Vural¹, Ali Akbaba^{2,3}, Fatma Rabia Fidan¹, Ekin Sağlıcan¹, N. Ezgi Altınışik⁴, Dilek Koptekin⁵, Kamilla Pawłowska⁶, Ian Hodder⁷, Sarah E. Adcock⁸, Benjamin S. Arbuckle⁹, Sharon R. Steadman¹⁰, Gregory McMahon¹¹, Yılmaz Selim Erdal⁴, Cemal Can Bilgin¹, Anders Götherstrom¹², Füsün Özer⁴, Mehmet Somel¹

¹Middle East Technical University, Department Of Biological Sciences, Ankara, Turkey

²Ankara University, Department of Anthropology, Ankara, Turkey

³University of Nevada, Department of Anthropology, Reno, NV, USA

⁴Hacettepe University, Department of Anthropology, Ankara, Turkey

⁵Middle East Technical University, Department of Health Informatics, Ankara, Turkey

⁶Adam Mickiewicz University, Department of Palaeoenvironmental Research, Poznan, Poland

⁷Stanford University, Department of Anthropology, Stanford, USA

⁸New York University, Institute for the Study of the Ancient World, NY, USA

⁹University of North Carolina at Chapel Hill, Department of Anthropology, Chapel Hill, NC, USA

¹⁰SUNY Cortland, Department of Sociology/Anthropology, NY, USA

¹¹University of New Hampshire, Classics, Humanities, and Italian Studies Department, Durham, NH, USA

¹²Stockholm University, Department of Archaeology and Classical Studies, Stockholm, Sweden

Equus hydruntinus, commonly known as European wild ass, is an equid once roamed across West Eurasia and went extinct in the Holocene. Morphological characteristics and ancient DNA studies on mitochondrial sequences presented a conundrum about its taxonomic status: either a distinct species or a subspecies of Asiatic wild ass, *Equus hemionus*. The timing and dynamics of its extinction have also remained unclear. In this study, we present ancient genomes of three morphologically ambiguous Anatolian equids dating to the 1st millennium BCE, sequenced to coverages 6.4-0.6x. Mitochondrial DNA signatures confirmed these individuals indeed were *E.hydruntinus* and were outside Asiatic wild ass genomic diversity. We also revealed a complex population history of non-caballine equids as sex biased gene flow between European and Iranian wild asses and different levels of genetic affinity between Eurasian and African asses. Finally, runs of homozygosity analyses indicate stark population decline in Anatolian wild asses by the mid-1st millennium BCE, consistent with their recent loss from the zooarchaeological record.

Keywords: Ancient DNA, *Equus hydruntinus*, demography, taxonomy, population genetics

Contact: mustafa.ozkan.sci@gmail.com

MICROBIAL EVOLUTION SESSION

Temperature Dependent Infection Risk of Plant Diseases: Peach-*Monilinia* spp. Pathosystem as a Model

Baran Taylan Fidanoğlu¹, Burcu Mestav², Hilal Özkılıç^{1,3}

¹Canakkale Onsekiz Mart University, School of Graduate Studies, MSc Program in Molecular Biology and Genetics, Canakkale/Turkey

²Canakkale Onsekiz Mart University, Dep. of Statistics, Canakkale/Turkey

³Canakkale Onsekiz Mart University, Dept. of Molecular Biology and Genetics, Canakkale

Temperature is an important factor on the onset, progression and severity of infection in fungal plant diseases. These effects may show different patterns on the basis of host and species. Understanding of the temperature adaptations of pathosystems is also important for appropriate disease managements, especially considering climate changes. The most important species that cause brown rot in peach fruits worldwide are known as *Monilinia fructicola* and *M. laxa*. In this study, *Monilinia*-peach infections were evaluated with in vitro pathogenicity tests at four different temperatures, considering both the relationships of the species with their hosts and the different temperature conditions they are exposed. Temperature significantly affected the both the incubation periods and relative area under disease progression curve (RAUDPC) values. While the incubation period was the shortest at 35°C and the disease severity was the highest at 4°C for both species. The piecewise regression (PWR) model identified statistically significant two main clusters for disease development, occurring at relatively cold (4°C and 11°C) and warm temperatures (23°C and 35°C). The PWR model also used to estimate the temperature value between these two clusters, which is the breakpoint leading to the sudden disease development. The PWR model was also used to predict different points on the function curve (such as the day when sudden disease severity is likely to occur). The dynamics of pathosystems are affected by climate and environmental changes, and the approaches used in the evaluation of this process will also make a significant contribution for the epidemiology predictions.

Keywords: *Monilinia*, peach, disease, temperature

Contact: barantaylanfidanoglu@gmail.com

LotuS2: An ultrafast and highly accurate tool for amplicon sequencing analysis

Ezgi Özkurt¹, Joachim Fritscher¹, Nicola Soranzo², Duncan Y. K. Ng¹, Robert P. Davey², Mohammad Bahram³, Falk Hildebrand¹

¹Quadram Institute Bioscience & Earlham Institute

²Earlham Institute

³Swedish University of Agricultural Sciences & University of Tartu

Amplicon sequencing is an established and cost-efficient method for profiling microbiomes. However, many available tools to process this data require both bioinformatics skills and high computational power to process big datasets. Furthermore, there are only a few tools that allow for long-read amplicon data analysis. To bridge this gap, we developed the LotuS2 (Less OTU Scripts 2) pipeline, enabling user-friendly, resource-friendly, and versatile analysis of raw amplicon sequences. In LotuS2, six different sequence clustering algorithms as well as extensive pre- and post-processing options allow for flexible data analysis by both experts, where parameters can be fully adjusted, and novices, where defaults are provided for different scenarios. We benchmarked three independent gut and soil datasets. When compared to other pipelines, LotuS2 was on average 29 times faster and could better reproduce alpha and beta diversity of technical replicate samples. Further benchmarking a mock community with known taxon composition showed that, compared to the other pipelines, LotuS2 recovered a higher fraction of correctly identified genera and species and a higher fraction of reads assigned to true taxa (83% & 98% and 48% & 57%, respectively). To conclude, LotuS2 is a lightweight and user-friendly

pipeline that is fast, precise and streamlined. High data usage rates and reliability enable high-throughput microbiome analysis in minutes.

Keywords: microbiome, short read sequencing, amplicon data analysis, 16S rRNA, ITS

Contact: ezgi140@gmail.com

Sampling Theorem for Biology

Yekbun Adiguzel

*Department of Medical Biology, School of Medicine, Atilim University, Kizilcasar Mah. 06836
Incek, Golbasi, Ankara, Turkey*

Nyquist-Shannon sampling theorem is a theory behind the means for determination of minimum sampling frequency that will result in apt data and distortion-free understanding of the system dynamics. Sampling theorem states that a signal must be sampled above the Nyquist rate. Associated theoretical framework was investigated separately for certain research fields in ecology, more specifically the movement ecology, not necessarily mentioning the theorem, e.g. in case of oceanography (1) and animal movements (2-7). Accordingly, it is suggested that frequency- and phase-dependent interactions, and hence sampling theorem, is of biological relevance and importance. Different oscillation vs observation rates can even result in misinterpretation of data, which may perhaps not be the case in the macroscopic world due to low frequencies, but the theorem can still be benefited. We will introduce the concept, give examples, and hopefully draw attention to this less known concept in the biology discipline. Microscopic, and hypothetical molecular examples are also aimed to be included.

Keywords: Sampling, sampling rate, sampling frequency, sampling duration, Nyquist-Shannon sampling theorem

Contact: yekbun.adiguzel@atilim.edu.tr

Game theoretical analysis of cooperation and cheating among lipase producing *Yarrowia lipolytica* sub-cultures

Özgür Yüksel¹ and Emrah Nikerel¹

¹*Yeditepe University*

Game theory is a mathematical tool for understanding social dilemmas and solving conflicts of interest between agents with set of strategies and goal of maximizing personal interests (payoffs). Among microorganisms, different phenotypes, such as complete or partial failure in exoenzyme production, can be regarded as strategies in a game where growth rates of cells represent fitnesses of each strategy. Consequently, the productivity of the population is determined by the interplay between the exoenzyme producer “Cooperator” and the exoenzyme non-producer “Cheater” sub-cultures. Among non-conventional yeasts, *Yarrowia lipolytica* can efficiently produce extracellular lipases to degrade hydrophobic substrates such as fats and fatty acids. In this thesis a game theoretical model is constructed to analyze the evolutionary dynamics and the lipase productivity of the *Y. lipolytica* population in terms of structured mathematical models. Fermentation model results indicate that fed-batch mode simultaneously promoted the Cheating and the lipolytic activity compared to batch mode which signifies the importance of the specific productivity independent from sub-culture frequencies. The evolutionary stability of the “Cooperator” and the “Cheater” sub-cultures are analyzed with a “stable

state finder algorithm". Two distinct game regimes were identified. When the lipase production cost is low, Cooperators dominate the population. At intermediate and higher costs, Cooperators coexist with Cheaters. These regimes correspond to "No-Conflict" and "Snowdrift" regimes respectively. The evolutionary stable states of the "multi-player fermentation game" is affected by the initial conditions. At higher initial cell densities equilibrium frequency of the Cooperators decreases. Cooperators benefit from higher initial olive oil concentrations and consequently the lipolytic activity increases. Also, Cheaters benefit from higher initial oleic acid concentrations and as a result the lipolytic activity decreases. The methodology of finding the Evolutionary stable state can also be applied to scenarios where different species are considered as players. In growing biotechnological literature, co-cultures are becoming prominent examples of such scenarios.

Keywords: Evolutionary Game Theory, Cooperation and Cheating, *Yarrowia Lipolytica*

Contact: ozguryuksel@live.com

Understanding individual heterogeneity in ageing from stochastic gene expression dynamics in *E.coli*

Murat Tugrul

Freie Universitat Berlin

Ageing structures populations and affects the pace of evolutionary dynamics such as the fate of a new mutation. Remarkably, ageing patterns and rates are not fixed and show variation across species, populations, and individuals. Most studies focused on genetic and environmental effects on the diversity and neglected the individual heterogeneity which is known to contribute significantly. At the molecular level, ageing is considered due to "damage" accumulation within cells, disrupting a healthy flow of bioprocesses. The damage accumulation can be considered under a direct influence of gene expression driven by genetic, environmental, and stochastic processes. We still stand in need of careful analyses to understand the relation between gene expression and ageing patterns at individual single-cells which is only be feasible using bacterial systems. Bacteria have been long considered as not ageing, based on arguments of symmetric divisions and observations at population level. This view was changed in the last two decades thanks to developed microfluidic and fluorescent microcopy techniques. Both reproductive and chronological ageing in bacteria have been showed but little is known for the link between stochastic dynamics of gene expression and individual heterogeneity in ageing. In our studies, we conduct experiments to obtain the expression dynamics of some key genes and the demographic fates at individual *E. coli* cells in microfluidic platforms under fluorescent microscope. We develop mathematical models to interpret stochastic gene expression and heterogenous demographic signals for damage and ageing as well as to project population dynamics and evolution.

Keywords: bacterial ageing, gene expression, mother machine, individual heterogeneity, stochastic dynamics, evolutionary demography

Contact: murat.tugrul@fu-berlin.de

ANCIENT DNA SESSION

Keynote address: Why theoreticians love their ‘what if?’ scenarios

Hanna Kokko

University of Zurich

I will reflect on theory building in evolutionary ecology: why theoreticians sometimes build models that intentionally keep out some factors known to operate in nature; we might even add features to their models that are not known to exist in nature. My examples will highlight some recent work on sexual conflict, mate choice in the presence of inbreeding, and the maintenance of polymorphisms. Towards the end of my talk I will also admit that eureka moments may actually come from field data... here I will show how a marine midge *Clunio marinus* manages to ‘transform time into space’, with important eco-evolutionary consequences for maintaining diversity in temporal niches.

Contact: hanna.kokko@ieu.uzh.ch

Best practices for DNA extraction from charred seeds: The Kaymakçı archaeological case

Funda Ö. Değirmenci¹, Asiye Uluğ², Çiğdem Kansu³, Christina Luke⁴, Christopher H. Roosevelt⁴, Zeki Kaya⁵

¹Ahi Evran University

²Kafkas University

³Tekirdağ Namık Kemal University

⁴Koç University

⁵Middle East Technical University

The Marmara Lake basin in the middle Gediz Valley hosted a variety of small to large, unfortified and fortified settlements and citadels in the Middle and Late Bronze Ages of the second millennium BCE. Excavations at Kaymakçı, the largest citadel site in the region, yielded large numbers of archaeobotanical samples that suggest diverse traditions of crop cultivation for both human and animal consumption. Among these 3500–4000 year-old samples were highly charred seeds of *Triticum aestivum/durum* L., *Hordeum vulgare* L., *Vicia ervillia* (L) Willd., *Cicer arietinum* L., and *Vitis vinifera* L. To ensure high DNA yield, it is essential to research and identify best practices for ancient DNA extraction and to optimize them for various charred crop seeds. Among the methods tested, the modified CTAB method yielded high concentrations of DNA compared to several commercial kit protocols. In general, low quantity and degraded quality are the major constraints in PCR amplification of DNA from charred plant seeds. Thus, high quantity and good quality genomic DNA is needed. Using the whole genome amplification kit, as an alternative to the tedious template DNA amplification process, through several PCR runs was a good solution to overcome this problem. As proof of endogenous DNA, partial fragments of 26SrDNA and the ribulose-1,5 biphosphate carboxylase (rbcL) gene were amplified successfully. Comparative sequence analysis of partial 26SrDNA and the rbcL gene from ancient seeds and their modern relatives showed high levels of similarity. These homologous sequences have distinct substitutions and indels at specific positions. Following these methods, paleogenetic analysis of amplifiable aDNA can then provide multiple, well-characterized, and potentially highly polymorphic genetic loci to answer archaeobotanical and archaeological questions regarding crop practices (including domestication and transport) across Anatolia.

Keywords: Ancient DNA, charred seeds, 26SrDNA, ribulose-1,5 biphosphate carboxylase gene

Contact: funda07@gmail.com

The effect of Neolithization on complex diseases in Anatolia: preliminary results

İdil Taç¹, Ulaş Işıldak², Hande Çubukcu¹, Damla Karadavut¹, Kıvılcım Başak Vural², Ezgi Altınışik³, Yılmaz Selim Erdal³, Mehmet Somel², Füsün Özer^{3,4}, İdil Yet¹ and Gülşah Merve Kılınç^{1,2}

¹Department of Bioinformatics, Graduate School of Health Sciences, Hacettepe University, 06100, Ankara, Turkey

²Department of Biological Sciences, Middle East Technical University (METU), Ankara, Turkey

³Department of Anthropology, Hacettepe University, Ankara, Turkey

⁴Human G Lab, Department of Anthropology, Hacettepe University, Ankara, Turkey

With Neolithization, human societies experienced profound changes in subsistence strategies, cultural and social relations, encountered new pathogens with animal husbandry and gradually transitioned to a settled life. Anatolia acting as a bridge between east and west, has closely witnessed these drastic changes in cultural process. In this study, we focused on obesity and type 2 diabetes (T2DM), two complex metabolic diseases with high prevalence in Turkey. We analyzed ancient and modern genomes to understand the evolutionary history of this traits after the Neolithization. To maximize the use of low-coverage ancient genome sequencing data, we calculated frequency for each SNP using an algorithm that finds values that maximize the log-likelihood calculated for each population using the binomial probability distribution. To determine whether the frequency change between periods was statistically significant, we used logistic regression, followed by ANOVA and Tukey's test. We also calculated the genetic distance between ancient and modern Anatolian periods for trait-associated SNPs using the F_{st} statistic and compared the results with evolutionary neutral regions. Our preliminary analyses revealed that the frequency change of trait-associated SNPs between periods was similar for neutral and obesity (p -value=0.1376115) and significantly different for T2DM (p -value=0.0000310). Using the F_{st} comparison method, we found that frequency of T2DM (p -value=0.0179) and obesity (p -value=0.0159) differed more between Neolithic and present-day Anatolia than expected for neutral. The significantly higher mean allele frequencies in regions associated with obesity and T2DM compared to neutral regions may signal adaptive changes to the changing processes between the Neolithic and present-day Anatolian periods.

Keywords: Ancient DNA, population genetics, complex disease, obesity, type 2 diabetes, Anatolia, Neolithization

Contact: idiltacc@gmail.com

Determination of DNA preservation in human bones from Anatolian Neolithic by a pre-screening method based on FTIR spectroscopy

Fatma Küçük Baloğlu¹, Merve Nur Güler², Sevgi Yorulmaz², Nergis Bilge Karabulut², Damla Kaptan², Ayça Küçükakdağ Doğu², Mehmet Somel², Füsün Özer³, Yılmaz Selim Erdal³

¹Giresun University

²Middle East Technical University

³Hacettepe University

The most important problem encountered in ancient DNA (aDNA) studies is the gradual loss of human or animal DNA as a result of factors such as pH, temperature, humidity, bacterial activity in bone samples remaining under the soil for a long time. In temperate regions such as Anatolia, obtaining aDNA is a particularly serious problem and most of the genome sequenced samples contain limited endogeneous DNA. Genome sequencing of hundreds of samples that are not known to have good or bad DNA preservation imposes a heavy burden on projects in terms of budget and time. The aim of this study is to optimize a pre-screening method based on Fourier Transform Infrared (FTIR) spectroscopy, which is used to differentiate good and bad DNA preserved human bone samples, and to apply this

method to human bones belonging to the Neolithic period in Anatolia. Accordingly, we optimized a sample preparation method and continued with the determination of spectral bands, spectral band ratios and threshold values to be used in Attenuated total reflection (ATR)-FTIR spectroscopy technique with ancient human bone samples with known DNA preservation. Following this process, we examined unsupervised and supervised chemometric analysis based on these spectral bands to complement and confirm the results obtained in our ATR-FTIR spectroscopy studies. When all these results were evaluated together, we found that the pre-screening method based on FTIR spectroscopy coupled with chemometrics can achieve a high discrimination rate, indicating the power of this method in determination of DNA preservation in ancient human bones.

Keywords: Ancient DNA, Neolithic Period, FTIR Spectroscopy, Chemometric Analysis, DNA Preservation

Contact: fatmakucuk1984@gmail.com

ABSTRACTS OF POSTER PRESENTATIONS

Population genomics of Boğazköy: preliminary results

Mehmet Somel¹, Anders Götherström², Andreas Schachner³, Damla Kaptan¹, Dilek Koptekin¹, Duygu Deniz Kazancı¹, Füsün Özer⁴, Handan Üstündağ⁵, Kanat Gürün¹, N. Ezgi Altınışik⁴, Sevgi Yorulmaz¹

¹METU, Turkey

²U Stockholm, Sweden

³DAI, Germany

⁴Hacettepe, Turkey

⁵Anadolu U, Turkey

Ancient genomics today allows in-depth analysis of past human mobility dynamics as well as certain social traditions, such as consanguinity. Here we study the population of Boğazköy (Boğazkale), Çorum, Turkey, through seven millennia. The site hosted human settlements in the Early Chalcolithic (c.5000 BCE), a Hatti settlement, and an Assur trading post in the Middle Bronze Ages (c.2000 BCE), and most notably, the Hittite capital Hattuša (c.1500 BCE). After the fall of the Hittites and a period of abandonment, Boğazköy was the site of relatively modest sized settlements from the Iron Age to the Hellenistic, Roman, and Ottoman periods. A luring question is how much inter-regional immigration did Boğazköy experience through this time frame of significant social and political change. To address this, we generated 20 shotgun ancient genomes dating between the Early Bronze Age to the Ottoman periods, between 0.02x to 2.2x coverage (median 0.10x), and joined these with 13 published early and late Chalcolithic genomes from the same area. We use this dataset to study a number of questions: To what degree do we observe population genetic continuity in Boğazköy between the Chalcolithic and Middle Ages? How has overall genetic diversity changed over time? Can we observe genetically outlier individuals of migrant descent? Which periods have experienced the highest degree of change through gene flow, and were these events sex-biased? Can we observe changes in consanguinity patterns from the Bronze Age to the Middle Ages?

Keywords: ancient DNA, Bogazkoy, Hittites, mobility, demography

Contact: somel.mehmet@gmail.com

Which taxonomic character is more plastic in allopatric populations of the species?

Ebru Kıran Özdemir¹, Hasan Sevgili¹

¹Ordu University, Turkey

Understanding the speciation process is one of the most important and interesting topics in evolutionary biology. Adaptation and genetic drift are the key to biological phenomena that motivate the speciation process. In particular, geographical isolation separating populations from each other is the most important factor that initiates and accelerates speciation. It has been proven by many studies that there may be genetic/epigenetic and morphological differentiations from the ancestral population with the effect of genetic drift and natural selection in different ecological conditions due to the decrease or complete termination of gene exchange between geographically separated local populations of the ancestral parent population. However, the question of which of the evidences (morphological, behavioral and biochemical characters) is a better indicator of speciation is always on the agenda of systematics. Bush-crickets are one of the best model organisms in the study of ecological and evolutionary causes of genetic, morphological and bioacoustic differences within and between the species. In particular, the species with short wings, limited mobility and distribution in narrow areas provide very useful information for this type of research. In this study, possible variations in morphological characters, bioacoustics and cuticular hydrocarbon profiles (CHC) were investigated in the five allopatric populations of the short-winged bush-cricket *Isophya autumnalis* Karabağ, 1962. Morphological and bioacoustic characters were

found to be more flexible than CHC. These results indicate that morphology and behavioral characters can evolve faster than biochemical characters in allopatric populations. This study was partially supported by TUBITAK (No: 117Z068).

Keywords: Cuticular hydrocarbon, bioacoustic, allopatric population, Isophya, plasticity

Contact: hsevgili@gmail.com

Ecological and Climatological Investigation of Karagöl Alpine Lake at Bolkar Mountains Using Sedimentary Records

Betül Bitir¹ Soylu Korhan Özkan¹

¹Middle East Technical University / Institute of Marine Sciences, Turkey

Alpine lakes are sensitive ecosystems similar to polar regions. Understanding how ecosystems behave and adapt under climate changes due to human impacts could be hard due to their complex signals. Sedimentary archives in Alpine Lakes are important sources to observe recent changes in climate. The effects of climate change on these ecosystems can be easily monitored based on their limited catchment interactions. In particular, studies on diatom communities have important roles in assessing changing environmental conditions due to the good preservation of diatom frustules in the sediment and their strong response to climatic drivers. Assessing the abundance and alteration of the populations over time helps to identify historical different environmental conditions. It provides complementary information to apply different paleoecological methods together like XRF analysis, loss on ignition values, pigment, and diatom analysis to interpret the alterations over time. The aim of this study is to determine how biochemical properties have changed over time in Karagöl Alpine Lake at Bolkar Mountains. A further objective is to define the abundance and composition of diatom communities as key species to understand past environmental changes. Here, we use the paleoecological reconstruction approach by analyzing core sample from the Karagöl lake sediment via diatom analysis, XRF, pigment and LOI analysis. Our first results show different patterns of biogeochemical properties occurs through the core via XRF, pigment and LOI analysis. We will be able to provide an understanding of these high-altitude-sensitive ecosystems and their history. It will contribute to identifying the environmental changes and dynamics.

Keywords: Paleoecology, climate change, diatoms, alpine lakes, sedimentary records

Contact: betul.soylu@metu.edu.tr

Archaeogenetic analysis of Neolithic sheep from Anatolia

Damla Kaptan¹, Kıvılcım Başak Vural¹, Gözde Atağ¹, Eren Yüncü¹, Mehmet Somel¹, Füsün Özer²

Middle East Technical University, Turkey

Hacettepe University, Turkey

Among the first domesticated livestock, sheep was one of the most important protein sources for Neolithic societies in Southwest Asia. The zooarchaeological record suggests that domestication may have taken place in central to east Anatolia, although the exact location and timing is unknown. The wild ancestor of sheep is thought to be the Asian mouflon (*Ovis gmelinii*), which was by the early Holocene, distributed from West Anatolia to East Iran. Genetic studies on present-day breeds provide two major patterns: First, high levels of nuclear and mitochondrial DNA diversity are observed, which may indicate

that domestication involved multiple centers, or alternatively a large, heterogenous wild population. Secondly, present-day domestic sheep clusters into two groups; west (Europe) and east (Asia, Africa and Mediterranean Islands) based on genome-wide polymorphism data and proportions of mitochondrial haplogroups. However, it is still not very well understood when and how these patterns emerged. To address this, we used present results from our recent work as well as unpublished genomes produced from 15 individuals of early Holocene sheep bones from central and west Anatolia. Comparing these profiles with published modern breeds and ancient genomes from Neolithic and Bronze Age Kyrgyzstan sheep, we show that divergence between West and East appeared early, by 6000 BCE, and that the European and Anatolian sheep gene pools changed significantly since the Neolithic period.

Keywords: ancient sheep, ancient DNA, archeogenetics, population genetics, demography

Contact: damlakaptan@gmail.com

Sampling Theorem for Biology

Yekbun ADIGUZEL¹

¹ATILIM UNIVERSITY, Turkey

"Nyquist-Shannon sampling theorem is a theory behind the means for determination of minimum sampling frequency that will result in apt data and distortion-free understanding of the system dynamics. Sampling theorem states that a signal must be sampled above the Nyquist rate. Associated theoretical framework was investigated separately for certain research fields in ecology, more specifically the movement ecology, not necessarily mentioning the theorem, e.g. in case of oceanography (1) and animal movements (2-7). Accordingly, it is suggested that frequency- and phase-dependent interactions, and hence sampling theorem, is of biological relevance and importance. Different oscillation vs observation rates can even result in misinterpretation of data, which may perhaps not be the case in the macroscopic world due to low frequencies, but the theorem can still be benefited. We will introduce the concept, give examples, and hopefully draw attention to this less known concept in the biology discipline. Microscopic, and hypothetical molecular examples are also aimed to be included.

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Keywords: Sampling, sampling rate, sampling frequency, sampling duration, Nyquist-Shannon sampling theorem

Contact: yekbun.adiguzel@atilim.edu.tr

The Impact of Randall's Threadfin Bream, One of the Last Fish to Arrive in the Mediterranean Sea via the Suez Canal, on the Food Web and Fishery

Yagmur Akgun¹, Ekin Akoglu¹

¹METU, Turkey

The Eastern Mediterranean Sea is one of the most invaded marine ecosystems due to the impact of Lessepsian species, which migrated from the Red Sea to the Mediterranean Sea after the construction of the Suez Canal. The impacts of Lessepsian species on the indigenous fish and fisheries can be both positive and negative. Some Lessepsian species may positively affect the fishery at the expense of negatively impacting the native species and, hence, the ecosystem. This study was conducted to understand the impact of the Lessepsian species Randall's threadfin bream (*Nemipterus randalli*) on the food web and fishery dynamics in the Mersin Bay, using one of the most widely adopted marine food-web models, the Ecopath with Ecosim. Scenarios were applied to compare *N. randalli*'s impacts on other species and fishery. The results showed that *N. randalli* has a significant role in the Eastern Mediterranean food web. The findings highlighted that *N. randalli*'s increasing population in the Eastern Mediterranean negatively affects commercially exploited native fish species, red mullet, striped mullet, common pandora, and axillary seabream. We suggest that targeted fisheries exploitation of the species as an alternative management measure can reduce its negative impacts on the food web in the Eastern Mediterranean Sea.

Keywords: food web, Lessepsian, marine ecology, Mediterranean, Suez Canal

Contact: yagmur.drive22@gmail.com

The Relationship Between Zooplankton Community Structure and Methane Emission From Urban Ponds

Feride Avci¹, Sarah S Hasnain¹, Hilal Kiran¹, Nur Filiz¹, Meryem Beklioğlu¹

¹Middle East Technical University, Turkey

"CO₂ and CH₄ emissions from shallow freshwater bodies such as ponds are significant because of the large amounts of nutrient loading. In freshwaters, respiration produces CO₂ when there is oxygen; when there is no oxygen respiration produces CH₄. Methane can be oxidized by methane oxidizing bacteria (MOB) when the water is oxic again.

Zooplankton are a crucial component of freshwater food webs. Depending on their size and feeding type, they can prey upon other zooplankton, phytoplankton, or bacteria. MOB can be grazed by bacteria, and this would result in a decrease in methane oxidization. The hypothesis was that different zooplankton communities observed in different urban ponds can have a direct association with the amount of methane emission observed from these ponds. The research was conducted in 2021 summer in 15 urban ponds in Ankara between Lake Mogan and Imrahor River Valley. The results showed that there was an association between zooplankton community structure and methane emissions."

Keywords: limnology, ponds, zooplankton, greenhouse gas, methane emissions

Contact: ferideavci18@gmail.com

Zooplankton Size in Urban Ponds is Influenced by Bottom Up and Top Down Process

Hilal Kiran¹, Sarah S Hasnain¹, Feride Avcı¹, Nur Filiz¹, Meryem Beklioğlu¹

¹Middle East Technical University, Turkey

"Abstract: Zooplankton is an important element of the aquatic food chain. They serve as an intermediary species in the food chain, having a role in transferring energy from planktonic algae to the larger invertebrate predators and wish who in turn feed on them. Body size is the main trait in freshwater zooplankton since it is a strong determinant of predation pressure, performance in competition, and top-down control of algae.

The hypothesis was that zooplankton size diversity in urban ponds can be affected by bottom-up and top-down processes. The research was conducted in 2021 summer in 18 urban ponds in Ankara between Lake Mogan and Imrahor River Valley. The results showed that fish, macroinvertebrates, and DOC influenced zooplankton mean community size and size diversity. These results suggest that both top-down and bottom-up processes influence zooplankton size across ponds in Ankara"

Keywords: limnology, ponds, zooplankton, bottom-up and top-down effects, fish, invertebrate

Contact: hilalkiran16@gmail.com

Ecological niche modelling and phylogeography to reveal climate driven range shifts of white-throated dipper *Cinclus cinclus*

Sinem Özcan¹, Utku Perktas^{1,2}, Can Elverici¹, Özge Yaylalı¹

¹Hacettepe University, Turkey

²American Museum of Natural History, University of Kansas

"The dipper (*Cinclus cinclus*) is a species which lives across a wide range in the Palearctic region. Climatic fluctuations during the Quarternary caused many temperate zone species to alter their distributions, for example, during Last Glacial Maximum (LGM) some species had to narrow their distributions into refugial areas to survive. In this study we asked if historical refugia exist and whether there will be a threat for the species in the future according to future climatic projections.

Detailed status of the species during the Quarternary has not yet been investigated. Therefore, by combining mitochondrial DNA based Bayesian demographical analysis and ecological niche modelling, we tried to fill this gap. For niche modelling, we obtained elevation and bioclimatic data for present, past, and future by using three global climate models and three different representative concentration pathways. For the Bayesian-based demography analysis, we obtained previously published mitochondrial DNA markers (cytochrome b, ND2 and D-loop) and estimated effective population size change over time by using Extended Bayesian Skyline Plot analysis. Additionally, we created parsimony network.

Results of the demographic analyses and niche modelling were consistent. An allopatric Caucasian refugium was found during the last interglacial period compatible with haplotype network. After LGM, there was an increase in the effective population size. This study shows evidence of multiple refugia during climatic oscillations that took place over different time periods during the Quarternary. It has also been predicted that the distribution of the species will dramatically contract in the future."

Keywords: mitochondrial DNA, ecological niche modelling, phylogeography, passerine birds

Contact: sinemozcan1994@gmail.com

Monitoring Medium-Large Carnivores and Human-Wildlife Conflict in Sakarya

Melis Töke¹

¹Istanbul University, Turkey

"Medium-large carnivores such as Brown bears (*Ursus arctos*), Gray wolves (*Canis lupus*), Golden jackals (*Canis aureus*), and Red foxes (*Vulpes vulpes*) are keystone species for healthy ecosystems. In Turkey, carnivore populations have been facing anthropogenic pressures due to logging activities, overgrazing, livestock activities, retaliation killings, and many other reasons. These anthropogenic pressures cause conflict between humans and wild animal populations. Such carnivores are killed as a result of this conflict. Although the news in the press does not reflect all the cases where animals were killed, in reality, these cases are much higher. However, nature conservation and public awareness projects focused on the level of this conflict are extremely limited all over Turkey.

In this context, a monitoring study was designed to examine the level of conflict in Sakarya, where human activities and habitat fragmentation are intense. First, in 2021, a preliminary study was carried out by trace tracking of target species and interviewing the local people in the field. In the last 6 months, data on medium-large carnivores have been collected periodically through camera trap and trace tracking studies. The GPS data and habitat characteristics obtained from the stations were analyzed within the scope of QGIS, and the levels of conflict areas were tried to be determined. In addition, SWOT analyzes of these regions were made. The first step of the long-term monitoring study required in the region started with this project. For the continuation of their populations, further investigations must continue and nature conservation techniques should be implemented in the study area."

Keywords: Conservation, Wildlife, Cameratrapp, Carnivores, Conflict

Contact: tokemelis@gmail.com

CNV analysis of ancient human genomes

Eren Yüncü¹, Arda Söylev², Sevim Seda Çokoğlu¹, Dilek Koptekin³, Mevlüt Köz², Dila Nur Çakal², Can Alkan⁴, Mehmet Somel¹

Middle East Technical University, Biological Sciences, Turkey

Konya Food and Agriculture University, Computer Engineering, Turkey

Middle East Technical University, Health Informatics, Turkey

Bilkent University, Computer Engineering, Turkey

Copy number variations (CNVs) are structural variations (such as deletions and duplications of >50 bp), that have been described to evolve under purifying selection, associated with adaptation mechanisms and can have phenotypic influences. However because of the difficulties of genotyping CNVs from low coverage ancient DNA data, investigating CNV evolution has yet been mainly limited to modern-day genomes. by using the recently developed algorithm, "Copy number variation genotyping in ancient genomes and low-coverage sequencing data (CONGA)" we successfully genotyped >1 Kb deletions in ancient human genomes with coverages down to 0.5x and replicated stronger negative selection signal on deletions when compared to SNPs. In this study, we are presenting preliminary

findings on the effect of deletions on overall mutation load of Eurasian ancient genome dated between 1000 BP to 50,000 BP.

Keywords: copy number variations (CNVs), ancient DNA, CONGA, negative selection, mutation load

Contact: eyuncu@metu.edu.tr

Assessment of Genetic Relatedness Tools for Ancient DNA Using Pedigree Simulations

Şevval Aktürk¹, Igor Mapelli¹, Merve Nur Güler¹, Kanat Gürün¹, Ekin Sağlıcan¹, N. Ezgi Altınışık²,

Dilek Koptekin¹, Kuvılcım Başak Vural¹, Füsün Özer², Elif Sürer¹, Mehmet Somel¹

¹Middle East Technical University, Turkey

¹Hacettepe University, Turkey

Understanding the biological relationships among individuals retrieved in archaeological excavations has drawn attention for a long time in the ancient DNA field. The increasing number of SNP genotype or whole-genome sequence data has recently opened up the opportunity to estimate genetic relatedness using genome-wide markers. However, shotgun sequencing of ancient genomes at low depth causes low precision in genotype calling. To overcome these challenges different tools have been developed, including algorithms relying on genotype likelihoods and population allele frequencies (e.g. NgsRelate, Hangzhou et al. 2019), or tools comparing genotype mismatch rates between a pair (e.g. READ, Monroy-Kuhn et al. 2018). To systematically evaluate the reliability of these two most commonly used tools, NgsRelate and READ, in the presence of a limited number of SNPs and inbreeding, we used ancient genome data produced from simulated pedigrees. Our results show that related pairs can be accurately classified as first-degree, even down to 1K shared SNPs with 85% and 96% F1 scores using READ and NgsRelate, respectively. Distinguishing unrelated pairs from close relatives down to third-degree is possible with high accuracy (F1 = 99%) at 5K shared SNPs using NgsRelate. Further, with 10K shared SNPs, NgsRelate outperforms READ in the differentiation of third-degree from second-degree relatedness with a 94% F1 score (%80 for READ). Last, inbreeding (e.g. first cousin mating) leads to the overestimation of kinship coefficients. These results are promising but also call for exploring novel approaches for kinship estimation with ultra-low coverage genomes.

Keywords: ancient DNA, kinship coefficient , simulation, pedigree , inbreeding

Contact: sevvakturk96@gmail.com

The nematode assemblages of a lake ecosystem (Lake Korugöl Natural Park, Duzce, West Black Sea Coast of Turkey): ecology and biodiversity patterns with first reports of 10 genera to Turkey's nematofauna.

Taylan Çakmak¹

Düzce University Faculty of Agriculture, Department of Agricultural Biotechnology, Turkey

This research was carried out to reveal the nematode fauna of Korugöl, Düzce and to contribute to the nematode diversity of the Western Black Sea Region of Turkey. The research area is under the influence of the Euro-Siberian and Mediterranean biogeographical regions. Field studies within the scope of the study were carried out in 2021. As a result of the study, 29 family, 45 total under genus 46 taxa were identified from the total number of 855 individuals. 10 nematode taxon, namely Aporcelinus,

Baladorylaimus, Dorylaimoides, Euteratocephalus, Labronemella, Laimidorus, Lindseyus, Metateratocephalus, Paractinolaimus and Tripylrella are the first report for Turkey's nematofauna. Classification of nematodes according to their feeding forms were: 233 taxon (27.27 %) bacteriovore, 18 taxon (2.10%) fungivore, 13 taxon (1.51 %) herbivore, 140 taxon (16.35 %) predator and 451 taxon (52.77 %) omnivorous. Collected samples are stored in Düzce University Faculty of Agriculture Agricultural Biotechnology Nematode Collection.

Keywords: Biodiversity, Düzce, Korugöl, Lake, Nematofauna, Turkey

Contact: cakmaktaylan@gmail.com

An Archeogenomic Study of Bronze Age South West Anatolia

Sevgi Yorulmaz¹, Gözde Atağ¹, Kivılcım Başak Vural¹, N. Ezgi Altınışik², Sevinç Günel², Marie-Henriette Gates³, Umay Oğuzhanoğlu⁴, Füsün Özer², Mehmet Somel¹, Ali Metin Büyükkarakaya²

Middle East Technical University, Turkey

Hacettepe University, Turkey

Bilkent University, Turkey

Pamukkale University, Turkey

Western Anatolia, with its multitude of natural harbors, has been an important region for interregional maritime interactions since prehistoric times. The Early Bronze Age (EBA) presents notable evidence of widening trade routes, with Western Anatolia playing a crucial role within the "Anatolian Trade Network", through which transfer of goods across the Aegean and Southwest Asia intensified especially in the second half of 3rd millennium BCE. Focusing on South West Anatolia (SWA), EBA settlements in this region have not yet been studied genetically in detail, and current knowledge is based on a few sites. Previous archeological research on material culture data from SWA settlements has suggested strong relations within and between the coastal (and possibly overseas) settlements in the west and south. Here, we study genomic data from three SWA settlements, dating back to the Bronze Age (BA), in terms of population structure and demography. We find that SWA BA populations have a genetic affinity towards certain Neolithic populations from the Aegean region (both modern-day Greece and Turkey), when compared with Central Anatolian Neolithic populations. However, SWA individuals show equal affinity to Bronze Age Anatolian and Greek populations, and also show similarity in their mitochondrial haplogroup profiles. Beyond this general genetic similarity, we can identify individuals and groups that show slightly different genetic profiles from the rest, suggesting human mobility in the region.

Keywords: Ancient DNA, Bronze Age, Southwest Anatolia, Archeogenomic

Contact: yorulmazsevgi3@gmail.com

Do high altitudes break down behavioral isolation in grasshoppers?

Tunca Deniz Yazıcı¹, Ricardo Pereira¹

Ludwig-Maximilian-Universitaet München, Germany

Closely related species can co-exist in the presence of strong enough reproductive barriers. The strength of reproductive isolation in sympatric populations depends on the total effects of sexual selection, and natural selection, including their interactions, counteracting gene flow. *Chorthippus biguttulus*, *C. brunneus*, and *C. mollis* are closely related grasshopper species that coexist in sympatry due to strong behavioral isolation which is based on male and female preferences towards chemical

and acoustic cues. In laboratory conditions, once the males are muted, it was observed that these species hybridized. These hybrid lines had intermediate songs of parental lines. Individuals with the intermediate songs were not found in wild until now, yet some intermediate songs were reported in higher altitudes of Alpine ecosystems, suggesting potential hybrid zones. In this project, by using ddRAD-seq data of Alpine populations with intermediate songs, and new genomic methods, we measure the hybridization index between taxa and test whether if the rate of hybridization increases with altitude. Our work will answer how the coexistence of species is affected in extreme conditions and serve as a guide to understanding how species would be affected when migrated to higher altitudes due to the ongoing crisis of increasing temperature.

Keywords: Behavioral isolation, ecological speciation, hybridization, sympatric populations, ddRAD sequencing

Contact: Yazici.Tu@campus.lmu.de

Genomic Factors Influencing Coverage Variability in Ancient DNA Libraries

Mevlüt Köz¹, Safa Kerem Aydın¹, Dila Nur Çakal², Utku Gürs¹, Mevlüt Köz², Mehmet Emre Özkan¹, Nergis Yasav¹, Elif Dönmez¹, Kanat Gürün¹ Mehmet Somel¹

¹Middle East Technical University, Turkey

²Konya Food and Agriculture University, Turkey

"Background/aim: Next Generation Sequencing has revolutionized studies on ancient DNA (aDNA), as it substantially increased the amount of genomic sequence data obtained from extinct populations. However, aDNA can be highly fragmented and lost due to long periods of decay. This effect depends on several factors and thus, we observe various read lengths and read depths for different parts of the genome. In this project, we aim to determine the factors that affect the variability of these statistics for aDNA, making use of epigenetic and genomic data.

Materials and methods: We used sequence data from four aDNA libraries of archaeological human bone and tooth tissue remains. After aligning the reads to the human reference genome we divided Chromosome 1 into 1000 base-pair windows. We then analyzed the coverage of the chromosome using various tools. For variability, we have not only used four different libraries, but also different coverages of these libraries. To catch positive/negative correlations, we compared our coverage output for the libraries with GC content, homopolymer density, ATAC-seq peaks, CpG islands, exon density, and mappability across bins.

Results: The results show that coverage of aDNA is affected by GC content and mappability. The former could reflect aDNA preservation biases, as well as technical biases in PCR and sequencing. The latter is a direct consequence of short-read alignment being constrained in repeat-rich regions. Meanwhile, we did not observe significant effects of genomic characteristics that related to chromatin state or DNA structure in this dataset."

Keywords: Ancient DNA, genomics, GC, coverage, mappability

Contact: kanatgurun@yahoo.com

Modelling the population history of Anatolia: A summary of ongoing attempts to create a plausible model

Hande Çubukcu¹, Ezgi Altınışik², Eren Yüncü³, Dilek Koptekin³, İdil Taç¹, Mehmet Somel³, Füsün Özer², Yılmaz Selim Erdal², İdil Yet¹, Gülşah Merve Kılınç¹

¹Department of Bioinformatics, Graduate School of Health Sciences, Hacettepe University, Ankara, Turkey

²Department of Anthropology, Hacettepe University, Ankara, Turkey

³Department of Biological Sciences, Middle East Technical University (METU), Ankara, Turkey

Anatolia has been a dynamic region in human history with multiple migration and admixture events since the Mesolithic era. Local hunter gatherers in Anatolia adopted farming and formed the first sedentary communities around 10000 BP. Early Anatolian Farmers are ancestral to the European Early Farmer populations. Populations located between Western Anatolia and Southern Caucasus during the Late Neolithic and Early Bronze Age had variable amounts of a mixed ancestry formed among the regions during the Neolithic. The genetic pool of Anatolia has remained the same with limited gene flow from the outside until the Middle Bronze Age. Admixture models produced using the qpGraph tool of the Admixtools software package offer a glimpse into the prehistory by showing possible interactions among prehistoric populations. The models are inferred from the genetic relatedness among the populations which is calculated using the allele frequency differences between them. Previously, admixture models made with this tool for the Caucasus and the Levant have been published, which included some important populations for the Anatolian prehistory. Here presented is a summary of the ongoing attempts to find a suitable admixture model of Anatolia. The models mainly include populations shown before to be closely related to Anatolian Early Farmers such as Western Hunter Gatherers and Iran Early Farmers, and populations that have interacted with Anatolian populations socially and demographically like the farmer populations from the Caucasus and Levant.

Keywords: ancient DNA, Neolithic age, admixture model, population genetics, Anatolian prehistory

Contact: handecubukcu4@gmail.com

Differences Between Two Middle European Water Frogs: *Pelophylax ridibundus* and *Pelophylax lessonae*- in Four Sex Determination Genes

Diyar Hamidi¹, Çiğdem Akın Pekşen², Montserrat Torres³, Jörg Plötner⁴

¹Christian-Albrecht University of Kiel, Kiel, Germany

²Baskent University, Ankara, Turkey

³Institute of Clinical Molecular Biology, Christian Albrecht University of Kiel, Kiel, Germany

⁴Museum für Naturkunde, Leibniz Institute for Evolution and Biodiversity Science, Berlin, Germany

Sex differentiation during gonadal maturation in amphibians occurs through complex networks involving mainly sex genes or sex chromosomes, transcription, and epigenetic factors. Here, we studied four genes (*sox3*, *dmrt1*, *amh*, and *irf9*) of Central European water frogs (*Pelophylax esculentus* complex) known to be involved in germline development and differentiation. Using testes transcriptomes of *Pelophylax lessonae* and *Pelophylax ridibundus*, we analyzed the intron-exon structure and interspecific sequence divergence (*p*) of these genes. As a result, *dmrt1* exhibited the highest sequence variability with a *p*-value of 2%, while *sox3* was the most conserved gene with a value of 1.1%. *P. ridibundus* and *P. lessonae* are the parental species of the hybridogenetic hybrid *Pelophylax esculentus*, which usually excludes one parental genome from its germline prior to meiosis and forms fertile gametes containing the remaining, non-recombined genome. In this way, the hybrid is able to reproduce by crosses with only one of its parental species, i.e., with *P. lessonae* in the so-called *lessonae-esculentus* (L-E) system and *P. ridibundus* in the *ridibundus-esculentus* (R-E) system. Although water frogs have been intensively studied for more than five decades, little is known about the molecular mechanisms underlying genome exclusion and clonal gamete formation in the germline of *P. esculentus*. In this context, the role that sex determination genes might play as putative meiotic drivers of genome elimination should be clarified, especially because in the L-E system, the clonally transmitted *ridibundus*

genome usually contains female determinants, whereas the lessonae clone inherited by hybrids in the R-E system contains male-determination factors.

Keywords: Water frogs, *Pelophylax ridibundus*, *Pelophylax lessonae*, sex determination, hybridogenesis

Contact: cerigensis@gmail.com

Warming summers, mass-emerging aquatic insects, and late-breeding endangered ducks: The perfect recipe for trophic mismatch

Alaz Uslu¹, Deniz Mercan², İbrahim Kaan Özgencil³, Gülümser Genç⁴, Dilan Melisa Özsoy⁴, Gencer Yaprak³, Melisa Soyluer³, Akın Karahasan², Ahmet Akkoç⁴, Pedro Seixas⁵, Beril Tezel⁴, Nur Filiz⁶, Cihangir Kirazlı⁷

¹Simurg Bird Sanctuary, Bolu Abant İzzet Baysal University, Turkey

²Eskişehir Osmangazi University, Turkey

³Middle East Technical University, Turkey

⁴Hacettepe University, Turkey

⁵Centro de Reprodução de Anatídeos, Portugal

⁶Middle East Technical University, Ecosystem Implementation and Research Center, Turkey

⁷Bolu Abant İzzet Baysal University, Turkey

Global climate change is threatening birds in many different ways. Trophic mismatch, the lack of phenological overlap between an organism and resources it consumes, is a widespread outcome of climate change, which has been documented in various habitats and bird groups, including waterbirds. Here, we studied the breeding phenology of two late-breeding endangered omnivorous diving duck species: White-headed Duck (*Oxyura leucocephala*) and Common Pochard (*Aythya ferina*) and their benthic macroinvertebrate food sources, non-biting midges (Chironomidae) larvae to investigate whether the two duck species are suffering from a trophic mismatch due to earlier mass-emergence of the larval midges at Lake Mogan in central Turkey. We conducted weekly surveys in spring and summer to locate all breeding female ducks and document the hatching time of their broods. We also collected mud samples and pupae pods from water surface at two-week intervals to study the demography, abundance, and emergence phenology of the midge populations in the lake. We found that the two endangered ducks species' broods hatch later than other duck species. We observed one mass emergence of midge flies in April and documented another one in mid to late July. Our results suggest that nearly one fourth of all broods of the endangered ducks might be suffering from a shortage of larval invertebrate food sources before they fledge, which may adversely affect their development and potentially have carryover effects. Further studies covering larger temporal and spatial scales are needed to have a better understanding of this seemingly partial trophic mismatch case.

Keywords: Diving ducks, Global warming, Trophic mismatch, Shallow lakes, Waterbirds

Contact: alazuslu@gmail.com

Widespread close-kin patterns among co-buried individuals in Southwest Asian Pre-Pottery Societies

N. Ezgi Altınışik¹, Duygu Deniz Kazancı², Ayça Aydoğan¹, Hasan Can Gemici², Ömür Dilek Erdal¹, Savaş Sarialtun³, Kivilcim Başak Vural², Dilek Koptekin², Kanat Gürün², Ekin Sağlıcan², Meliha Melis Koruyucu¹, Cansu Karamurat², Mustafa Özkan², Gülşah Merve Kılıncı¹, Anders Götherström⁴, Çiğdem Atakuman², Yılmaz Selim Erda¹, Füsün Özer¹, Aslı Erim Özdoğan³, Mehmet Somel²

¹Hacettepe University, Turkey

²Middle East Technical University, Turkey

³Çanakkale Onsekiz Mart University, Turkey

⁴Stockholm University, Sweden

"During the Neolithic period in Southwest Asia, it was common practice to bury the deceased under the floors of domestic buildings. The biological relationship patterns of sub-floor burials also provide valuable knowledge on understanding the social organisation in society. In recent years, ancient DNA technology has made it possible to effectively estimate these relationships.

Here in this study, we produced ancient DNA shotgun data from 13 samples excavated from Çayönü Tepesi, representing the Upper Mesopotamian society dated to pre-pottery Neolithic Period. Nine of these thirteen individuals were co-buried under the floors of three buildings. By exploring the kinship patterns of these individuals, we revealed that all close kin pairs identified were buried in the same buildings.

In recent studies, a similar pattern was observed in contemporaneous Pre-Pottery Neolithic populations in Central Anatolia, represented by Aşıklı and Boncuklu. However, this phenomenon seems altered in Pottery Neolithic in Central and Western Anatolia (i.e., Çatalhöyük and Barcın Höyük) where co-buried individuals, mostly subadults, were not frequently biological kin. These exciting results represent early steps toward uncovering widespread burial custom practices in Neolithic Southwest Asia."

Keywords: ancient DNA, Uppuer Mesopotamia, kinship, social organisation

Contact: ezgialtinisik@hacettepe.edu.tr