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evolutionary biology symposium

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Symposium Programme & Abstract Book



ISTANBUL UNIVERSITY FACULTY OF SCIENCE
FEZA GÜRSEY HALL

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Ecology and Evolutionary Biology Society



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SYMPOSIUM PROGRAMME

FEZA GÜRSEY HALL

DAY 1st (17.07.2023, Monday)

Time Slot	Presentation Title	Presenting Author	
09:00-09:30 On-site registration			
09:30-10:00	Welcome from the Organizing Committee and EkoEvo President	Efe Sezgin	
Session I: Evolutionary Biology	10:00-10:15	The role of cephalopod-specific microsynteny in the evolution of novel gene regulation	Gözde Yalçın
	10:15-10:30	Social disruption in female guppies leads to a diversification of reproductive strategies	Alessandro Macario
	10:30-10:45	The adaptive introgression of MHC genes in multiple vertebrate taxa	Tomasz Gaczorek
	10:45-11:15	Coffee Break	
	11:15-11:30	Selection inference in inversion rich genomes	Julia Morales-Garcia
	11:30-11:45	Cancer's vulnerability to food availability is evolutionarily conserved: fasting inhibits tumorigenesis in both Hydra and zebrafish	Sophie TISSOT
	11:45-12:00	A Study on Phylogenies of Homing Endonuclease Genes Found in Mitochondrial Genomes of Monilinia Species	Sibel Öncel
	12:00-13:30	Break for Lunch	
13:30-14:30	Keynote Speaker <u>Genomics of adaptation and speciation in crater lake cichlid fishes</u>	Axel Meyer	
Session II: Population Genetics & Phylogenetics	14:30-14:45	Genetic rescue or human-mediated massive contamination: Investigation of genomic differences between farm-reared and wild populations of <i>Alectoris chukar</i> with high-density SNPs data	Sarp Kaya
	14:45-15:00	Genomic Insights into the Endangered Mouflon Populations of Anatolia and Cyprus	Gözde Atağ
	15:00-15:15	Genetic polymorphism in the VKORC1 gene in house mice (<i>Mus musculus</i>) and Norway rats (<i>Rattus norvegicus</i>) in Russia	Aleksey Maltsev
	15:15-15:30	Comprehensive analysis of circulating viral DNA in maternal plasma at population-scale using low-pass whole-genome sequencing	Selim Can Kuralay
	15:30-16:00	Coffee Break	
	16:00-16:15	Phylogenetic Analysis of Brown Bear (<i>Ursus arctos</i>) Populations Across Turkey	Elif Çeltik
	16:15-16:30	A Phylogenetic Study on <i>Crocus gargaricus</i> Herb. Species Complex	Ceyda Yazıcı
	16:30-16:45	Genetic alteration in the chloroplast and nuclear gene regions of 3500-year-old charred crop seeds from the archaeological site of Kaymakçı	Asiye Uluğ
16:45-18:00	Poster Session / Panel: The Evolution Curriculum in Turkey		

FEZA GÜRSEY HALL

DAY 2nd (18.07.2023, Tuesday)

Time Slot	Presentation Title	Presenting Author
09:00-09:30	On-site registration	
09:30-10:30	Keynote Speaker <u>Quantifying Uncertainty in Evolutionary Analyses</u>	Alexandros Stamatakis
10:30-10:45	Phylogeny-based inferences in protein function	Ogun Adebali
10:45-11:00	Deep convolutional and conditional neural networks for large-scale genomic data generation	Burak Yelmen
11:00-11:15	Coffee Break	
11:15-11:30	Coevolution of Transcription Factor Protein Structure and DNA Binding Sites in Crustaceans	Murat Tugrul
11:30-11:45	Comparative transcriptome provides insights into thermal adaptation among aquatic insect communities	Maribet Gamboa
11:45-12:00	Incorporating functional information into selection scans using ancient DNA	Pelin Poyraz
12:00-12:15	Prediction of Long non-Coding RNAs in Monilinia Fungal Pathogens and First Insights on Mito-LncRNAs	Hilal Özkılınç
12:15-13:45	Break for Lunch	
13:45-14:45	Keynote Speaker <u>The evolutionary history of Turkish Hipparchonine horses</u>	Ray Bernor
14:45-15:00	Noise and bio-acoustic monitoring of coastal waters in Northern Portugal	Ana Bio
15:00-15:15	Temporal resolution in fire occurrence models: implications for model performance and climate change projections	İsmail Bekar
15:15-15:30	From Local Ecological Knowledge to Long-term Monitoring Surveys: Addressing the Importance of Marine Top Predators	Nur Bikem Kesici
15:30-15:45	Climatic, Geographic, and Anthropogenic Drivers of Honey Bee Subspecies Distribution and Winter Losses in Türkiye	Mert Kükrer
15:45-16:15	Coffee Break	
16:15-16:30	The Role of Cuticular Waxes in Drought Response and Tolerance in Populus trichocarpa (Black Cottonwood)	Melike Karaca-Bulut
16:30-16:45	Investigation of the Effect of Sexual Cannibalism on Sex Ratio in a Natural Population of Two Different Praying Mantis Species	Kaan Yılmaz
16:45-17:00	Climate Change and Anthropogenic Interactions Modulates Habitat Suitability of Brown Bears Across Türkiye	Ercan Şıkıdokur
17:00-18:30	General Meeting of the EkoEvo Society	Efe Sezgin

AHMET YÜKSEK ÖZEMRE HALL

DAY 2nd (18.07.2023, Tuesday)

Special Session: Paleobiological and Paleoanthropological Studies	Moderator: Ferhat Kaya	Time Slot	Presentation Title	Presenting Author
		14:45-15:00	Mammal Paleontology of Turkey in the 21st Century: Challenges, Research Opportunities and Future Prospects	Ferhat Kaya
		15:00-15:15	New Reconstruction of the Oldest Homo erectus from Turkey (Kocabaş 3). Discussion on Evolutionary Perspectives	Amélie Vialet
		15:15-15:30	Evolution and paleoecology of Late Miocene Eastern Mediterranean Proboscidea	Juha Saarinen
		15:30-15:45	When Did the Beaver Become Extinct in Anatolia?	Elçin Ekşi
		15:45-16:15	Coffee Break	
		16:15-16:30	Pollen Productivity Estimates for Past Land Cover Reconstruction in Turkey	Esra Ergin
		16:30-16:45	Preliminary Paleobiology and Paleoecology of two Late Neogene Mammal Fossil Sites in Cappadocia, Turkey	Özge Kahya
		16:45-17:00	Metagenomic Analysis of Three Chewed Pitch Pieces from Huseby Klev	Emrah Kırdök

ŞEVKET ERK HALL

DAY 2nd (18.07.2023, Tuesday)

Special Session: Emerging Themes in Eco-Evo-Devo	Moderator: A. Matteen Rafiqi	Time Slot	Presentation Title	Presenting Author
		15:00-15:15	The Evolutionary and Developmental Mechanisms of Caste-Specific Traits in Ants: Insights from Ocelli on Formicinae	Angelly Vasquez-Correa
		15:15-15:30	Bacteriocyte origins from specific posterior cells of early embryo in hemipteran insects	Mauricio Alarcon
		15:30-15:45	Segregation and Transmission of Bacteria with a novel structure	Zelal Özgür Durmuş
		15:45-16:15	Coffee Break	
		16:15-16:30	Gene Regulatory Networks Altered by Endosymbiosis	Nihan Sultan Milat
		16:30-16:45	A trait-based morphometric assessment on spiders (Araneae) from Anatolia adapted to suł Mert Elverici	

FEZA GÜRSEY HALL

DAY 3rd (19.07.2023, Tuesday)

Time Slot	Presentation Title	Presenting Author	
09:00-09:30	On-site registration		
Session V: Microbial Ecology	09:30-10:30	Keynote Speaker <u>Making a microbiome: unravelling ecological and evolutionary influences in wild rodents</u>	Sarah Knowles
	10:30-10:45	Altitudinal Effect on Gut Microbiome Composition of Long-Living and Cancer-Free Blind Mole Rat (<i>Nannospalax xanthodon</i>)	Halil Mert Solak
	10:45-11:00	Rock structure drives the taxonomic and functional diversity of endolithic microbial communities in extreme environments	Emine Ertekin
	11:00-11:15	Coffee Break	
	11:15-11:30	Shore flies (Diptera, Ephydriidae) adaptation to extreme habitats: morphology and symbiotic microbiota	Ekaterina Iakovleva
	11:30-11:45	Conserved gut microbial guilds across the human life stages	Ezgi Özkurt
	11:45-12:00	Destabilising effect of climate change on population persistence	Arpat Özgül
	12:00-13:30	Break for Lunch	
	13:30-13:45	Harmonized estimation of wild ungulate densities throughout Europe	Tamar Uguzashvili
	13:45-14:00	Wolves' feeding ecology across the Anatolia	Hüseyin Ambarlı
Session VI: Biogeography and Spatial Ecology & Population and Wildlife Ecology	14:00-14:15	Higher functional diversity is associated with higher functional stability in bird communities	İbrahim Kaan Özgencil
	14:15-14:30	A Hybrid Modeling Framework to Project <i>Impatiens glandulifera</i> Invasion in North America	Oğuzhan Kanmaz
	14:30-15:00	Coffee Break	
	15:00-15:15	Investigating the changes in spring phenology of <i>Fagus orientalis</i> in Turkey using remote sensing	Tuğçe Şenel
	15:15-15:30	Nitrate Availability Can Inhibit Methane Emissions in Central and Western Anatolian Shallow Saline Lakes	Gültekin Yılmaz
	15:30-15:45	Time, not resource availability, is a better predictor of successional patterns of saproxylic beetles on decaying wood	Didem Ambarlı
	15:45-16:00	Drivers of among-population variability in fire-related traits in Turkish Red Pine (<i>Pinus brutia</i> Ten.)	Duygu Deniz Kazancı
	16:00-17:00	Awards and Closing Ceremony	

DAY 1st (17.07.2023, Monday)

	Time Slot	Presentation Title	Presenting Author
Poster Session	17:15-18:00	Population Genomics of Crohn's Disease Susceptibility	Bengisu Narlı
	17:15-18:00	Investigation of microplastic concentration in commercial fish species in Gemlik Bay (Marmara Sea)	Serda Kececi Gündüz
	17:15-18:00	Genetic mechanisms of adaptation in <i>Isophya rizeensis</i> bush cricket along environmental gradient	Ufuk Topalan
	17:15-18:00	Determination of Microplastic Characterization of Turkish Endemic frog <i>Pelophylax caralitanus</i> from Isparta Province, Türkiye	Hale Tatlı
	17:15-18:00	Ancient DNA illuminates population dynamics of the central Levant in the 2nd to 1st millennium BCE	Suzanne Freilich
	17:15-18:00	Distinguishing First-Degree Relationships From Ancient Samples With Machine Learning	Merve Nur Güler
	17:15-18:00	Rhizosphere microbiome profile of the local endemic and critically endangered <i>Thymus pulvinatus</i>	Gökçe Ercan
	17:15-18:00	Comparison of Flammability in Two Serotinous Mediterranean Trees	Çağatay Tavşanoğlu
	17:15-18:00	Identification of Anterior Determinants in Ants	Sevim Nur Akyüz
	17:15-18:00	Molecular evolution of Myh7 proteins among mammals: a comparative, phylogenetic, structural, and interactional analysis	Dilara Sönmeztekin
	17:15-18:00	Molecular evolution of Maa proteins among mammals: a comparative, phylogenetic, structural, and interactional analysis	Buminhan Özgültekin
	17:15-18:00	Hox gene function in ants that have intracellular endosymbiotic bacteria	Birgül Çolak-AI
	17:15-18:00	Investigating genomic processes underlying rapid divergence and speciation in <i>Phonochorion</i>	Seray Altıntaş
	17:15-18:00	Tracing Spatiotemporal Changes in Skin Pigmentation Diversity in Holocene Anatolia	Arta Nezirli
	17:15-18:00	First step to understand thermal adaptation in the fungal pathogen <i>Monilinia fructicola</i>	İrem Ece Kadioğlu
	17:15-18:00	Genetic assimilation of host genes responding to the signal from endosymbionts	Yesim Erol
	17:15-18:00	Human Brown Bears Conflict Risk Across Türkiye's Human Dominated Landscapes	Ercan Sıkdokur
	17:15-18:00	Evolutionary genomics underlying the response of the life history traits to the fluctuating and deteriorating thermal conditions	Nikola Petkovic
17:15-18:00	Purifying selection on old-biased genes and the evolution of human lifespan	Melih Yıldız	
17:15-18:00	Patterns of sex-biased long-distance mobility in humans inferred from paleogenomes	Mehmet Somel	

Poster Session	Time	Title	Author
	17:15-18:00	Species-specific best-fit inspection for the model developed through an information-theoretic approach relating the lengths of protein and the encoding DNA	Yekbun Adıgüzel
	17:15-18:00	Gene regulatory networks altered by endosymbiosis	Nihan Sultan Milat
	17:15-18:00	Signal peptides from endosymbiont influencing gene expression of the ant host	Fatma Zehra Çağlı
	17:15-18:00	Contribution of the symbiotic microbiota to the change in the lifespan of <i>Drosophila melanogaster</i> selected for late reproduction	Daniil Merzlikin
	17:15-18:00	The Combined Effects of Ocean Acidification, Microplastic and Lanthanum in Sea Urchin <i>Arbacia lixula</i>	Berna Şahin
	17:15-18:00	The Effect of gut microbiome size on the evolution of bacterial resistance	Onur Erk Kavlak
	17:15-18:00	A research on desiccation tolerance of stream macrobenthic invertebrates	Ahmet Anhan Erözden
	17:15-18:00	Genetic characterization of ancient charred wheat seeds from the archaeological site of Kaymakçı using <i>glu-1</i> loci	Göksu Tunçer
	17:15-18:00	The NR1L subfamily grows larger: gene annotation and evolutionary analyses of a unique group of nuclear receptors in Branchiopoda (Crustacea: Allotriocarida)	Ferran Palero
	17:15-18:00	CNV analysis of two endangered wild sheep	Eren Yüncü
	17:15-18:00	Revealing the draft genome sequence of the invasive pest <i>Ricania simulans</i> (Walker, 1851) (Hemiptera: Ricaniidae)	Yusuf Ulaş Çınar
	17:15-18:00	Uncovering the knowledge gaps in Triglidae family biology in Turkish Waters	Yunus Gönül
	17:15-18:00	Identification of genomic regions regulating sex determination in European anchovy (<i>Engraulis encrasicolus</i> L., 1758) by whole-genome sequencing approach	Selahattin Barış Çay
	17:15-18:00	Effects of ocean acidification on the ark clam (<i>Anadara kagoshimensis</i>) physiological processes	Narin Sezer
	17:15-18:00	Temporal variation in the evolutionary potential of quantitative immune traits in a wild invertebrate population	Cansu Çetin
	17:15-18:00	2023 Spring soaring bird migration	Yiğit Ergün
	17:15-18:00	The effect of presence and abundance of European bee-eater on honey bee activity	Melisa Soylyuer
	17:15-18:00	Assessment of population genetic structure and differentiation of the <i>pelodytes caucasicus</i> (Boulenger 1896) from Giresun and Rize	Tuğba Ergül Kalaycı

ABSTRACT OF ORAL PRESENTATIONS

SESSION I: EVOLUTIONARY BIOLOGY

Keynote Address: Genomics of adaptation and speciation in crater lake cichlid fishes

Axel Meyer

University of Konstanz

The transition from 'well-marked varieties' of a single species into 'well-defined species' especially in the absence of geographic barriers to gene flow (sympatric speciation) has puzzled evolutionary biologists ever since Darwin. Gene flow is expected to counteract the buildup of genome-wide differentiation through the evolution of irreversible reproductive barriers (incompatibilities) that complete the process of speciation. Theory predicts that the genetic architecture of divergently selected traits can influence whether sympatric speciation occurs, but empirical tests of this theory are scant because comprehensive data are difficult to collect and synthesize. Within a young species complex of Neotropical cichlid fishes, we analyzed genomic divergence among populations and species across several crater lakes in Nicaragua where repeatedly and parallel several species originated in these isolated small lakes. Also, several adaptations such as hypertrophied lips, differences in dentition, coloration and body shapes evolved convergently in these lakes. By generating a new genome assembly and re-sequencing 500 genomes, we uncovered the repeated genetic architecture of traits that have been suggested to be important for divergence. Species that differ in monogenic or oligogenic traits that affect ecological performance and/or mate choice show remarkably localized genomic differentiation. By contrast, differentiation among species that have diverged in polygenic traits is genomically widespread and much higher overall, consistent with the evolution of genome-wide barriers to gene flow. Simple trait architectures might not always be conducive to sympatric speciation, but polygenic architectures can promote rapid speciation in sympatry. We also discovered a case of homoploid hybrid speciation (i.e., hybrid speciation without a change in ploidy). Only few accepted empirical examples of homoploid hybrid speciation exist, and in only one previous case was it convincingly shown that this process occurred in complete sympatry. Here, we report an instance of sympatric homoploid hybrid speciation in cichlid fishes in Crater Lake Xiloá. The hybrid lineage, albeit at an early stage of speciation, has genomically and phenotypically diverged from both of its two parental species. Together with a distinct stable isotope signature this suggests that this hybrid lineages occupies a different trophic niche compared to the other sympatric Midas cichlid species.

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The role of cephalopod-specific microsyntenies in the evolution of novel gene regulation

Gözde Yalçın¹, Oleg Simakov¹, Thea F. Rogers¹

¹University of Vienna

Coleoid cephalopods have many species-specific innovations, such as their uniquely structured and large invertebrate brain, the light organ that houses symbiotic bacteria in the bobtail squid, as well as complex behaviors such as camouflaging ability. Comparative genomic studies are starting to investigate how these distinctive morphological and behavioral traits have evolved at the macroevolutionary level in these species, however, we know less about the role of local gene neighborhoods and regulatory evolution underlying cephalopod novel traits. Previously, we identified hundreds of genomic microsyntenies associated with cephalopod innovations (MACIs). Using ATAC-seq and genomic data in the Hawaiian bobtail squid (*Euprymna scolopes*) we show that MACIs have distinct 'types' of microsynteny blocks that are different from ancestral, metazoan microsynteny. Next, we use Micro-C data from *E. scolopes* and the California two-spot octopus (*Octopus bimaculoides*) to show that MACIs tend to be located in multiple TADs, often within one larger TAD, forming large regulatory blocks. Overall, our study suggests a distinct 'unit' of gene regulation underlying in the evolution of coleoid cephalopod-specific traits.

Keywords: gene regulation, genomics, evolution of complex traits, Cephalopods

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Social disruption in female guppies leads to a diversification of reproductive strategies

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Animal living in groups display complex social organization based on non-random interactions amongst individuals. Perturbation to the composition of these groups alters social cohesion and the level of social familiarity that results from stable relationships between members, however little is known about individual fitness consequences when established social ties are weakened or otherwise disrupted. Using guppies (*Poecilia reticulata*) as a model system, we aimed at quantifying the potential costs of disrupting females' social bonds and analyzed whether and how females adapt to social instability. To do so we experimentally manipulated the degree of social stability amongst unrelated females and explored how key life-history traits were affected. We found that both females' growth, an indicator for survival ability, and females' reproductive investment in terms of fecundity and egg size varied in response to social instability; females with the highest level of experimentally induced social instability incurred direct physiological and reproductive costs as they grew less, were less fecund and produced on average smaller eggs than females experiencing no or mild social disruption. Moreover, our results suggest that some of the phenotypic plasticity found in females' reproductive efforts and somatic growth represents adaptive trade-offs and bet-hedging strategy in response to the unpredictable environmental conditions to which they were exposed. To the best of our knowledge, this study is the first to demonstrate the fitness consequences of social disruption on a group of familiar individuals, highlighting the life-history strategies implemented by these individuals to mitigate the costs associated with such social instability.

Keywords: sociality, social instability, fitness consequences, life-history strategies, adaptive phenotypic plasticity

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The adaptive introgression of MHC genes in multiple vertebrate taxa

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The Major Histocompatibility Complex (MHC) is a key component of adaptive immunity and contains the most polymorphic genes in the vertebrate genome. Its extraordinary diversity is largely driven by host-pathogen coevolution, favoring novel or rare alleles. Since novel MHC alleles can be easily acquired by introgression from related species, MHC introgression is likely to be adaptive. However, its extent and prevalence remain an open question. Here, we used comparative analysis to test for adaptive MHC introgression across all major vertebrate groups by directly comparing the extent of MHC and genome-wide introgression in natural hybrid zones. In total, we tested 29 hybrid zones formed by 32 species of fish, amphibians, reptiles, birds and mammals. The extent of MHC and genome-wide introgression was compared using four methods, including geographic and genomic clines, and the results were synthesized in a comparative framework that controlled for the effect of phylogeny. We found extensive evidence for widespread adaptive introgression of MHC genes - almost all hybrid zones showed the signals of increased MHC introgression, regardless of divergence time or MHC variability. We found no significant difference in the overall rate of introgression between MHC classes. Taken together, our results suggest that MHC is among the last genes to stop flowing between incipient species before speciation is complete. Introgression thus appears to be a general mechanism that introduces new and restores previously lost MHC variation, increasing the adaptive potential of hybridizing species and influencing the dynamics of host-pathogen arms-races.

Keywords: adaptive introgression, MHC, hybrid zones

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Molecular characterization of coronavirus in bats living in close contact with humans, in Camargue, France

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The fight against viral infectious diseases remains a challenging and endless task despite the tremendous efforts and significant advances in public healthcare. The COVID-19 crisis has demonstrated the need for surveillance of potentially zoonotic viruses in wildlife in order to predict future spillovers and to prevent outbreaks. Bats are major reservoirs of zoonotic viruses, including coronaviruses. Their extraordinary genetic characteristics (high rate of mutations, ability to recombination, poor fidelity of the RNA polymerase...) allows coronaviruses to easily cross the species barrier between animals and to spillover to humans. In Camargue, southern France, the high promiscuity between humans and bats, hosting the roofs of houses, increases the risk of virus transmission through respiratory route. In order to investigate coronavirus infection in bats and to assess the risk of bat-to-human transmission, we collected guanos throughout the Tour du Valat park. The results reported the detection of virus from the *Alphacoronavirus* genus in *Pipistrellus pygmaeus* bat species, with a prevalence as high as 50%. Moreover, genomic sequences detected were very different from known human coronavirus, suggesting low zoonotic risk. However, since humans are often infected from bats through intermediate animal species, the investigation of coronavirus infection of the whole Camargue wildlife is required.

Keywords: bats, coronavirus, zoonotic risk, Camargue, molecular biology

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Cancer's vulnerability to food availability is evolutionarily conserved: fasting inhibits tumorigenesis in both Hydra and zebrafish

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Although cancer is a disease that arose with the emergence of multicellular organisms and is still common in present-day species, little is known about the degree of conservation of the biological traits that characterize and regulate tumorigenesis across the metazoan tree. In this work, using scientific reasoning based on evolutionary ecology, we tested the hypothesis that the vulnerability to food availability, regardless of the multicellular organism considered, should govern several aspects of tumorigenesis. We considered two phylogenetically unrelated model systems, namely the cnidarian *Hydra oligactis* and the fish *Danio rerio*. Healthy individuals (including wild ones for hydra) and individuals from tumor-prone lines were placed on four diets that differed in feeding frequency and quantity. We also considered individuals at the beginning of tumorigenesis or at a more advanced stage. For both models, frequent overfeeding favor tumor emergence, while lean diets seem to be protective against tumor initiation. With regard to tumor progression, the high availability of food promotes the proliferation of the tumor cells present, whereas lower resource levels help to control tumor progression without being curative. From an evolutionary medicine perspective, these results support that fluctuations in food availability may have acted in the past as a purging mechanism for premalignant cells in the host body, and that the recent increases in food availability by-passes this evolutionarily conserved anti-cancer mechanism and generates evolutionary mismatches leading to higher cancer risk.

Keywords: cancer, food availability, evolutionary medicine, Hydra, zebrafish

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A Study on phylogenies of homing endonuclease genes found in mitochondrial genomes of *Monilinia* species

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Homing endonucleases are enzymes that cleave DNA at specific target sites. Homing endonuclease genes (HEGs) are remnants of mobile genetic elements, so they are mainly studied for their intron splicing properties, which contribute to evolution. Regardless of their origin, they are found in a wide range of fungal taxa. In our previous studies, many HEGs were detected, both in genic and intergenic regions, in the mitochondrial genomes of brown rot pathogens *Monilinia fructicola* and *Monilinia laxa*. These HEGs are separated into two groups, depending on their conserved motifs, which are GIY-YIG and LAGLIDADG. We found that these species have unique and common HEG sequences. Thus, understanding of these genetic elements phylogenetically has been questioned. Initially, common genic HEGs of the two species were studied, where the common HEGs mostly appeared within the COX genes and the NAD5 gene. In Maximum Likelihood trees, the two *Monilinia* species were diverged based on most of the HEG sequences considered, although there was an exceptional result where for a common HEG found in NAD5 gene, all *M. fructicola* isolates except one clustered together with *M. laxa* isolates. Additionally, homologs of the genic HEGs in different species were detected using BLASTX, where homologies were discovered among HEGs with Basidiomycete species along with several other Ascomycetes such as *Sclerotinia sp.* and *Ascochyta sp.*, with a wide range of fungal taxonomy being detected. Overall, this study provides insights on the phylogenetic relationships between mitochondrial HEGs of *Monilinia* species and potential research plans to be developed are discussed.

Keywords: mitochondrial genome, homing endonucleases, phylogenetics

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Genetic rescue or human-mediated massive contamination: Investigation of genomic differences between farm-reared and wild populations of *Alectoris chukar* with high-density SNPs data

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Restocking of wild populations by releasing farm-reared individuals is a complex dilemma in the context of conservation genetics. An uncontrolled genetic release can result in a genetic swamp in the native population due to the loss of local adaptations or the replacement of individuals with hybrid individuals via hybrid vigour. The chukar partridge (*Alectoris chukar*) is one of the most economically and culturally important bird species in Türkiye. However, wild chukar populations are decreasing as a result of anthropogenic factors such as habitat fragmentation and loss, overhunting, and pollution. As a game species, the General Directorate of Nature Conservation and National Parks (NCNP) annually releases thousands of chukar partridges into the nature. However, partridges released into the wild are typically individuals bred and raised in breeding farm conditions, and knowledge of their genetic source, their inbreeding degree, and genomic selection signals depending on the farm conditions are still limited. In this study, therefore, we investigated the genetic similarity and inbreeding depression level of farm-reared and wild populations and the possible selection signals in the farm-reared populations using samples both from farm-reared and wild chukar individuals. To archive these objectives, a genomic library was prepared with 96 samples from 5 different farms, 10 different wild populations, China and Greece and sequenced in Illumina HiSeq X Ten platform (2x150bp), and about 700 million reads were obtained. Our preliminary results indicate the presence of intense China clade-B contamination on the chukar breeding farms of the General Directorate of Nature Conservation and National Parks.

Keywords: *Alectoris chukar*, genetic rescue, conservation genomics, FROH, FST statistics.

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SESSION II: POPULATION GENETICS AND PHYLOGENETICS

Genomic insights into the endangered Mouflon populations of Anatolia and Cyprus

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Once widespread in their native habitats, Anatolian mouflon and Cypriot mouflon were driven to near extinction during the 20th century, and are currently categorized as endangered subspecies by the IUCN. Despite conservation efforts, their populations continue to decline, and they are now limited to a few locations with population sizes estimated to be less than 2,500. Here, we analyze whole genome sequences of five Anatolian mouflons and ten Cypriot mouflons to explore their historical population dynamics and their outcomes. We find that the two subspecies diverged approximately 5-10 thousand years ago. Past population size estimations show that Cypriot mouflon underwent an extended period of population decline, beginning at the end of the Pleistocene epoch. Both subspecies exhibit a high prevalence of runs of homozygosity (ROH) blocks, indicating recent severe inbreeding. Compared to Anatolian mouflons, the Cypriot mouflons have more pronounced patterns of low pairwise genetic diversity, high degrees of relatedness, and elevated non-synonymous to synonymous variant ratios. These genomic characteristics can be attributed to the human-mediated introduction of the mouflon to Cyprus during the early Holocene epoch and long-term isolation. We also discover a peak in local heterozygosity estimates covering 1-2Mb, in which copies of a locus with homology to a candidate paratuberculosis resistance gene (ABCC4) were found. We use data from other sheep genomes and paleogenomes to investigate the history of this locus. Overall, our study demonstrates how these endemic mouflon populations have been affected by demographic decline, which can inform conservation management strategies.

Keywords: conservation genomics, population genetics, endangered mouflons

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Genetic polymorphism in the VKORC1 gene in house mice (*Mus musculus*) and Norway rats (*Rattus norvegicus*) in Russia

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Genetic anticoagulant resistance due to arising and fixed by natural selection by mutations in the VKORC1 gene. The aim of our research was to analyze the polymorphism of the Vkorc1 gene in population of house mice and Norway rats in the settlements of Russia and to reveal the presence or absence of mutations responsible for the resistance. Two exons of the Vkorc1 gene were analyzed in 80 Norway rats from four cities (Moscow, Tyumen, Chita, Rostov-on-Don) and 126 house mice from cities and small settlements. In Norway rats' resistance-associated genotypes were limited to Moscow samples: several individuals have one of the mutations (Tyr139Ser) in a heterozygous state. The percentage of resistant individuals from Moscow was 15.7%. The resistant to warfarin rats were captured in three districts of Moscow: South-West, North and North-East. House mice were not found to have mutations in the Vkorc1 gene responsible for resistance to anticoagulants of the first and second generation in the Leu128Ser and Tyr139Cys positions located in the third exon. In this scenario, it may be that heavy use of anticoagulants has removed them from the population. However, in cities in the first exon, we identified two heterozygous mutations have not be described previously in the scientific literature: Lys58Arg and Ser31Trp. In Russia, the genetic resistance to rodenticides in settlements in the populations of house mice and Norway rats is significantly lower than in Western Europe.

Keywords: *Mus musculus*, *Rattus norvegicus*, Vkorc1 polymorphism

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Comprehensive analysis of circulating viral DNA in maternal plasma at population-scale using low-pass whole-genome sequencing

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As the most readily adopted molecular screening test, low-pass WGS of maternal plasma cell-free DNA for aneuploidy detection generates a vast amount of genomic data. This large-scale method also allows for high-throughput virome screening. NIPT sequencing data, yielding 6.57 terabases of data from 187.8 billion reads, from 12,951 pregnant Turkish women was used to investigate the prevalence and abundance of viral DNA in plasma.

Single-end clean reads aligned with the most recent human genome assembly on GENCODE (GRCh38.p13) using Bowtie2 v2.4.2. The unaligned non-human reads were extracted from the Bowtie2 output.

To identify viral sequences in maternal plasma, we performed a BlastN search to align unmapped sequences to the NCBI RefSeq viral reference sequences. We removed alignments containing bacteriophages and remaining alignments were considered significant hits for eukaryotic viruses. We used only individuals with at least two hits for a specific virus.

Among the 22 virus sequences identified in 12% of participants were human papillomavirus, herpesvirus, betaherpesvirus and anellovirus. We observed a unique pattern of circulating viral DNA with a high prevalence of papillomaviruses. The prevalence of herpesviruses/anellovirus was similar among Turkish, European and Dutch populations. Hepatitis B prevalence was remarkably low in Dutch, European and Turkish populations, but higher in China. WGS data revealed that herpesvirus/anelloviruses are naturally found in European populations. This represents the first comprehensive research on the plasma virome of pregnant Turkish women. The reuse of existing NIPT data generated by low-coverage WGS should hopefully further prove the potential power of NIPT in population-scale virome studies.

Keywords: NIPT, population genetics, low-pass whole genome sequencing

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Phylogenetic Analysis of Brown Bear (*Ursus arctos*) Populations Across Turkey

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Brown bears (*Ursus arctos*) are carnivores distributed across Eurasia and North America. Previous studies based on mtDNA revealed significant differences in genetic variation between European and Middle Eastern brown bears with each region characterized by distinct haplogroups. Turkey, as a crossroads between three continents, is an important region for brown bear diversity as it harbors haplotypes from both regions. However, previous information on the genetic diversity of Turkey was based on only mtDNA sequences and limited sample sizes therefore the role Turkey has played in the evolutionary history of brown bears is still largely unknown. Here using genome wide sequencing data together with the mtDNA D-loop region sequences we aim to fill this gap by investigating patterns of genetic diversity and differentiation across Turkey and nearby regions. Our results show three distinct mtDNA haplogroups clustered into western and eastern geographic groups. Genome-wide SNP analysis supported this conclusion, with high patterns of genetic diversity and distinct geographic structuring. Turkish and nearby Middle Eastern brown bear populations displayed high genetic diversity, admixture across populations, and significant genetic divergence based on both PCA and F_{st} values, contrasting with other world populations. Population size estimates across time indicated high effective population sizes with an upward trend, a stark contrast to lower effective population sizes observed in other populations. Collectively our results indicate that the evolutionary dynamics influencing brown bear populations across Turkey and the Middle East are distinct from other world populations, potentially related to novel adaptations targeted towards living under human dominated landscapes.

Keywords: phylogenetic analysis, *Ursus arctos*, genetic diversity, mtDNA, haplogroups, SNP

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A Phylogenetic Study on *Crocus gargaricus* Herb. Species Complex

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Crocus gargaricus Herb. is an endemic species complex living in high mountain areas in Western Anatolia. In the past, it was known from three populations (1 *Crocus thirkeanus* Koch and 2 *C. gargaricus*) whose taxonomic position has changed over time. As a result of our literature review and field studies, two more populations emerged. We investigated the various populations of this species complex from distant mountain ranges in both morphological and molecular biological contexts. Morphological measurements were performed on at least 20 randomly selected individuals. Statistically significant results were determined by One-Way ANOVA (Analysis of Variance) in morphological quantitative data. Then, Principle Coordinate Analysis (PCoA) was performed in the PAST program using the quantitative and all qualitative data found to be significant, and the morphological distances of the populations were determined. For molecular study, we used both nuclear (ITS and ETS) chloroplast (trnI-f) markers. The sequenced samples were aligned in the PhyDE program and a phylogenetic tree was constructed using the Bayesian method. Morphological analyses indicate significant differences between populations in terms of corm size, tunic structure, and filament and anther lengths. As a result of this study, the speciation process of the *C. gargaricus* taxon was revealed and new species will be introduced to the scientific world.

Keywords: *Crocus*, phylogenetic tree, morphology

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Genetic alteration in the chloroplast and nuclear gene regions of 3500-year-old charred crop seeds from the archaeological site of Kaymakçı

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Archaeobotanical and archaeological materials from different archaeological sites in Anatolia provide valuable information about past agricultural activities, domestication, and social life. Archaeological research at the archaeological site of Kaymakçı in the Gediz Valley reveal how western Anatolian farmers grew agricultural products for both their own consumption and as animal feed in the Middle and Late Bronze Age. Ancient DNA from 3500-year-old charred seeds of *Triticum aestivum/durum* L., *Hordeum vulgare* L., *Vicia ervillia* (L.) Willd., *Cicer arietinum* L., and *Vitis vinifera* L. excavated from the archaeological site of Kaymakçı was successfully extracted using various DNA extraction methods. The chloroplast (rbcl) and nuclear ribosomal (ITS, IGS) gene regions of the charred seeds were amplified successfully and aligned with their contemporary relatives with a high level of homology. By observing similar changes in modern samples, it was revealed that the base changes in the sequenced gene regions were not caused by the DNA degradation to which the charred seeds were exposed. Since the studied specimens have been continuously cultured to increase their nutritional value and yield, they showed nucleotide substitutions resulting from intense domestication and breeding activities over 3500 years. Some specimens of the charred species indicated the same sequence as seen in modern relatives, while some of them differed. This result revealed that charred species with different genotypes were cultured in agricultural practices in the Gediz valley. The obtained genomic data, supported by more sequenced gene regions in later studies, will answer many questions about past agricultural and social life.

Keywords: archaeological site, ancient DNA, charred seeds, ribulose-1,5 biphosphate carboxylase gene

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SESSION III: BIOINFORMATICS

Keynote address: Quantifying uncertainty in evolutionary analyses

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Uncertainty in results of evolutionary analyses can be present for a plethora of reasons such as, numerical deviations, lack of signal, ad hoc analysis parameter settings etc. Hence, instead of depicting discrete and monolithic analytical results one should summarize their inherent uncertainties. In this talk I will present novel approaches for better quantifying and displaying, but also predicting the expected uncertainties in phylogenetic inference.

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Phylogeny-based inferences in protein function

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Co-evolution trends of amino acids observed within or between genes provide valuable insights into protein structure and function. The most common approach to detect co-evolving residues is to analyze co-varying amino acids in multiple sequence alignment (MSA). However, alignments alone do not reflect the shared evolutionary history, and thus, this approach does not necessarily take into account only the independent changes in evolution. To avoid this bias, we developed a novel approach based on substitution mapping of amino acid changes onto the phylogenetic tree. We perform ancestral reconstruction and use the probability values of amino acids at each node to evaluate the independent changes. Starting from the root of the tree, we walk through the nodes and compute the total amount of substitution per branch based on the probability differences of ancestral amino acids between neighboring nodes. Our coevolution scoring consists of three major components: i) the total amount of change per branch obtained by the tree traversal process; (ii) repeated and parallel changes for both positions; (iii) the total number of affected leaves from a substitution. Compared to CAPS, iBIS2Analyzer, PSICOV, and CoMap, our approach identifies the coevolving position pairs with higher accuracy by ruling out the MSA-based problems and considering phylogenetic dependency that is commonly overlooked by existing tools. Our approach is useful not only in revealing co-evolving positions but also in the prediction of the functional effect of amino acid substitutions in health and disease.

Keywords: phylogenetics, pathogenicity prediction, missense mutations, co-evolution, loss-of-function, gain-of-function

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Deep convolutional and conditional neural networks for large-scale genomic data generation

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Applications of generative models for genomic data have gained significant momentum in the past few years, with scopes ranging from data characterization to generation of genomic segments and functional sequences. In our previous study, we demonstrated that generative adversarial networks (GANs) and restricted Boltzmann machines (RBMs) can be used to create novel high-quality artificial genomes (AGs) which can preserve the complex characteristics of real genomes such as population structure, linkage disequilibrium and selection signals. However, a major drawback of these models is scalability, since the large feature space of genome-wide data increases computational complexity vastly. To address this issue, we implemented a novel convolutional Wasserstein GAN (WGAN) model along with a novel conditional RBM (CRBM) framework for generating AGs with high SNP number. These networks implicitly learn the varying landscape of haplotypic structure in order to capture complex correlation patterns along the genome and generate a wide diversity of plausible haplotypes. We performed comparative analyses to assess both the quality of these generated haplotypes and the amount of possible privacy leakage from the training data. As the importance of genetic privacy becomes more prevalent, the need for effective privacy protection measures for genomic data increases. We used generative neural networks to create large artificial genome segments which possess many characteristics of real genomes without any apparent privacy leakage from the training dataset. In the near future, large-scale artificial genome databases can be assembled to provide easily accessible surrogates of real databases, allowing researchers to conduct studies with diverse genomic data within a safe ethical framework in terms of donor privacy.

Keywords: genomics, generative models, population genetics, genetic data privacy, deep learning

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Coevolution of transcription factor protein structure and DNA binding sites in crustaceans

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Transcription factors (TFs) regulate gene expression and play an important role in an organism's development and adaptation. Nuclear receptors (NRs) are special TFs that control the expression of genes in response to signaling molecules and environmental stimuli and can have profound effects on physiology and fitness. The evolution of NRs is therefore considered to play an important role in the diversification and adaptation of animals. However, little is known about the coevolution of the protein structure and DNA binding sites of NRs. In this study, we focus on the nuclear receptor group NR2B (e.g. *usp/rxr* genes) of crustaceans, a very diverse group of invertebrate animals adapted to various ecological niches. Our preliminary results indicate that the evolution of NR2B protein sequences is in agreement with the phylogeny of Crustacea, suggesting that Copepoda and Cirripedia might share a common ancestor and that Euphausiacea and Decapoda diverged latest within Malacostraca. Moreover, we used ModCre, a machine learning prediction tool, to obtain the binding motifs of this NR group. Interestingly, the binding motifs have also evolved along the phylogeny, but conserving the essential parts responsible for recognising specific DNA sequences. Finally, we have explored how the number of binding sites evolved within the crustacean genomes. Our findings provide new insights into the coevolution of nuclear receptors and their binding motifs in crustaceans and highlight their role in the evolutionary processes of these organisms.

Keywords: gene regulation, protein structure, transcription factor binding sites

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Comparative transcriptome provides insights into thermal adaptation among aquatic insect communities

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Temperature variation has been known to create strong selection pressure for genomic variation that enables the adaptation of organisms. By altering gene expression patterns, organisms can modify their adaptive potential to heterogeneous environmental conditions along a latitudinal gradient; however, there is a gap in our understanding of how physiological consequences in wild species are affected and act on multiple species. Here, we investigated how seven stream stonefly species sampled from four geographical regions in Japan differ in their responses to latitudinal variations by measuring gene expression (RNA-seq) differences within species and gene co-expression among species. Several genes (622) were differentially expressed along the latitudinal gradient. The high species-specific gene expression diversity found at higher latitude regions was probably associated with low temperatures and high-water discharge, which suggests their adaptive potential. In contrast, similar gene expression patterns among species were observed at lower latitudes, suggesting that strong environmental stress occurs in warmer regions. Weighted gene co-expression network analysis (WGCNA) identified 22 genes with similar expression patterns among species along the latitudinal gradient. Among the four geographical regions, high differential expression patterns in the co-expressed genes from two regions were found, suggesting that the local environment strongly affects gene expression patterns among species. Respiration, metabolism, and developmental co-expressed genes exhibited a latitudinal cline, showing clear evidence of divergent adaptive responses to latitude. Our findings demonstrate that stonefly species are differentially adapted to local environmental conditions and imply that adaptation in gene expression could be shared by multiple species under environmental stress conditions.

Keywords: transcriptomics, local adaptation, temperature, aquatic insects

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Incorporating functional information into selection scans using ancient DNA

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Ancient DNA can directly reveal the contribution of natural selection to human genomic variation. However, while ancient DNA based methods have been successful in identifying genomic signals of selection, inferring the phenotypic effects of that selection has been difficult. Evidence from genome-wide association studies suggests that most trait-associated variants are non-coding, so we expect that a large proportion of the phenotypic effects of selection will also act through non-coding variation. Since we cannot measure gene expression directly in ancient individuals, we used an approach (PrediXcan) developed to predict gene expression from genotype data. We incorporated this approach into a gene-level test for regulatory shifts due to selection across a time transect of 4500 years. We predicted the expression of 17,834 protein coding genes for each individual in a population of 91 modern and 684 ancient individuals from Britain. Based on linear regression models of expression against time, 36 genes (FDR < 0.05) had evidence for non-neutral shifts in expression levels in this time period. Our approach allowed us to highlight several genes with directional regulatory change from genomic signals for selection that in some cases span tens of genes, including LCT, FADS1, OAS3 and C4A. Importantly, we identified signals of selection on gene expression not captured by scans based on genomic signatures of selection that do not incorporate functional information. These results demonstrate the potential of combining this information and ancient DNA to elucidate the consequences of selection.

Keywords: selection scan, gene regulation, time series

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Prediction of long non-coding RNAs in *Monilinia* fungal pathogens and first Insights on mito-lncRNAs

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Long non-coding RNAs (lncRNAs) are RNA transcripts that have length higher than 200 nucleotides. Their interaction with the transcription differs from cis interference with the transcription of adjacent or overlapping sense or antisense-oriented target genes (NATs), to nucleosome repositioning, trans interactions with proteins, DNA, or other RNAs. Therefore, lncRNAs are expected to play important roles in the adaptation of the organism. *Monilinia fructicola* and *Monilinia laxa* are phytopathogenic fungal species that cause brown rot of pome and stone fruits. Our first preliminary study to identify lncRNAs included in silico studies of lncRNA predictions based on all transcriptome data from *M. fructicola* and *M. laxa* available at NCBI (Accession numbers: SRX10743191 and SRX3412422). For *M. laxa*, total of 24 novel lncRNAs and 18 novel NATs were predicted. For *M. fructicola*, 12 lncRNAs and 10 NATs were predicted. For *M. fructicola* 5 NATs were mapped to different positions in the mitochondrial genome. The most important finding of this prediction in *M. laxa* was the two antisense RNAs located in the Cob gene and Cox 1 in the mitochondrial genome. For *M. fructicola*, one of the lncRNAs was mapped to the GPAT gene in the nuclear genome and 5 of the NATs were mapped to vital genes such as the NAD and COX. Which suggests that these NATs may be involved in regulating vital genes in the mitogenome. Our research on further identification of lncRNAs in these pathogens and their specific functional effects is ongoing. This study is supported by TÜBİTAK-COST, Proje No: 122Z863.

Keywords: fungal pathogen, lncRNAs, bioinformatics, transcriptomics.

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SESSION IV: GENERAL ECOLOGY

Keynote address: The evolutionary history of Turkish Hipparionine horses

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The current NOW database records 222 late Miocene-Pleistocene occurrence of *Hipparion sensu lato*. Of these, 94 are from the oldest late Miocene interval, MN9, 11.2-9.937 Ma. There are 33 MN10, 22 MN11, 43 MN12, 3 MN13, 3 MN14, 3 MN15, 1 MN16, 3 MN17 and 11 MQ1 reported occurrences. Bernor et al., 2021 reported 63 species of Late Miocene – Quaternary hipparions within a lineage-based biogeographic, paleoecologic and paleoclimatic context. These taxa were referred to 10 genus-level clades. Of these 10 clades, the Turkish late Miocene-Quaternary includes 7 genus level clades: *Cormohipparion sinapensis* and *Cormohipparion sp.* in MN9, *Hippotherium sp.* in MN12, *Hippotherium brachypus* in MN11 and 12, “*Hipparion ankarynum*”, “*H. uzungazili*”, “*H. kecigibi*” and “*H. sp.*” in MN9. The genus *Cremohipparion* includes 5 species in MN12, *C. moldavicum*, *C. macedonicum*, *C. mediterraneum*, *C. proboscideum*, *C. matthewi* in MN12 and *C. nikosi* in MN13. Ukraine, Greece, Turkey and Iran represent the nexus of *Cremohipparion* origin and this clade extended its range during the late Miocene into Western Europe, the Siwaliks, China and North Africa. *Plesiohipparion* first appeared in MN12 of Russia, Turkey and the Arab Emirates and extended its range into Western Europe and China. *Proboscidipparion* originated in China and extended its range into Turkey in MN15 and continued to MN16. *Proboscidipparion* also occurred in Europe in the Pliocene and early Pleistocene last occurring in China 1.0 Ma. There are major turnovers in the Turkish equid fauna from the Vallesian to Turolian and the late Turolian to the Ruscinian. Climate change across this interval is characterized as being a progressive shift from wet to drier environments. The apogee of *Hipparion* evolution was later MN12 and MN13 with a collapse in species diversity at the Mio-Pliocene boundary. Lineages that persisted into the later Pliocene-Pleistocene included *Proboscidipparion*, *Plesiohipparion* and *Cremohipparion*.

Noise and bio-acoustic monitoring of coastal waters in Northern Portugal

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Underwater noise, caused by human activities at sea and along the coast is ubiquitous and increasing. This has a negative impact on marine life and particularly on marine mammals which use sounds to sense their surroundings, communicate, locate food, and protect themselves.

The present work aimed to map the underwater soundscape of the northern Portuguese coast to: quantify ambient noise levels; assess the presence and distribution of cetaceans in the area based on acoustic data; and relate cetacean presence to environmental conditions, particularly ambient noise levels.

Short hydrophone recordings of 10 min each were collected on a grid of 32 stations, twice a year, for two years, during 4-day multidisciplinary survey boat campaigns. Acoustic recordings were analyzed: computing ambient noise levels; manually processing the spectrograms for biotic sounds; and, using AI-based methods for an automated detection of sound nature, i.e. biophonic and anthropophonic acoustic events.

Noise level exposure varied locally, with comparatively higher levels detected along shipping routes and close to the main harbours. Noise from small offshore wind farm (3 wind turbines) could also be detected. Biotic sounds from dolphin (vocalizations and clicks) and from snapping shrimps were identified during records analysis. Results suggest that cetacean distribution is affected by noise levels. Furthermore, cetacean distribution showed seasonality, with more cetacean sound records during summer than during winter, indicating that part of the population is probably resident and part migrating.

Keywords: passive acoustic monitoring, cetaceans, noisescape, spectrogram analysis

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From local ecological knowledge to long-term monitoring surveys:
Addressing the importance of marine top predators

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Top predators occupy the higher trophic levels in the food web and play a key role as ecosystem regulators. Their presence supports the diversity of species and is linked with it in various ways, including trophic cascades, reliance on ecosystem productivity, susceptibility to disturbances, and connections to various elements of the ecosystem therefore, predator-centered conservation is believed to deliver certain biodiversity goals. However, the lack of available information on the local biodiversity and other important ecosystem variables is a major obstacle in conservation planning. A number of studies on the marine top predators in Turkish waters are not going any further than first records or range expansion reports. The very first database on these species around Gökçeada Island is established through visual, acoustic, and drone-based aerial surveys, supported by Local Ecological Knowledge (LEK). Marine top predators of the Gökçeada Island have been monitored since 2019 in order to gain a clearer understanding of these inhabitants. Individuals were reported via social media platforms and questionnaires were applied to stakeholders. Short-beaked common dolphins, bottlenose dolphins, and a sperm whale were detected during approximately 15 hours of acoustic recording. The study also covers the records of the critically endangered Mediterranean monk seal and other top predators such as the Great White shark, shortfin mako, and vulnerable marine mammals. Swordfish and Atlantic bluefin tuna were determined to be the most abundant top predators in the area.

Keywords: top predator, marine conservation, acoustic survey, drone-based monitoring, local ecological knowledge

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Climatic, geographic, and anthropogenic drivers of honey bee subspecies distribution and winter losses in Türkiye

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Honey bee populations worldwide face significant challenges, including anthropogenic factors, climate change, and winter losses. In this study, we investigate the climatic, geographic, and anthropogenic drivers of intra-specific turnover in honey bee subspecies compositions and winter losses in Türkiye. We employed Gradient Forests (GF) and Generalized Dissimilarity Modeling (GDM) to explore the patterns of intra-specific turnover across environmental gradients and quantify the relative importance of geographical and climatic factors. We sampled 691 stationary colonies across the country and two reference populations and genotyped them at 30 microsatellite loci. Our results identify the core zones where subspecies are found in unmixed form, the transition areas where they exchange genes, and the critical boundaries where sudden changes occur in subspecies compositions. Additionally, we surveyed 392 stationary beekeepers and utilized generalized linear mixed models to examine the factors influencing winter losses. We found that weather, climatic conditions, geography, land cover, genetic background, and beekeeping operation profiles contribute to winter losses to varying degrees. We also make predictions on the short, medium, and long-term impact of climate change on winter losses and distributions under various scenarios. Our study highlights the importance of considering multiple factors in understanding the distribution and survival of honey bee populations and provides essential information for policymakers and beekeepers to improve the management and protection of honey bee populations. Overall, our study represents a significant advancement in our understanding of the factors driving intra-specific turnover and winter losses and helps us better predict the impacts of climate change on biodiversity.

Keywords: honey bee subspecies, winter losses, climate change, anthropogenic factors, gradient forests, generalized dissimilarity modeling, genetics, land cover, beekeeping operations, biodiversity

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The role of cuticular waxes in drought response and tolerance in *Populus trichocarpa* (black cottonwood)

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The study investigates the effects of drought stress on the productivity of *Populus trichocarpa* (black cottonwood) trees, a species with high transpiration rates, by examining changes in the composition of leaf cuticular waxes. Cuticular waxes are crucial for regulating non-stomatal water loss and include long-chain fatty acid metabolites, flavonoids, tocopherols, triterpenoids, and phytosterols. By comparing the cuticular wax composition of natural populations grown under control and drought conditions, the study identified candidate genes associated with cuticular wax biosynthesis and regulation using GWAS. The study found that the overall wax content of black cottonwood is less sensitive to drought than individual wax constituents, with alkenes, alcohols, and esters contributing to drought response and tolerance. The study uncovered two known genes, CER1 and FATB, linked to fatty acid biosynthesis and novel components involved in coordinating drought responses in poplar trees, highlighting the plasticity of cuticular waxes in responding to drought environments. This research has important implications for understanding the potential impacts of climate change on poplar trees and identifying strategies for improving their drought tolerance.

Keywords: black cottonwood, drought stress, leaf cuticular waxes, GWAS

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Investigation of the effect of sexual cannibalism on sex ratio in a natural population of two different praying mantis species

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Sexual cannibalism is the behavior of one sex to consume the other sex as food, and it can cause a skewed sex ratio. The possible effects of sexual cannibalism in the mantises on the sex ratio in the population have not been adequately clarified, and related studies have only been studied in species with similar phenology and known to show cannibalism. The effects of cannibalism on sex ratios in populations can be better investigated by utilizing this difference in strategy in closely related species where cannibalism is common and absent. There is no evidence that *Empusa fasciata*, which has a different phenology from the mantid species studied so far, exhibits cannibalism behavior in nature. In this study, cannibalism was tested in *Mantis religiosa*, where cannibalism is common, and *E. fasciata*, where cannibalism is common, with two different diets and phenologies, and sex ratios in natural populations were followed. While 30% cannibalism was observed in *M. religiosa*, no cannibalism was detected in *E. fasciata*. As a result of this study, while female-biased sex ratio was observed in the nymphal stage in *M. religiosa*; The male-biased sex ratio at the adult stage turned to female-biased from the breeding season. In *E. fasciata*, the sex ratio, which was close to 1:1 in the nymphal stage, shifted towards female bias over time and continued with female bias in the adult stage. This result can be interpreted as cannibalism is effective in shaping the sex ratio of the population in the adult stage.

Keywords: sexual cannibalism, sex ratio, *Empusa fasciata*, *Mantis religiosa*, population dynamic

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Climate change and anthropogenic interactions modulates habitat suitability of brown bears across Türkiye

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Climate change and increasing human land use in natural areas change the land cover synergistically and lead to fragmented habitats, reducing suitable patches for species. Large carnivores are one of the most vulnerable groups to such changes. In this study, we predicted the spatial distribution of brown bears, the largest carnivores living in Türkiye, using the ensemble modeling approach, considering the anthropogenic, bioclimatic, and topographic variables for both current and future projections. Accordingly, while suitable habitats correspond to 20% of the country (154,302 km²), most suitable area is in the Euro-Siberian, Irano-Turanian, and Mediterranean biogeographic regions. The most important contributing variables were Distance to forest (27%), Mean diurnal range (BIO2) (17%), Annual mean temperature (BIO1) (10%) and Isothermality (BIO3) (10%). When the averages of different general circulation models (MIROC6, CNRM-CM6-1, MPI-ESM1-2-LR) were taken for future projections, we determined that habitat loss will vary between 42-51% in 2050 and between 42%-70% in 2070, depending on the scenario (RCP2.6, RCP7.0, RCP8.5). While the biggest losses were in the Mediterranean, Irano-Turanian, and Euro-Siberian regions, an 80% loss was projected for the Mediterranean region in 2070. Furthermore, we show that brown bears are expected to shift further north due to climate change and that the extent of range shifts varies with respect to elevation. As the impact of climate change increases, the decreasing proportion of protected areas in suitable habitat indicates that a conservation gap will occur in the near future. These findings indicate the need to develop urgent conservation strategies to protect the suitable habitats of brown bears and to plan connectivity studies to support their fragmented populations.

Keywords: species distribution modeling (SDM), brown bear (*Ursus arctos*), climate change, land use land cover (LULC), habitat suitability

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SESSION V: MICROBIAL ECOLOGY

Keynote address: Making a microbiome: unraveling ecological and evolutionary influences in wild rodents

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The mammalian gut teems with a dense and diverse community of microbes, the gut microbiota. More than just passengers, these symbiotic microbes are now known to play key roles in a diverse range of biological processes within the host – shaping nutrition, metabolism, immune development and pathogen resistance. Despite the gut microbiota's biological importance, these communities display staggering variability in free-living animal populations and we are just beginning to understand how different forces combine to shape them over ecological and evolutionary timescales. In this talk, I'll present our recent work exploring how host evolutionary history, social interactions and other factors all shape the microbiome of wild mammals, and the implications for understanding the role of these symbiotic communities in the lives of their hosts.

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Altitudinal Effect on Gut Microbiome Composition of Long-Living and Cancer-Free Blind Mole Rat (*Nannospalax xanthodon*)

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The mammalian gut is colonized by microorganisms that affect development, immunity, energetics, and reproduction. Since most studies focused only on laboratory animals and in artificial setups, more studies based on the wild species are necessary. Altitude is an environmental factor associated with numerous biotic and abiotic variables involved in modulating gut microbiota in the wild. However, current knowledge on altitudinal differences in gut microbiota is based on only a few empirical studies and species with similar ecology.

Anatolian Blind Mole Rat, *Nannospalax xanthodon* is a subterranean rodent with very unique adaptations to subterranean life, and wide altitudinal distribution. Using two populations in three altitude categories each ranging from ~1000 m. asl to ~3000 m. asl, a total of 56 individuals, we tested the effects of altitude on microbiome composition using 16S rRNA. The study addresses the following two main questions; (i) Is altitude a major factor affecting the microbiome composition? and (ii) Does the microbiome diversity correlate with the altitude?

Gut microbiome composition generally aligned well with previous studies on same or closely related species. The middle altitude animals have higher alpha diversity, which is also seen on the OTU differential abundance testing: middle altitude samples have highest number of the most unique OTUs compared to other altitudes. Besides the alpha diversity, there is a (significant) linear effect of altitude on the gut microbiome composition, the microbiome composition is significantly getting richer with increasing altitude.

Keywords: 16S rRNA, metabarcoding, microbiota, wild, rodent, mole rats

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Rock structure drives the taxonomic and functional diversity of endolithic microbial communities in extreme environments

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In the driest and hottest deserts around the world, as a last refuge for life, microorganisms colonize insides of the rocks (endoliths) to seek shelter from water scarcity and extreme UV radiation. These are simple communities composed of Cyanobacteria as the main primary producers along with an assortment of heterotrophic taxa like Proteobacteria, Actinobacteria, Chloroflexi and Deinococcus. Understanding what the eco-evolutionary mechanisms are that drive the diversity of these endolithic communities is essential for predicting the fate of the ecosystem during climate change and desertification scenarios. Here, our goal was to explore how key environmental variables like water availability and rock structure shaped community composition and functions of gypsum (calcium sulfate) endoliths in the Atacama Desert, one of the oldest and driest deserts on earth. Using computed tomography scanning together with amplicon and metagenomic sequencing, we compared the taxonomic and functional composition of gypsum endoliths that colonized distinct micro-habitats in terms of water availability and rock structure. We found that surprisingly, regardless of lower water availability, the diversity increased in a more fragmented rock structure due to a potentially higher number of micro-niches available for colonization, reflected also in the types of microbial associations. Gypsum communities were functionally similar, yet adapted to their unique micro-habitats by modulating their carbon and energy acquisition strategies and their growth modalities. Reconstructed population genomes showed that these endolithic microbial populations encoded potential pathways for anoxygenic phototrophy and atmospheric hydrogen oxidation as supplemental energy sources.

Keywords: endolithic communities, Atacama Desert, gypsum, extreme environments, metagenomics

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Shore flies (Diptera, Ephydriidae) adaptation to extreme habitats: morphology and symbiotic microbiota

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Larvae of many shore-fly species (family Ephydriidae) develop in water with high or extremely high salinity, which is unusual enough for insects to live in seawater. Our goal is to clear up the mechanisms of the manifold adaptations to such extreme habitat. We study *Ephydra riparia* and *Paracoenia fumosa* flies inhabit White Sea littoral and describe morphological features and symbiotic yeast microbiome that can contribute to halotolerance of that species.

For the first time, by silver-staining and SEM, we proved that the larvae of both studied species had anal organs (AO) – specialized structures serve osmoregulatory function and responsible for the transport of ions from the environment to the larval hemolymph, and compared AO with homological structures of extremely halophilic and freshwater shore-flies and *Drosophila melanogaster*.

Experiments on the laboratory lines of *Drosophila* proved the contribution of yeast to fly adaptation to salty substrate. We suggested that halophilic and halotolerant flies may be associated with special groups of symbiotic yeasts. By seeding experiments and analysis of sequences of the ITS rDNA region we studied the content of yeast microbiome of shore-flies, substrate, water, and algae. We found that the yeast community of flies was not identical to one of the substrates; the microbiome of imagoes, pupae and larvae differ significantly. *P. fumosa* had poor enough yeast community, but the intestines of *E. riparia* are filled with yeasts. Yeast living in larval gut didn't find in the surrounding substrate. They might contribute to success adaptation of their host to salt water.

The study was funded by the Russian Science Foundation, project No.22-24-00156, <https://rscf.ru/en/project/22-24-00156/>.

Keywords: shore flies, *Ephydra riparia*, *Paracoenia fumosa*, yeast microbiota, anal organs, halotolerance

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Conserved gut microbial guilds across the human life stages

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The gut microbiome plays a crucial role in human health, but its significance during different life stages remains uncertain. Nevertheless, research has shown that the gut microbiota follows a predictable transition from infancy to adulthood. As the gut microbiome ages, it becomes less diverse, has a more unique composition, and a lower abundance of bacteria that produce short-chain fatty acids (SCFAs). Although certain bacteria are commonly associated with early or late life stages, our knowledge of associated bacterial guilds and their interactions is still limited.

Our study examined age-type gut microbiomes and their evolution over time by analyzing nearly 9,700 publicly available faecal metagenomes from 36 studies worldwide. We found that individuals in the same life stage tend to have consistent microbial guilds coexisting in their gut despite differences in genetic background and lifestyle. We hypothesize that these microbial guilds form the basis of a healthy gut flora. Analyzing microbial composition and intricate interaction networks among bacteria revealed crucial colonization patterns that decline in the mature adult microbiome but reappear in the elderly. Finally, we investigated the evolutionary forces shaping microbial communities in different age groups, contextualizing our findings within an evolutionary framework. Our study underscores the importance of microbial guilds in the gut and their evolution during different phases of human life.

Keywords: gut microbiome, metagenomics, meta-analysis, ageing

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SESSION VI: BIOGEOGRAPHY AND SPATIAL ECOLOGY&POPULATION AND WILDLIFE ECOLOGY

Destabilising effect of climate change on population persistence

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Seasonal tropical environments are among those regions that are the most affected by shifts in temperature and rainfall regimes under climate change, with potentially severe consequences for wildlife population persistence. This persistence is ultimately determined by complex demographic responses to multiple climatic drivers, yet these complexities have been little explored in tropical mammals. We use long-term, individual-based demographic data (1994-2020) from a short-lived primate in western Madagascar, the gray mouse lemur (*Microcebus murinus*), to investigate the demographic drivers of population persistence under observed shifts in seasonal temperature and rainfall. While rainfall during the wet season has been declining over the years, dry season temperatures have been increasing, with these trends projected to continue. These environmental changes resulted in lower survival and higher recruitment rates over time for gray mouse lemurs. Although the contrasting changes have prevented the study population from collapsing, the resulting increase in life-history speed has destabilised an otherwise stable population. Population projections under more recent rainfall and temperature levels predict an increase in population fluctuations and a corresponding increase in the extinction risk over the next five decades. Our analyses show that a relatively short-lived mammal with high reproductive output, representing a life history that is expected to closely track changes in its environment, can nonetheless be threatened by climate change.

Keywords: demography, gray mouse lemur, population dynamics, environmental change, seasonal rainfall, seasonal temperature, reproduction, survival, population persistence, primate, life history, Madagascar

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Harmonized estimation of wild ungulate densities throughout Europe

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The European Observatory of Wildlife (EOW, <https://wildlifeobservatory.org/>) is an EFSA-funded (European Food and Safety Authority) initiative run by the ENETWILD project (www.enetwild.com). The EOW aims to improve harmonizing wildlife monitoring methods throughout the Europe and provide the possibilities to estimate the density of wildlife across the continent. In 2022, synchronic camera-trapping surveys were conducted in 37 European areas, grouped in four bioregions. This provided a unique scenario where the same methodology and protocols are applied by trained teams, covering a varied and widely distributed set of study areas all over Europe. We assessed the variation in daily range and activity level of terrestrial mammals by using camera traps and identified factors determining their variability: species, population, geographical, environmental, biological, and management. Our recommendations for monitoring and conservation programs will help to estimate movement parameters for the target population and survey, ideally from camera-trap data.

Keywords: density estimation, camera traps, harmonizing methods, wildlife monitoring, European observatory of wildlife

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Wolves' feeding ecology across the Anatolia

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The diet of wolves can reveal their feeding behavior and their prey-predator relationships. In Türkiye, wolves have a wide range of habitats, from the coast to the alpine mountains, and their diet varies across different regions. However, the causes of this variation are unclear. To understand the dietary patterns of wolves in Anatolia and their influencing factors, we collected feces from two areas with different vegetation, ungulate population densities, and livestock numbers: the northwestern deciduous and mixed forests (n=76, mean elevation=1000 m a.s.l) and the northeastern coniferous forests and alpine grasslands (n=35, mean elevation 1850 m a.s.l). We analyzed the diet items in the feces using point frame methods and rarefaction curves. We also compared the human-wolf conflicts with the proportions of domestic livestock and wild ungulates in the wolf diet. We found 17 different food items in the wolf diet. The volume of wild animals decreased from 91% in the western region to 59% in the eastern region, while the volume of domestic livestock increased from 4% to 36%, respectively. This also correlated with the severity of human-wolf conflicts, which were mainly food-based, although the livestock numbers were lower in the eastern region. We concluded that the wolf diet and the human-wolf conflicts were more related to the availability of wild animals and the animal husbandry practices than to the livestock numbers, compared to previous studies. We suggest more personalized small regional conflict preventive measures regarding small animal husbandries.

Keywords: wolf, diet, human-wolf conflict, wildlife

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Higher functional diversity is associated with higher functional stability in bird communities

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Aim: Bird communities worldwide are suffering from declines in abundance and diversity as a result of human-induced land cover changes and climate change. The aim of this study is to test whether the taxonomic and functional stability of breeding bird communities, measured as the inverse of temporal beta diversity, is affected by the diversity of the communities. We expected that communities with high functional diversity would resist change better, while communities with higher taxonomic diversity would be less stable due to the presence of many rare species in richer communities.

Materials and methods: We focused on Gediz Delta, which is an important bird area in western Türkiye. We obtained data from two breeding bird atlases conducted in 2006 and 2021, both of which had 1x1 km spatial resolution, resulting in usable data from 184 grid cells. A total of 122 breeding birds were included in the analysis. We selected 14 functional traits representing different niche dimensions and retrieved data from the Elton Traits and AVONET databases. We calculated several functional diversity metrics, representing different aspects of functional diversity.

Results: We found that higher values of some functional diversity measures, such as functional divergence and functional dispersion, were associated with higher functional stability of the communities. Contrary to our expectations, none of the diversity metrics were significantly associated with taxonomic stability.

Discussion and conclusion: Our results suggest that the functional diversity of the communities may be an important conservation target to ensure the persistence of ecosystem functions and services.

Keywords: compositional stability, functional diversity, functional stability, ecosystem functions, temporal beta diversity

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A Hybrid Modeling Framework to Project *Impatiens glandulifera* Invasion in North America

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Biological invasions are a major component of global environmental change and cause severe ecological and economic impacts. Since the post-entry eradication of an invasive species is extremely costly and even futile in many cases, prevention is considered the most effective strategy. In this respect, the models to project areas under risk and evaluate the potential invasion scenarios are crucial tools. *Impatiens glandulifera* is considered one of the most notorious invasive species. Its invasive range spreads across the Northern Hemisphere, primarily in Europe, in highly diverse habitats. While its occurrence is reported in both the east and west parts of North America, studies on its fate under climate change are quite limited, considering that it is thought to be far from reaching its geographical potential. In this study, we constructed a hybrid and spatially explicit modeling framework by utilizing Maxent and an agent-based model developed in R to project the fate of *Impatiens glandulifera* invasion in North America for the 2020-2050 period under RCP 4.5 scenario. The results of the simulations showed a predominant northward progression and aggressive expansion to the interior parts, which implies a potential formation of a continuous range across the continent.

Keywords: invasion ecology, invasive species, *Impatiens glandulifera*, species distribution modeling

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Investigating the changes in spring phenology of *Fagus orientalis* in Turkey using remote sensing

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Plant phenology is accepted as one of the most sensitive bioindicators of climate change and phenological shifts, e.g., a shift of the start of season (SOS) date, are considered a vegetation response to climate change. However, phenological observation records are not available for many countries, regions, and ecosystems. Land surface phenology (LSP) constitutes a valuable tool to track vegetation phenology in the absence of observational data and provides long-term, continuous data from local to global scales. This study aimed to investigate the phenological shifts of *Fagus orientalis* forests in Turkey by extracting SOS, the length, and the end of season (LOS and EOS) parameters from normalized difference vegetation index (NDVI) time series, which was calculated from daily MODIS surface reflectance data (MOD09GA) for 2002 – 2020 period and the entire Turkey extent. This extent was masked for pure *F. orientalis* pixels to minimize the mixed pixel effect. The remaining pixels were filtered with temporal and spatial coverage thresholds. Trend analysis for the study period showed an earlier spring with an advancing SOS pattern, in accordance with the results frequently reported in the literature. Relationships between the mean SOS trend and climate variables (mean, maximum and minimum temperature, growing degree days, and chilling hours) over the study period were also assessed.

Keywords: phenology, land surface phenology, MODIS, *Fagus orientalis*

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Nitrate Availability Can Inhibit Methane Emissions in Central and Western Anatolian Shallow Saline Lakes

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Field surveys were conducted in early summer in 33 shallow, saline, and brackish lakes (salinity ranging from 0.4 to 220 ppt) based in two closed basins in central-western Anatolia and southwest and eastern Mediterranean coastal zone to quantify the greenhouse gases (CH₄, CO₂, N₂O) emissions and to elucidate the environmental drivers controlling them. The diffusional fluxes of GHGs were determined in the littoral and pelagic zones of the lakes using flux chambers. The average CH₄, CO₂ and N₂O fluxes ranged between 0.05-134, -44-2576 and 0-0.99 mmol m⁻² d⁻¹, respectively, with shallower and less saline water bodies generally having higher methane emissions. Salinity was the main control of methane emissions from the studied lakes as in the lakes with 5+ ppt salinity CH₄ emissions were strongly inhibited, while CO₂ emissions showed a more complex response to salinity. Moreover, NO₃ availability was also inhibitory for CH₄, especially over 100 µM, which can be plausibly attributed to the anaerobic (nitrate) oxidation of methane while on the other hand, NO₃ concentration and low pH was usually associated with high CO₂ fluxes, which can be indicative of high respiration/mineralization activity. In the sub-saline range (0-5 ppt), where the control posed by salinity become less prominent, methane emissions are positively associated with the TN and TP, which can be interpreted as a result of enhanced methanogenic activity with the availability of organic substrate.

Keywords: saline lakes, GHGs, methane, climate change

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Time, not resource availability, is a better predictor of successional patterns of saproxylic beetles on decaying wood

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Decaying wood is a declining habitat in forest ecosystems yet it supports diverse insect communities. There is no clear information on the effect of host trees and their decay stages on temporal patterns of saproxylic, i.e. deadwood-dependent, beetle diversity. To fill this gap, we conducted an experiment over eight years with logs of several angiosperm and gymnosperm tree species. At logs that have decayed 34-71% in eight years, alpha diversity peaked earlier in gymnosperms than angiosperms and then decreased similarly in hosts from both plant divisions. We also found differences in temporal patterns of tree species within each division. Annual gamma diversity of saproxylic beetles increased in time in both divisions. Angiosperms were richer in terms of alpha and annual gamma diversities. Year, not the wood density as a proxy for the decomposition stage, was a better predictor of alpha and annual gamma diversities, indicating the importance of other factors such as ordered emergence patterns, priority effects of fungi and beetles. We found no correlation between decay levels of trees, a proxy for the diversity of microhabitats, and gamma diversities at the end of the experiment. Still, the overall gamma diversity differences between some tree species at the end of eight years diminished when wood decay stages are taken into account. Our findings imply that there is no single richest host species along the decay. On the contrary, pines, which are commonly used in plantations, supported relatively poor communities. Therefore it is important to maintain a diversity of deadwood in terms of taxonomy and decay stages to support insect diversity in forests.

Keywords: succession, brown food web, decomposition, deadwood, saproxylic, insect communities, alpha diversity, gamma diversity

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Drivers of among-population variability in fire-related traits in Turkish Red Pine (*Pinus brutia* Ten.)

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Mediterranean pines have many traits that enable adaptation to fire regimes. These traits exhibit variability among species, populations, and individuals. We investigated the variability of fire-related traits, namely serotiny, bark thickness, and self-pruning in Turkish red pine (*Pinus brutia* Ten.) across different spatial scales. Additionally, we examined whether fire regime and climate explain the variability of these traits and evaluated their broad-sense heritability. Field studies were conducted in long-unburned Turkish red pine forests in southwestern Anatolia (Turkey) to collect leaf samples and make measurements on individuals, and followed by genetic analysis in the laboratory. Turkish red pine had relatively lower serotiny levels compared to other serotinous Mediterranean pines, but exhibited thick bark, and signs of self-pruning. All traits displayed significant variability across the spatial scales studied, with fire regime zones and some climatic variables accounting for part of this variability. We detected heritability in serotiny, bark thickness, and self-pruning to some extent. Our results suggest that the fire regime is an important factor influencing trait variability in Turkish red pine, and reveal that fire-related traits possess a genetic basis in this species. Our study contributes to understanding the role fire in shaping the ecology and evolution of Mediterranean pines, specifically Turkish red pine.

Keywords: fire, *Pinus*, trait variability

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ABSTRACTS OF POSTER PRESENTATIONS

Population Genomics of Crohn's Disease Susceptibility

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Crohn's disease (CD) is an inflammatory bowel disease that causes chronic inflammation of the gastrointestinal system. The clinical features, genetics, and epidemiology of CD vary considerably between geographic regions and ethnic groups. Available data suggest an interaction between genetic predisposition and environmental factors in the development of CD. The genetic makeup that increases CD susceptibility in modern populations claimed to be a derived trait that provides selective advantage against certain environmental stressors, such as resistance to infections and pathogens. Therefore, there must be signs of selection in the genes associated with CD. To test whether CD risk is a derived selected trait, CD-associated genes and variants were identified through literature searches. Ancient and modern population data were collected through the Allen Dataset and 1000 Genomes Project. Data was analysed using Plink and custom R scripts. We identified 352 CD risk alleles, and compared the disease risk status (protective vs. susceptible) of CD-associated alleles with their ancestral and derived status. The differentiation of five worldwide metapopulations with respect to these alleles is examined. Moreover, allele frequency differences between ancient and modern populations are compared. Genetic differentiation and discrimination between metapopulations were determined to be due to the effect of the CD-related PUS10, PPBP-CXCL5 and HERC2 genes in particular, and was evident where populations with higher CD prevalence had higher risk allele frequencies. Variants in CD-associated IRGM, OR2B11 and IL10 genes showed high allele frequency changes through time when ancestral and modern populations were compared. Extended haplotype structure analysis-based tests suggested recent selection acting on several CD genes.

Keywords: Crohn's disease, genetics, GWAS, selection, susceptibility

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Investigation of microplastic concentration in commercial fish species in Gemlik Bay (Marmara Sea)

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Microplastic pollution is a worldwide phenomenon. Microplastic density has enhanced and accumulated over decades in aquatic ecosystems and caused many physiological problems in living organisms. In this study, we aimed to evaluate and characterize the microplastic pollution in the commercial fish species in Gemlik Bay, the Marmara Sea. Thus, microplastic pollution in this important bay, surrounded by industrial facilities and well known for the intensity of fishing and tourism activities, was revealed in detail for the first time. Attention was paid to the fact that the fish species selected for the study have different nutritional and habitat preferences and are also consumed by humans. To detect microplastics in the gill and gastrointestinal tract, the organic material was fragmented and filtered off. Plastics from the remaining inorganic materials were counted under the microscope and Raman analysis was performed for polymer characterization. Our results showed that the highest microplastic concentration per individual was in the gills of *Synapturichthys kleinii* (Risso, 1827) (14.5 pieces.ind⁻¹) and the lowest in *Diplodus annularis* (Linnaeus, 1758) (0.33 pieces.ind⁻¹). The highest concentration (8.75 pieces.ind⁻¹) was indicated in the gastrointestinal tract of *Chelidonichthys lucerna* (Linnaeus, 1758), but the lowest concentration (0.88 pieces.ind⁻¹) was in that of *D. annularis*. The fiber-type particles were the most determined microplastics in the samples. The Micro-Raman Spectrometer revealed that polyoxymethylene and polyphenylene sulfone polymers dominated fish species. Our results encompassing commercial fish species have provided a perspective about the effects of microplastic pollution on the human population.

Keywords: microplastic, Micro-Raman, commercial Fish

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Genetic mechanisms of adaptation in *Isophya rizeensis* bush cricket along environmental gradient

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This study aims to understand the genetic mechanisms of adaptations that enable species to survive under changing environmental conditions using the univoltine bush cricket species *Isophya rizeensis* as a model system. The species has a remarkable altitudinal distribution, starting from sea level to 2500 meters, and shows distinct clinal patterns in dorsal coloration and body size variation along the steep altitudinal gradient. These patterns are associated with temperature and precipitation, making *I. rizeensis* an excellent system for studying the genetic mechanisms of adaptation. To this end we sampled individuals from the total range of *I. rizeensis* and from an altitudinal gradient ranging from 350 to 2500 meters within the Firtina Valley and used RAD sequence data to determine genome-wide polymorphisms in a total of 96 individuals. To understand genetic structure and genetic differentiation along this gradient and to discover genomic regions associated with altitudinal change we conducted PCA and discriminant analysis based on genome-wide data. Preliminary results show a transitional area between pale and dark populations around 1400 meters supported by PCA and admixture analysis which show three distinct genetic clusters correlated with altitude. Discriminant analysis discovered 138 genomic regions with major contributions to differentiation between populations along the altitudinal gradient. These findings contribute to our understanding of the genetic mechanisms underlying adaptation to changing environmental conditions in ectotherms with fast generation times and wide distribution ranges.

Keywords: genome sequencing, evolutionary genetics, population genetics, landscape genetics, genome wide association studies, adaptation genomics, environmental change, biodiversity

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Determination of Microplastic Characterization of Turkish Endemic frog *Pelophylax caralitanus* from Isparta Province, Türkiye

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Amphibians are dual inhabitants of aquatic and terrestrial environments, making them valuable indicators of pollution levels in both habitats. In this study, we aimed to determine the microplastic (MP) accumulation in the digestive system of a population (n=11; Eğirdir Lake, Isparta province, Türkiye) of *Pelophylax caralitanus*, which is endemic to the lakes region in Türkiye. The species has been considered Near Threatened by the IUCN since 2008. The adult frogs' gastrointestinal tract (GIT) was removed, and its weight was determined. Next, each GIT was digested using 150 mL of 30% H₂O₂ at 65 °C at 80 rpm for three days. Then, the samples were passed through a Whatman GF/C filter. To confirm the origin of the polymer, a total of 20 particles, randomly selected from those visually identified as MP, were examined by Fourier Transform-Infrared spectroscopic analysis using a PerkinElmer Spectrum 100 spectrophotometer coupled with Attenuated Total Reflection. All of the MPs detected were fiber. Polymer type was determined as follows: 30% Poly cyclohexylene dimethyl terephthalate (PCT), 20% Ethylene-vinyl acetate (EVA), 20% Poly(hexamethylene dodecanediamide) (PD), 10% PR Poliamit resin (PR), 10% Polyethylene terephthalate (PET), 10% Polyvinyl alcohol (PVA). The minimum polymer length was 900 µm, the maximum was 2700 µm, and the average size was 1273 µm. The results indicate that it is critical to create appropriate waste management techniques to maintain the fragile water ecosystems of Eğirdir Lake and ensure the sustainable use of living resources in this region.

Keywords: amphibians, bioindicator, microplastic, pollution, polymer

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Ancient DNA illuminates population dynamics of the central Levant in the 2nd to 1st millennium BCE

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The 2nd to 1st millennium BCE in the central Levant has been extensively researched in historical records. Influenced by major political forces such as Assyria, Babylonia and the Persian empire, the Levant was marked by extended human mobility. However, this period remains genetically understudied, with inland sites particularly lacking from the genetic record. Therefore, it is unclear whether genetic interactions mirrored the cultural transformations apparent in the historical record. To address this, we have used in-solution target enrichment techniques to reconstruct ancient genome-wide data from c. 30 individuals excavated at present-day Lebanon, with a particular focus on a genetic time transect from the tell site of Kamid el-Loz, spanning from the Middle-Late Bronze Age to the Persian-Hellenistic period (approximately 1900 – 200 BCE). This site developed into a fortified city in the Middle Bronze period, with palace, temple and administrative structures, private dwellings and cemeteries. With this new genomic dataset and comparative genomes from other central Levantine sites, we present findings of genetic population structure during the Bronze Age, together with evidence of genetic continuity and change from the Bronze to Iron Age periods at Kamid el-Loz. These results offer new insights into regional genetic structure and human mobility from the 2nd to 1st millennium BCE, reflecting both local and inter-regional genetic interactions.

Keywords: conservation genomics, FROH, FST statistics.

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Distinguishing First-Degree Relationships From Ancient Samples With Machine Learning

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Estimating genetic relatedness between individuals using genomic data from ancient samples is of utmost importance; however, almost all current tools only distinguish between first, second, and third-degree relationship categories. This study aims to differentiate between parent-offspring and sibling pairs using deep learning in low-coverage ancient genomes. The ability to distinguish between these two first-degree relationship categories is vital for investigating long-gone cultural practices. The study began by simulating founders using the population genetic simulator msprime and the pedigree simulator ped-sim to create sibling and parent-offspring pairs under realistic demographic scenarios. Then we applied ancient DNA simulation in order to obtain ancient genomes. Next, using an allele-sharing coefficient statistic, we estimated the kinship coefficient across genomic windows containing 250 SNPs, i.e., the probability that two alleles at a given locus are identical by descent. We applied two-dimensional binning on them and trained a Central Neural Network algorithm using the resulting fixed-length vectors for each pair. We tested the algorithm under scenarios of the different numbers of shared SNPs and achieved 98% and 92% precision for pairs sharing 50K and 20K SNPs, respectively. Additionally, to improve the algorithm's accuracy, we studied the performance of curriculum learning and increased the sample size. This study demonstrates the potential for deep understanding to differentiate between first-degree relationships in low-coverage ancient genomes precisely and provides a foundation for future research in this field.

Keywords: deep learning, ancient dna, kinship

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Rhizosphere microbiome profile of the local endemic and critically endangered *Thymus pulvinatus*

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Plants are in strong relationship with the microorganisms in their environment and have their own microbiome. Thus, the plant microbiome consists of dynamic and specialized networks that increase the plant's adaptation for the relevant environment. Understanding the plant-microbiome dynamics is important in developing effective new strategies to protect endangered plant species from extinction and prevention of biodiversity loss. Kazdağı National Park, which is one of the most-known biodiversity hotspots of Türkiye, is home to numerous endangered endemic and rare plants. Among the endemic plants in this region, narrowly distributed local endemic *T. pulvinatus* is classified as critically endangered. In this study, we characterized the bacterial and fungal microbiomes of bulk and rhizosphere soil of *T. pulvinatus* by 16S rRNA gene and ITS amplicon sequencing. We revealed that bacterial microbiome profiles differentiated between soil types while fungal microbiome profiles were similar. According to estimated functional analyses, profiles of rhizosphere and bulk soil did not overlap while the rhizosphere samples were mostly found to consist of specific bacterial groups that can function in plant protection and survival mechanisms. This study presents an overview of differences and similarities between rhizosphere and bulk soil microbiome profiles of *T. pulvinatus*. Highlighting the importance of these interactions, these results provide a basis for research on plant endemism and rhizosphere microbiomes.

Keywords: plant endemism, *Thymus pulvinatus*, Kazdağı National Park, rhizosphere, soil, microbiome, amplicon sequencing

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Comparison of Flammability in Two Serotinous Mediterranean Trees

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Fire plays a crucial role in the life history of plants in Mediterranean ecosystems. Both evolutionary and filtering processes have shaped plant traits leading to flammable communities in these ecosystems, and many species with post-fire regeneration abilities possess traits that make them more flammable. Serotiny is one of these regeneration traits that involve the long-term storage of seeds within cones on the plant. In this study, we investigated the flammability of two serotinous conifer species, *Pinus brutia* (Turkish red pine) and *Cupressus sempervirens* (Mediterranean cypress) in the Marmaris region, southwestern Turkey. We measured several flammability parameters, including leaf functional traits (leaf moisture content, specific leaf area, leaf dry matter content, leaf thickness, and leaf curliness), flammability metrics (time to ignition, flame duration, fuel consumption, and mass loss rate), and branch traits (branch moisture content and branch fuel consumption). The results revealed significant differences in some flammability parameters between two species, with both species displaying either low or high flammability level depending on the traits examined. Contrary to the widespread belief that Turkish red pine is more flammable tree than Mediterranean cypress, our findings indicate that Mediterranean cypress also exhibited higher flammability than Turkish red pine in several traits examined. In summary, both species can be considered flammable trees when taking into account different aspects of the flammability concept. Our comparison offers valuable insights for evaluating afforestation and post-fire restoration activities, as well as "let it burn" and "green belt" strategies for fire management purposes in Mediterranean Basin forests.

Keywords: fire, flammability, functional traits

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Identification of Anterior Determinants in Ants

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Anterior-posterior (AP) axis formation is a critical process that occurs during embryonic development in bilaterian organisms, including insects. Several maternal anterior determinant genes are known to initiate the AP axis formation such as: TCF/Pangolin in *Anopheles*, *Parish* in *Chironomus*, *Curoid* in *Aedes* and *Culex*, *Zic/opa* in *Clogmia*, *Bicoid* in *Drosophila*, *Otd* in *Nasonia* and *Tribolium*. However, anterior determinant has not been identified in ants. Moreover, our previous study has shown that embryo formation in the carpenter ant *Camponotus* spp., occurs in the anterior region of the egg compared to those ants which lack endosymbiont. Here we propose a study to investigate anterior determinant candidate genes in *Camponotus floridanus*. Within the scope of this study, we will knockdown candidate genes by RNAi to test their function in anterior determination. The discovery of anterior determinant in ants will help us understand axis formation in this lineage. It will also shed light on how this pathway changed when the position of the embryo in the egg changed. Since anterior formation of embryo correlates with the presence of endosymbionts, this study will also help us understand interaction between endosymbiosis and AP axis formation.

Keywords: anterior-posterior axis formation, embryonic development, endosymbionts, *Camponotus floridanus*

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Molecular evolution of Myh7 proteins among mammals: a comparative, phylogenetic, structural, and interactional analysis

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Background/aim: Myosin heavy chain 7 (Myh7), is a protein involved in the control of cardiac and skeletal muscle function. It makes up a significant portion of the thick filaments in muscle sarcomeres, which are in charge of contracting the muscle. Cardiomyopathy and hypertrophic cardiomyopathy are two heart and muscle disorders that have been associated to mutations in the Myh7 gene. This study aims to reveal the molecular evolution of the Myh7 protein among mammals at comparative, phylogenetic, structural, and interactional levels.

Materials and methods: To do this, the Myh7 protein sequences of different mammalian species including human, chimpanzee, bonobo, gorilla, orangutan, macaque, and mouse were aligned, and then 3D protein structures were modeled and compared. Finally, phosphorylation profiles and protein interaction networks were predicted.

Results: Human Myh7 protein was more similar to chimpanzee one at the sequence level while it was more similar to gorilla one at the structural level. Human, chimpanzee, bonobo, gorilla, and orangutan Myh7 proteins were found more similar than mouse and macaque ones at the structural level. Humans and gorillas were more closely related to each other. Macaques and mice were more distantly related to them. PolyA region was found in all analyzed species. Also, a tyrosine residue (position 65) was only found in human among the compared mammals. All analyzed mammalian Myh7 proteins were found to have highly phosphorylated, especially in human, gorilla, and chimpanzee ones. Myl2, Myl3, Myl4, Tnni1, and Mybpc3 proteins were predicted in the interaction network of Myh7 proteins in all analyzed mammals.

Conclusion: Among all analyzed mammals, the Myh7 protein was evolutionarily conserved at the sequence, structural, and interactional levels with a high phosphorylation profile. The outcomes of this study bring new perspectives into the molecular evolution of Myh7 proteins in mammals.

Keywords: Myh7, molecular evolution, structural modeling, protein interaction, mammals

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Molecular evolution of Maa proteins among mammals: a comparative, phylogenetic, structural, and interactional analysis

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Background/aim: Monoamine oxidase A (Maa) is an oxidoreductase that facilitates the oxidation of neurotransmitters like dopamine, serotonin, and norepinephrine. Maa also undergoes posttranslational modifications such as N-glycosylation and phosphorylation for its proper folding and stability. Dysfunctions in Maa can lead to neuropathologies in mammals. This study aims to reveal the molecular evolution of the Maa protein among mammals at comparative, phylogenetic, structural, and interactional levels.

Materials and methods: Maa protein sequences of different mammalian species including human, chimpanzee, bonobo, gorilla, orangutan, macaque, and mouse were aligned, and then 3D protein structures were modeled and compared. Finally, N-glycosylation and phosphorylation profiles and protein interaction networks were predicted.

Results: Human Maa protein was found structurally more similar to gorilla among all analyzed species. At the initial part of the alignment, a gap was found in chimpanzee according to alignment outcomes. However, chimpanzee and bonobo had more matches from other species in relation to the length of the alignment. N-glycosylation profiles of the human, gorilla, bonobo, and orangutan species were found conserved between them. Additionally, two conserved phosphorylation profiles were found in macaque, chimpanzee, and bonobo, orangutan. These two groups were more likely to have similar phosphorylation sites. Also, macaque and chimpanzee species were found to have highly phosphorylated Maa than the other ones. Ddc, Comt, and Aldh2 proteins were predicted in the interaction network of Maa proteins in all analyzed mammals.

Conclusion: Maa of human, gorilla, and bonobo were more similar according to their post-translational profiles and structural comparison. Maa is responsible for catabolizing amine neurotransmitters, so these findings in the study give us a new aspect of the molecular evolution of Maa proteins among mammals.

Keywords: Maa, molecular evolution, structural modeling, protein interaction, mammals

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Hox gene function in ants that have intracellular endosymbiotic bacteria

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Hox genes encode highly conserved transcription factors that define identity of the segments during embryogenesis in all bilaterian animals including insects. In ants so far, the homeotic function of hox genes has not been explored. It has been suggested through differences in expression of hox genes of bithorax complex that the defining body parts of petiole and post-petiole evolved under the influence of these genes. Here we explore the expression and homeotic function of Bithorax complex genes in *Camponotus floridanus*. However, the homeotic function of these genes has not been possible to assess due to an early lethal phenotype attributed to the presence of endosymbiont. These genes are expressed maternally, and their loss-of-function phenotype causes lethality by truncation of the abdomen. This is a departure from the known homeotic phenotype attributed to these genes and disallows study of their homeotic function. To circumvent this limitation, in this project, we selectively target the zygotic genome using CRISPR/Cas9-mediated knockout to test the homeotic function of these Hox genes and use in situ hybridization to test the expression of these genes in *C. floridanus*. This study paves the way for understanding the role of these Hox genes in the evolution of novel body parts in ants.

Keywords: Hox genes, Bithorax complex, petiole, post-petiole, endosymbiont, *Camponotus floridanus*

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Investigating genomic processes underlying rapid divergence and speciation in *Phonochorion*

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The phenomenon of rapid divergence and speciation in high-altitude species due to repeated patterns of isolation and secondary contact has been observed in the cricket genus *Phonochorion*, which is found only in the sky islands of the Caucasus Mountains in the Northeastern Black Sea region of Türkiye. Previous studies have shown that these crickets diverge rapidly between species and show higher rates of reproductive isolation when in sympatry versus allopatry. This study aims to examine the genomic processes underlying this observed rapid divergence and speciation by comparing the levels of diversity and adaptation across the genome in two species of *Phonochorion*.

The hypothesis of this study is that populations of *Phonochorion* species in sympatry should exhibit relatively higher levels of genomic diversity compared to conspecifics in allopatry. Additionally, it is expected that genomic loci responsible for local adaptation should differ in nature and intensity between species in sympatry versus allopatry. Understanding these genomic processes can shed light on the mechanisms responsible for the rapid divergence and speciation observed in these crickets.

Overall, the study seeks to investigate the role of genomic diversity and adaptation in the rapid divergence and speciation of high-altitude species. The results of this research will provide valuable insights into the genomic processes that drive the evolution of biodiversity in the unique and fragile ecosystems of the sky islands of the Caucasus Mountains.

Keywords: *Phonochorion*, speciation, local adaptation, rapid divergence, sympatry, allopatry

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Tracing Spatiotemporal Changes in Skin Pigmentation Diversity in Holocene Anatolia

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The Neolithic era was a period of significant socio-economic and cultural changes, comprising major shifts in lifestyle, from nomadic to sedentary, with the adoption of agriculture and animal domestication. These changes had genomic consequences as well, introducing novel selection pressures. Indeed, dietary shifts were suggested to induce such pressure, involving Vitamin D deficiencies related to a more plant-based diet. SLC24A5, a skin pigmentation associated gene, promotes Vitamin D synthesis, and was suggested to be advantageous during times of change. As skin color variation presents a diversity of phenotypes among different human groups, adaptive selection on SLC24A5 has been studied extensively in both modern and ancient populations. Accordingly, a strong signal of selection was observed in Early Neolithic European farmers, whereas the selected alleles were found to be already fixed in Neolithic Anatolians. Considering an earlier selection pressure on the SLC24A5 alleles in Anatolia, we study these alleles throughout Neolithic Anatolia, using n=81 ancient genomes from literature. Comparing with neutral alleles of similar frequencies, we tested whether the observed signals can be a product of genetic drift alone. We also extend our analysis to subsequent time periods until present day. Overall, we present a spatiotemporal scan of allelic changes in the well-known skin pigmentation gene SLC24A5, through a time span of c.10,000 years and 46 sites in Anatolia.

Keywords: ancient DNA, Anatolia, selection, skin pigmentation

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First step to understand thermal adaptation in the fungal pathogen *Monilinia fructicola*

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Temperature is an important factor affecting growth in fungal organisms. Temperature adaptations of different fungal species and their success in adapting to changing temperatures may differ. Considering climate change, knowing the temperature adaptations of pathogenic organisms is important to be prepared for possible epidemic scenarios. In this direction, we aimed to understand the effect of temperature on the mycelial growth of *Monilinia fructicola*, the fungal pathogen of brown rot disease in stone fruits such as peach. As an initial step, a total of 15 isolates were selected from six different cities in Turkey. Mycelial growth values were determined at five temperatures between 17-29°C by 3°C gradual temperature difference based on 23°C, which is the optimum in vitro growth temperature of the pathogen. The ANOVA models were used to compare the mycelial growth of the isolates at each temperature tested. The factors 'temperature' and 'city' were highly significant ($P < 0.001$). The smallest colony areas were recorded at 17 °C and 29°C. Moreover, the heritability of the temperature growth response of the isolates at each temperature was estimated by using a one-way model. The proportion of variation of the the ANOVA models were found to be approximately 0.90 and above, and the 'isolate' term was highly significant ($P < 0.0001$) in all analyses. These results provided the first data on the thermal adaptation of this important phytopathogen and indicated that the success of adaptation to stressing temperatures should be considered. This study was supported by the Scientific Research Projects Coordination Unit of Çanakkale Onsekiz Mart University, Project No: FLÖAP-2023-4304.

Keywords: *Monilinia fructicola*, fungal growth, thermal adaptation

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Genetic assimilation of host genes responding to the signal from endosymbionts

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Endosymbionts have been shown to influence the gene regulatory regions of their hosts during the co-evolution of the interacting partners. The exact molecular interactions between the signal molecules and the regulatory regions are relatively unknown. During the continued persistence of the endosymbiotic association, some of the target host genes undergo genetic assimilation such that the continued presence of the endosymbiont is not needed for their regulation. Target genes that do not undergo assimilation continue to depend on the endosymbiont for their regulation. We exploit these types of interactions to understand the continued communication between the endosymbiont signals and the host genes. More specifically, we focus on identifying the enhancer region within the *Camponotus floridanus* genome that responds to the signal of its endosymbiotic bacteria *Blochmannia* causing novel expression of the gene abdominal A, a gene that actively responds to the experimental removal of the endosymbiont. We designed a reporter gene assay that contains the enhancer fragments of this gene. This will help identify the putative target element responding to the bacterial signals. In the future, we plan to use this method to test other host gene enhancers and the enhancer region of abdominal A in closely related species. We will be able to address the question of how endosymbiotic signaling becomes genetically assimilated during the course of co-evolution of endosymbiont and host.

Keywords: enhancer, genetic assimilation, endosymbiosis

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Human Brown Bears Conflict Risk Across Türkiye's Human Dominated Landscapes

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Wildlife-human conflicts are one of the most challenging issues facing large carnivore conservation and can reduce the success rate of such programs. Brown bears, which suffer from reduced habitat suitability and quality, frequently conflict with humans. These animals need to cover large areas to fulfill their habitat requirements, therefore, they frequently make use of human based resources such as open garbage dumps, beehives and livestock in human dominated landscapes. As a country in which most of the natural areas are human-dominated, human-brown bear conflicts (HBCs) are a prominent event in Türkiye. In this research, we collected HBC events across the country through media coverage and compared the results by years, seasons, and regions to understand the spatial and temporal dynamics of HBCs. Moreover, we used an ensemble modeling approach to determine conflict risk probabilities across the country based on conflict events points and anthropogenic variables. The comparison among the frequencies of HBCs by years, seasons, and regions were all significantly different. The main contributing variables in the HBCs were Distance to villages (37%), Distance to protected areas (18%), Distance to farmland (16%), Human footprint (13%), and Population density (7%), respectively. Furthermore, we found that in total 21% of the country (164,548 km²) was under conflict risk. Dramatically, 24 to 43% percent of all conflict risk areas lay 5-10 km around the protected areas while 7.8% of conflict risks were found directly inside the protected areas. Our results indicate HBCs in Türkiye are mainly the result of increasing human encroachment into core wildlife habitats. Collecting detailed information on conflict events across the country, and planning long-term conservation strategies as well as conservation programs that support coexistence are emerging needs for understanding and preventing HBCs.

Keywords: species distribution modeling (SDM), protected areas, human- brown bear conflicts, spatial modeling

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Evolutionary genomics underlying the response of the life history traits to the fluctuating and deteriorating thermal conditions

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A growing body of experimental studies demonstrated that an increase of both the mean and variation of temperature significantly influences the response of several life history traits, namely reduction of development time and body size at maturation. However, most research has focused only on abrupt changes to thermal conditions. To incorporate ecological realism into our studies, we need experiments investigating the effects of gradually changing thermal environments over longer time scales, because the population genetics of adaptation to stressful environments is strongly influenced by the rate of environmental change. We have little information about the relative contribution of phenotypic plasticity and genetic adaptations underlying the response of life histories to the changing thermal regimes, which are often difficult to disentangle. Likewise, there are still outstanding questions concerning the genomic architecture of life history change under increasing and fluctuating temperatures.

To investigate evolution under fluctuating and deteriorating thermal environments, respectively, we will carry out the two experiments with a plankton crustacean, *Daphnia magna*. We will subject clonal populations of *D. magna* to two different thermal conditions: 1) a regime where temperatures will fluctuate in irregular intervals and 2) a regime with continuous increase of temperature in regular intervals. The experimental populations will be monitored in a series of common garden experiments by measuring three life history traits. To provide insight into the genomic architecture underlying the observed mechanisms, we will compare the ancestral vs evolved populations, by sampling genomic DNA at regular intervals, followed by whole-genome sequencing.

Keywords: experimental evolution; *Daphnia magna*; life history traits; fluctuating and deteriorating temperatures; genomic architecture

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Purifying selection on old-biased genes and the evolution of human lifespan

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Increased effects of drift and relaxation of selection have been shown to correlate with aging-related phenomena in various ways; studies in several species reveal genes associated with aging are under weaker purifying selection, expression of lowly conserved genes tend to increase with increasing age, and the rapid evolution of shorter life-span in certain taxa, namely killifish, has been correlated with genome-wide patterns of relaxation. However, the relationships between relaxation/intensification of selection, age-related gene expression changes, and life-span changes have not been directly investigated. Here, we asked whether the longer life-span in humans may be correlated with intensification of selection in old-biased genes, using aging brain transcriptome data from humans and shorter-lived mice. Our preliminary results suggest an increased effect of purifying selection acting on old-biased genes in humans compared to that of mice, which may have contributed to the extended human lifespan. Our research is thus opening a new avenue for studies on the causal relationship between relaxation of selection and changes in lifespan.

Keywords: evolution of aging, human life-span, drift, purifying selection

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Patterns of sex-biased long-distance mobility in humans inferred from paleogenomes

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The demographic analysis of ancient genomes can provide new insights into past mobility patterns, including sex-biased mobility. To address this, we recently used a dataset of c.400 ancient partial genomes from Southwest Asia spanning the Holocene (i.e. the last 10,000 years from the Neolithic period till today). Within each region, we compared the rates of genetic change measured on autosomes versus the X chromosome and how these autosome-X differences changed over time, which revealed a stark temporal pattern consistent with increasing male-bias and/or decreasing female-bias in interregional mobility. Here we make use of published ancient genomes compiled in the Allen Ancient DNA Resource (AADR) and extend this analysis to other regions that underwent independent Neolithic Transitions, including East Asia and the Americas.

Keywords: ancient DNA, mobility, sex-bias

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Germination responses to incubation temperature in four herbaceous plants at low and high elevations in a Mediterranean mountain

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Temperature is a crucial abiotic factor affecting seed germination, with climate change threatening species by disrupting germination through rising temperatures. The Mediterranean Basin is already experiencing such temperature increases, a trend expected to persist in the coming decades. Elevation also significantly impacts temperature. In this study, we investigated the effects of various incubation temperatures on the germination of four herbaceous Mediterranean plant species at different elevations in Bozdağ, a mountain in western Turkey. Seeds were collected from both lower and higher elevations for each species. We conducted experiments in climate chambers to assess the germination response of each population and species to constant (15°C, 20°C, 25°C, and 30°C) and alternating (20/10°C, 25/15°C, and 30/20°C) temperatures under 12h/12h photoperiod conditions. Our findings revealed no consistent patterns in germination behaviour across all studied species. Germination patterns were species-specific, as each of the four species displayed distinct responses to increased incubation temperatures and elevation. Additionally, the optimal germination temperatures varied among the species. Some species achieved higher germination percentages at lower elevations compared to higher elevations, while others showed no significant difference. For one species, increased temperatures up to 30°C resulted in decreased germination, whereas seeds from other species were capable of germinating at this temperature. We also found that alternating temperatures did not significantly improve germination compared to constant temperatures. Our results suggest that the germination response of Mediterranean herbaceous species to varying temperature regimes is highly species-specific. Consequently, climate warming may differentially affect the germination behaviour of plants in Mediterranean mountain ecosystems.

Keywords: germination, temperature, altitude

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In search of mountain gazelles: Examining diet, gastrointestinal parasites, and stress hormones

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Human activity and seasonal changes impact the feeding and reproductive behaviours, stress levels, and parasite load in large herbivores such as deer, gazelles, and wild goats. The mountain gazelle, *Gazella gazella*, is an endangered large herbivore whose global population has significantly decreased. One remaining and the northernmost population of this species is in Hatay province, Turkey, where it has rarely been ecologically studied. We are currently investigating the seasonal variation in dietary habits, gastrointestinal parasites, and stress hormones of this mountain gazelle population. We conduct field studies during different periods of the biological cycle of mountain gazelles and perform concurrent laboratory analyses. In the field, we collect fecal samples from mountain gazelles and domestic sheep at various locations throughout the mountain gazelle's range, as well as from captive individuals near the study area. We employ the metabarcoding method to identify plant and parasite species present in the fecal samples of mountain gazelles and sheep. We also use conventional methods for detecting gastrointestinal parasites and a specific technique for assessing stress hormone levels in fecal samples. By the end of the project, we will obtain not only descriptive data but also insights into the relationship between seasonal diet and parasites of mountain gazelles, the potential for competition for food between sheep and mountain gazelles, spatial and temporal dynamics of stress hormone levels of mountain gazelles, and the differences between captive and free individuals in these aspects. Our multidisciplinary methodological approach will contribute to the effective conservation of the mountain gazelle population in Hatay, Turkey.

Keywords: large mammals, metabarcoding, mountain gazelle

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Species-specific best-fit inspection for the model developed through an information-theoretic approach relating the lengths of protein and the encoding DNA

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Aim:

We previously generated a model for the relation of monomeric lengths of the proteins and encoding DNA. Then we looked for its fit with the averages of extracted data of species belonging separately to the plants, insects, fishes, birds, rodents, and primates. Respective max-length features revealed the best fit. Here we aim to make the comparison through individual species' data.

Materials and methods:

We previously developed an information-theoretic approach relating the protein and the encoding DNA lengths (Adiguzel 2021. Doi: 10.1111/cbdd.13988.) Here we utilized that model and the data retrieved at the same time, to make a similar comparison with the averages of the median and the maximum values. We further evaluated the comparison through individual species' data of the best-fitting averaged-data.

Results:

The best-fitting averaged-data belonged to that of the maximum values and comparison through the individual species' data revealed to be optimum for the individual species' data of the birds.

Discussion/conclusion:

We made comparisons with the data that is averaged or not averaged. Accordingly, the results are based on the selected parameter values in the model, which gives the best outcome with different parameters in the respective comparisons. This can be an expected outcome but should be interpreted in terms of the mathematical basis of the results, as well as the possible biological significance.

Keywords: Information theory, gene length, protein length, species-specific data

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Gene regulatory networks altered by endosymbiosis

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Gene Regulatory Networks are composed of interacting transcription factors, their enhancers, and signaling molecules that are responsible for pattern formation in multicellular organisms. In the case of insects, the presence of intracellular endosymbionts poses challenges to pattern formation because of the interactions between the host gene regulatory network and the endosymbiont. A recent study has shown that in ants of the tribe, Camponotini the position of extraembryonic membranes and dorsal-ventral axis is altered compared to non-Camponotini ants. These changes correlate with the presence of endosymbiont *Blochmannia*. This raises the possibility that the endosymbiont interacts with the gene regulatory networks in the host. The nature of these interactions still remains unexplored. To unveil the nature of these interactions, in this study, specific gene regulation was characterized in the carpenter ant *Camponotus floridanus*. We examined components of the Bone Morphogenetic Protein (BMP) signaling pathway using in situ hybridization. We show that BMP signaling is active during the early development of *C. floridanus* and the expression of the components of this pathway has been altered in comparison with other known cases of insects. We also present a fate map of tissues in early embryos in these ants.

Keywords: ants, endosymbionts, BMP, gene regulatory networks

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Signal peptides from endosymbiont influencing gene expression of the ant host

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Insects have evolved mutualistic and obligate interactions with bacteria. As the obligate partnership between the host and the endosymbiont persists, such long-term relationship can influence expression of genes, development of the organs, anterior-posterior axis determination, localization of mRNAs, and proteins of specific genes. In the carpenter ant *Camponotus floridanus*, the genetic changes induced by the endosymbiont, increase the efficiency of the endosymbiotic relationship. Here, using bioinformatics, molecular and embryological techniques, we present preliminary data for identification of the signal peptides of endosymbiont origin that target the gene regulation of the host ant. These data will help understand the molecular interactions between the endosymbiont and the host.

Keywords: endosymbiont, host, signal peptides, ant, evolution

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Contribution of the symbiotic microbiota to the change in the lifespan of *Drosophila melanogaster* selected for late reproduction

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One of the classical approaches to the study of the evolutionary foundation of the lifespan is experiments on artificial selection on convenient object like fruit flies.

In this study, the lifespan of flies from a line selected for late reproduction (Ma), a line with a depleted yeast microbiome (Mbd) and a control line (Mn) ancestral to the Ma and Mbd lines were studied.

Initially, we were selecting fruit flies for later reproduction. Having found a significant increase in lifespan of Ma line, we undertook to assess the genetic component of the observed changes. The inability to explain the change in the lifespan only by genetic factors prompted us to test hypotheses about the influence of microbiotic factor on this parameter of the life cycle.

We have identified a significant contribution of the microbiota to the results of the selection for longevity. In the presence of microbiota from the Mn control line, the lifespan of flies from different lines sharply decreased, which indicates the presence of Mn components (bacteria or yeast) in the microbiota of control flies that greatly shorten the life of flies. As a result, the low lifespan of Mn flies turned out to be a "contagious" sign.

Apparently, during the selection for later reproduction, a new microbiota was formed in flies from the Ma line that did not have a negative effect on the lifespan, and this was what explained most of the excess of the lifespan of Ma flies over the lifespan of flies from the ancestral Mn lineage. This result is a reliable confirmation of the homogenomic theory of evolution.

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Keywords: lifespan, symbiotic microbiota, *D. melanogaster*

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The Combined Effects of Ocean Acidification, Microplastic and Lanthanum in Sea Urchin *Arbacia lixula*

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Marine organisms are exposed to various stressors as a result of anthropogenic activities. Ocean acidification (OA), microplastics (MP) and lanthanum (La) are of importance due to their increasing trends and hazardous effects on marine species. The main purpose of the present study is to investigate the single and combined effects of those stressors (low pH: pH: 7.45, polyethylene MP: 26 g L⁻¹ and La: 9 g L⁻¹) on the physiology and histology of sea urchin *Arbacia lixula*.

Adult sea urchins were collected from Saros Bay, northeast Aegean Sea and they were transported to the laboratory. The experimental setup consisted of 8 aquariums on the basis of full factorial design. They were acclimated to the laboratory conditions for 9 days (20±2 °C, pH: 8.00 and salinity of 38). Then, they were exposed to single and combined stressors for 14 days. All the experimental setup consisted of three replications. The physiological and histological effects of OA, MP and La on the sea urchins were evaluated by considering respiration rate, the quantity and viability of coelomocytes, and histopathology.

According to the results, the stressors did not lead to mortality in the sea urchins. Coelomocyte viability was the most affected, however, the total coelomocytes were slightly affected by the stressors. The coelomocyte viability was suppressed most in the triple stressor group (OA-MP-La). The respiration rate was not affected by stressors.

We need further studies to better understand the chronic effects of those stressors with different levels and extended exposure periods.

Keywords: ocean acidification, microplastic, lanthanum, sea urchin, coelomocyte, histopathology

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The Effect of gut microbiome size on the evolution of bacterial resistance

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The gut microbiome of holometabolous insects changes significantly during metamorphosis, triggered by the secretion of immune effectors. *Galleria mellonella*, a holometabolous insect, upregulates three different antimicrobial peptides (AMPs) and lysozymes at the onset of pupation, which reduces the abundance of gut microbiome. This is believed to limit the evolution of resistance in opportunistic pathogens due to a smaller population's lower mutation supply. However, it is unclear how much the gut microbiome fluctuates during metamorphosis, and whether there are differences in resistance evolution among different population sizes. In this study, *Galleria mellonella* was used as an insect model to investigate changes in bacterial population size in the gut during different developmental stages. We analyzed the gut microbiome composition using 16S metabarcoding and conducted an experimental evolution study with different population sizes of gut bacteria. The results showed that the gut microbiome abundance declined from 10^7 to 10^6 CFU/gut upon gut replacement when AMPs are upregulated. The population size ranged between 10^5 – 10^8 CFU/gut during metamorphosis. The symbiotic *Enterococcus* genus was the most abundant bacteria through all stages. However, during experimental evolution, all populations went extinct, possibly due to the doubling cecropin-A concentration at each transfer cycle. The findings indicate that the gut microbiome abundance varies and experiences a reduction during metamorphosis. Still, the effects of AMP on resistance evolution were not observed. This study can provide more insight into how population size reduction can constrain resistance evolution against host immune effectors.

Keywords: population size, gut microbiome, microbial evolution

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A research on desiccation tolerance of stream macrobenthic invertebrates

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Global climate change poses a major threat to freshwater ecosystems, such as extended droughts of running waters like streams. Many species of macrobenthic invertebrates inhabit the substrates of streams and their natural life cycles evolved together with the natural hydrological cycles of these streams. The rapid climate change disrupts annual water cycles, for example causing droughts. Study material consists of macrobenthic invertebrates (n=270) collected from Karasu Stream and Davul Stream in İstanbul and Kocaeli respectively, in rainy and dry periods of 2021 and 2022. At least 18 species, from 9 orders were identified. Survival Times of individual specimens under complete desiccation were measured in hours through Desiccation Experiments. The Survival Times ranged from 1 hour to over 40 hours, with 66% of the specimens dying in first 8 hours. The general indicators of survival times were found to be the systematic group and body size. The body size is explained through the proportion between evaporation rate and volume/mass ratio of the specimen, which supports previous studies. The natural drying and rewetting cycles of streams worldwide are affected by changing climate and the dry periods are increasing. The results suggest that extended drought periods would impose serious threats to less tolerant species. In the experiments, more vulnerable species are mainly noted as the lower members of the food chain. Thus, our study suggests that even if the extended dry period is temporary, it is expected to leave a more significant negative impact on the freshwater community beyond the point of dehydration.

Keywords: macrobenthic invertebrates, Desiccation tolerance, Drought, Climate change

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Genetic characterization of ancient charred wheat seeds from the archaeological site of Kaymakci using glu-1 loci

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Wheat is one of the world's most essential crops, and understanding its evolutionary history is critical for improving its yield and nutritional quality. In this study, ancient DNA (aDNA) from wheat remains from Kaymakçı archaeological site, Manisa, Türkiye, was analyzed and compared the genetic data to modern wheat varieties to investigate the domestication and evolution of wheat. 26s rDNA, ITS2 and IGS regions were used to determine the genome type of the 3,500 years old charred wheat seeds. These DNA barcodes revealed previously undetermined *T.aestivum/durum* ancient wheat seeds were *T.aestivum*. Additionally, High molecular weight (HMW) subunits of wheat glutenin genes were investigated in this study since these genes are essential determinants of flour quality, and understanding their evolution is critical for improving breeding programs. Results of this study revealed that the HMW subunits of wheat glutenin gene GluB1 subunit in ancient samples were highly conserved while in the GluA1 subunit of the gene some changes were found. These findings underscore the potential of aDNA research in elucidating the genetic history of wheat in Türkiye.

Keywords: wheat, ancient DNA, agriculture, archaeobotany, genome type, plant domestication

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The NR1L subfamily grows larger: gene annotation and evolutionary analyses of a unique group of nuclear receptors in Branchiopoda (Crustacea: Allotriocarida)

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Nuclear receptors (NR) are transcription factors (TF) involved in a wide range of diverse biological processes, from development and reproduction to metabolism. Currently, there are eight NRs subfamilies described based on the similarity of their highly conserved DNA binding domain (DBD) and ligand binding domain (LBD). Apparently exclusive of arthropods, the NR1L group has been recently established within the NR1 subfamily to include three NRs (HR97A, HR97B and HR97G) first characterized as hormone receptor 97 on the crustacean genus *Daphnia*. In this study, we identify and annotate HR97 orthologs within several Branchiopoda species using in silico methods. Our results suggest that HR97 genes are absent in Anostraca, but present in Anomopoda, Spinicaudata and Notostraca. Therefore, the origin of this NR group can be traced back over 300 Mya, before the split between Notostraca and other branchiopods. Interestingly, HR97A and HR97B seem to have suffered several duplication events, passing from being a single-copy gene in Notostraca to showing more than one copy in Diplostraca. The methodology developed in this study opens a new discovery path to identify gene orthologs and characterize their evolution across Pancrustacea.

Keywords: nuclear receptors, branchiopoda, evolution, phylogenetics

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CNV analysis of two endangered wild sheep

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Copy number variations (CNVs) are a type of structural variation that consist of large deletions and duplications, ranging from 50 base pairs to several mega base pairs. They have an effect on a variety of adaptation mechanisms and impact on phenotypic traits. Moreover, large deletions are known to evolve under negative selection; hence, they can be an important cause of deleterious mutation load, especially in small, severely depleted populations. This study focuses on Anatolian mouflon (*Ovis gmelini anatolica*) and Cypriot mouflon (*Ovis gmelini ophion*), two wild sheep that went through severe bottleneck during 20th century with limited habitat range and estimated census size lower than 2,500. In order to characterize deletion profiles of these two sub-species, first, de-novo deletions from various high coverage (>5x) wild sheep, including one high coverage Cypriot mouflon, will be identified. Together with these de-novo CNV's and a CNV panel created from multiple domestic sheep breeds, genotype deletions of low coverage Anatolian mouflon and Cypriot mouflon samples will be genotyped. This way, deletion frequency changes and overall mutation load these engendered wild sheep will be explored in order to evaluate the genetic consequence of bottlenecks. Here, we are presenting preliminary results of de-novo deletion calling of these wild sheep.

Keywords: Copy number variations, negative selection, *Ovis gmelini anatolica*, *Ovis gmelini ophion*

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Revealing the draft genome sequence of the invasive pest *Ricania simulans*
(Walker, 1851) (Hemiptera: Ricaniidae)

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An invasive agricultural pest *Ricania simulans*, whose homeland is the Far East, entered Turkey through the trade of plant materials through Georgia and Russia and has spread to Istanbul today. Both the nymphal form and its adult individuals are fed with plant sap on all agricultural plants, shrubs and shoots of young trees, especially plants such as tea, kiwi, hazelnut, corn, beans, pepper and eggplant, which are frequently consumed and economically important for local areas. The genetic and -omic resources for *Ricania simulans* have not been as extensively developed as those for other insect agricultural pests, and they have not been made publicly available up to now. To better understand this pest's chemosensory abilities and insecticide resistance, as well as to come up with novel control strategies like gene editing, it is essential to develop genomic resources.

In this study, High molecular weight DNA was extracted from 10 nymphs of *Ricania simulans* were sequenced using long-read Oxford Nanopore reads and MGI DNBSEQ short reads and assembled using a hybrid assembly pipeline. The final genome assembly is ~1 Gb with 10x coverage and contains complete sequences for ~88% of the BUSCO Arthropoda dataset. Repetitive elements comprised ~26% of the draft genome.

As an invasive pest, *R. simulans* is undergoing an expansion in Turkey, necessitating novel managerial techniques, which may incorporate strategies made possible by genome assembly and annotation.

Keywords: insect genome, nanopore sequencing, *Ricania simulans*

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Uncovering the knowledge gaps in Triglidae family biology in Turkish Waters

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The Triglidae family, commonly known as sea robins, comprises 114 species distributed across world seas and divided into two subfamilies, Peristediinae and Triglinae. In Turkish seas, the family is represented by five genera (*Chelidonichthys*, *Trigla*, *Eutrigla*, *Lepidotrigla*, *Peristedion*) and eight species (*Chelidonichthys cuculus*, *C. obscurus*, *C. lastoviza*, *Eutrigla gurnardus*, *Lepidotrigla cavillone*, *L. dieuzeidei*, *Trigla lyra*, *Peristedion catapractum*). These species are demersal marine fishes that prefer muddy and/or sandy bottoms, and are distributed in the Eastern Atlantic to Mediterranean, Aegean and Black Seas. Despite the widespread occurrence of Triglidae in Turkish seas, only 29 studies have been conducted on their biology (i.e. age, growth, and reproduction), with a majority of these studies focusing on commercially valuable species. Overall in 29 studies conducted; some of the species are discussed far more than the others, such as *C. lucerna* (22 times), *C. lastoviza* (10 times), *L. cavillone* (9 times), *E. gurnardus* (8 times), *T. lyra* (8 times) and *C. cuculus* (2 times). Unfortunately, there is insufficient knowledge about triglids since most of the studies in Turkish seas have focused on commercially valuable species, which leads to a narrow literature on this topic. Overall, studying the biology of a species is critical for understanding its role in the ecosystem, managing its populations sustainably, and protecting it for future generations. This review aims to make an evaluation of these understudied species and reveal the number of research conducted in the Turkish waters, also to highlight that the existing literature is inadequate, and further research is necessary to fill the gaps.

Keywords: Triglidae, Turkish waters, age, growth, reproduction

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Identification of genomic regions regulating sex determination in European anchovy (*Engraulis encrasicolus* L., 1758) by whole-genome sequencing approach

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The European Anchovy (*Engraulis encrasicolus* L., 1758) is the most economically and ecologically valuable marine species in Turkey. The aim of this project was to identify genomic regions that determine the sex of the European Anchovy and to identify potential genomic regions and gene candidates that control sex determination and differentiation in these regions.

To achieve this, high molecular weight genomic DNA was extracted from lateral caudal muscle tissue from 50 female and 50 male individuals captured from local fisheries in the Eastern Karadeniz region. Reads belonging to genomic DNAs were obtained by a low-pass whole genome sequencing approach. The resulting reads were analyzed together with the European Anchovy genome data to reveal potential genomic locations and genes controlling sex.

An average of 2.5 Gb ".fastq" data were produced per 50 female and 50 male low-pass whole genome sequencing. The ".fastq" data from female and male individuals were transformed into a vcf (Variant Call Format) file, which includes information about genetic variants detected in genomic sequencing data. These files were then analyzed and identified using the GATK tools to identify sex-related genomic regions that differed between males and females. These regions were then mapped to the European Anchovy genome to determine their corresponding genomic locations.

Research on sex determination and differentiation, and the investigation of new genes responsible for sex determination in fish, are important for understanding the evolution of sex, as well as for the management and conservation of species. Furthermore, the discovery of these genes could enable more efficient and profitable production in industrial fish farming, while also helping to protect and manage native or invasive species.

Keywords: European Anchovy, *Engraulis encrasicolus*, Sex Determination, Sex Determining Genes

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Effects of ocean acidification on the ark clam (*Anadara kagoshimensis*) physiological processes

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Increasing CO₂ in the oceans is causing a series of changes in seawater chemistry. The most important of these is the decrease in seawater pH. The main purpose of this study is to reveal the physiological effects of ocean acidification and seawater carbonate system changes in the ark clam (*Anadara kagoshimensis*) by experiments performed under laboratory conditions. Bivalves, such as mollusks feed by filtering organic substances and phytoplankton in the water. Therefore, they are called bioindicator species. The clams, which have been collected in the Marmara Sea, were taken to 6 aquariums for the application of 3 repetitions at the same time, and the setup was ensured. Clams were acclimated to the laboratory conditions for 7 days (21±3 oC, pHT: 8.00 and salinity of 20). Then they were exposed to two different pH conditions (ambient pH: 8.0 and low pH: 7.5) for 12 days. In order to examine the effects of ocean acidification on physiological processes in clams, filtration rate, absorption efficiency, respiration rate and excretion rate tests were performed. In addition, total hemocyte count and hemocyte viability were measured to detect cellular changes in clams. Although hemocyte viability decreased under low pH conditions, there was no significant change in total hemocyte count under normal and low pH conditions. It has been noted that physiological processes in clams are affected after exposure to low pH conditions. In addition to ocean acidification in clams, there is a need to investigate how the effect will change with other stress factors.

Keywords: ocean acidification; physiology; *Anadara kagoshimensis*

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Temporal variation in the evolutionary potential of quantitative immune traits in a wild invertebrate population

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Parasites and pathogens are amongst the strongest selective agents in nature. The rate of evolutionary change in host defense traits when subject to selection depends on the amount of additive genetic variance (and covariance) in them. Here, we assessed the potential for evolutionary change in quantitative non-specific immune traits in a natural population of a freshwater snail, *Lymnaea stagnalis*. We estimated the genomic relatedness of 561 field-collected individuals using high-marker density genotyping (ddRADSeq, 19,339 SNP markers). We then applied the produced genomic relatedness matrix to determine additive genetic variance and covariance of three phenotypic immune traits: hemolymph phenoloxidase, laccase and antibacterial activity. Because the expression of these immune traits is context-dependent, we sampled the snails at several time points over one reproductive season and also examined the variation in snail condition (body size, fat and glycogen content) and trematode infection status. We found the evolutionary potential of snail immune activity to be low in the early season but high in the late season. The evolutionary potential was independent of snail condition and infection status. Temporal changes in estimates of evolutionary potential suggest the evolutionary potential being highly dynamic in heterogeneous environments, which could be due to changes in the additive genetic variance and/or environmental variance. Thus, our results highlight the importance of considering the possible temporal variation, as well as other potential ecological/environmental factors that may affect trait variation, in influencing the evolutionary potential of immune and other traits across taxa.

Keywords: evolutionary potential, ddRAD sequencing, quantitative traits, immune variation, genomic relatedness

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2023 Spring soaring bird migration

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Birds which have wide and big wings do not make active fly like other birds. They soar by thermal that occurs at day time when the weather is hot on land. Therefore, the migrating birds pursues the coast way in the morning because they can't fly over the big sea areas and they passe trough the region which seas are the closest to the lands such as straits. For instance, Bosphorus is the most important major migration path in Europe for the soaring birds.

For this reason, Bosphorus is the common place for the bird watchers and researchers for so many years. Researchers could use the watching points to observe the migration in Istanbul University Department of Science. The purpose of this research to find and dedicated the number of birds and their migration pathway and reduce to people lack of knowledge.

Keywords: spring migration, soaring birds, migration pathway

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The effect of presence and abundance of European bee-eater on honey bee activity

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European Bee-eaters (*Merops apiaster*) are considered as one of the biggest threats to apiculture. Here, we investigated whether the activity patterns of Anatolian (*Apis mellifera anatoliaca*) and Caucasian (*Apis mellifera caucasia*) honey bees are affected by the presence and abundance of European Bee-eaters, their migratory avian predator. To measure the number of bees entering and leaving the hive, the entrance of a commercial hive was recorded with a camera, while the number of European Bee-eaters was also counted simultaneously. The external factors known to affect honey bee activity, such as wind speed, temperature, cloud cover, and time of the day, were also measured and included in our analyses. We found that the honey bee activity may decrease in the presence of European Bee-eaters, and the higher number of European Bee-eaters was associated with the higher number of bees entering the hive to take refuge. Our results suggest that honey bees may actively avoid predation by their avian predators by taking refuge in their hives. Further studies are required to fully comprehend how honey bees behave in response to European bee-eaters.

Keywords: European Bee-eater, honey bee, apiculture, honey bee activity

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Assessment of population genetic structure and differentiation of the *Pelodytes caucasicus* (Boulenger 1896) from Giresun and Rize

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The Caucasian parsley frog, *Pelodytes caucasicus*, is an endemic species of the Caucasian Isthmus. The frog inhabits Turkey, Georgia, Abkhazia, South Ossetia, Azerbaijan, and Russia. Although *P. caucasicus* is studied from various perspectives, many issues related to the species' genetic diversity and population genetic structure have yet to be studied. We studied the population genetic structure of 31 individuals from Çat (Rize) and Cımbırtlık (Giresun) localities using eight different microsatellite loci (Ppu1, Ppu3, Ppu4, Ppu6, Ppu8, Ppu11, PPU5, and PPU10). We extracted genomic DNA using the DNA Purification Kit according to the manufacturer's instructions. The multiplex polymerase chain reaction (PCR) was run using the Type-it multiplex PCR Kit. The alleles were scored using the GENEMARKER program (Soft Genetics LLC). Genetic diversity indices, including the observed heterozygosity (HO), expected heterozygosity (HE), private allele, and the number of effective alleles, were calculated using the GenAEx program. We estimated the number of alleles per locus (Na), allelic richness (AR), and inbreeding coefficient (FIS) using FSTAT. We conducted a Bayesian-based individual assessment test with the program STRUCTURE to identify distinct genetic clusters. We computed a Principal Coordinate Analysis (PCoA) via multivariate analysis of microsatellite allele frequencies using the GenAEx and Factorial Correspondence Analysis (FCA) using the Genetix programs. We found minimal gene flow between (Nm= 0.78) the two localities. Genetic variation was higher in Çat than in Cımbırtlık. We found higher FIS in Cımbırtlık (Giresun) population. Population genetic structures between populations are differentiated according to Structure, PCoA, and FCA analysis. This is the first study using microsatellite markers that revealed the genetic relationship between two populations of *P. caucasicus*.

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Keywords: amphibia, genetic diversity, microsatellites, Caucasian frog

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