EEBST24

10th ECOLOGY AND EVOLUTIONARY BIOLOGY SYMPOSIUM

23-25 JULY 2024

SYMPOSIUM PROGRAMME
&
ABSTRACT BOOK

ÇANAKKALE 18 MART UNIVERSITY
TROIA CULTURE CENTER

ekoevo
Ekoloji ve Evrimsel Biyoloji Derneği

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ABSTRACT OF ORAL PRESENTATIONS

SESSION I: PHYLOGENETICS AND BIOINFORMATICS

Season-Long Monitoring of Peach Fruit Surface Mycobiome Biodiversity Detected Using High-Throughput Sequencing Data

Sibel Öncel[1], Hilal Özkılınç[1]

[1] *Çanakkale Onsekiz Mart University*

Fruit surfaces contain a diverse array of fungal species collectively known as the epiphytic mycobiome, encompassing both pathogenic and mutualistic organisms. Maintaining a balanced composition within this mycobiome is crucial for ecosystem functions and host health, yet it faces continual pressures from biotic and abiotic stressors, as well as interspecies interactions and competition. Addressing the dynamics of fungal colonization on host surfaces and its relationship to host growth stages is seen as important for the importance of mycobiome content in fungal diseases, especially considering our previous research on brown rot pathogens in peach fruit. To elucidate the extent of diversity within the mycobiome, we conducted sampling across various developmental stages in a commercial orchard. Using metabarcoding techniques, taxonomic identification and quantification of fungal species were performed. Initial findings revealed dominance of pathogenic Ascomycete species, with lesser presence of mutualistic or environmental fungi. It was also observed that the sampling location and time greatly influences the dynamicity of the mycobiome. The results indicated the complex interspecies interactions and competitive dynamics. In summary, this study provides valuable insights into the dynamic fluctuations of the mycobiome and the interplay among fungal species colonizing fruit surfaces throughout host growth stages. These findings enhance our understanding of fungal organisms and have implications for agricultural management strategies and disease mitigation. This project has been supported by Çanakkale Onsekiz Mart University The Scientific Coordination Unit under the project number FYL-2023-4385.

Keywords: Mycobiome, fungal biodiversity, metabarcoding, bioinformatics

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Evaluation of genotype imputation of ancient human genomes from West Eurasia

Hande Çubukçu[1], Gülşah Merve Kılınç[1]

[1]*Hacettepe University*

Genotype imputation presents a solution to the high amount of missing information in low coverage ancient DNA samples. By using the phasing and imputation tool GLIMPSE, we evaluate the accuracy of genotype imputation on biallelic SNPs and compare the amount of missing variants depending on the applied filters at four different coverages using ten high coverage and over a hundred low coverage genomes from West Asia and Europe. We then compare the effect of using imputed data in frequently used population genetics analyses. The accuracy of imputation measured as genotype concordance with high coverage data reaches 70% to 90% at common variants at 0.1x genome coverage, while losing less than 5% to 15% of the positions using posterior genotype probability filters between 80% and 99% in chromosome 22. Missing amount in common variants using the same data reaches %20 and %50 in commonly used Human Origins dataset positions. Pseudo haploid data have more affinity towards the reference genome compared to the imputed data, pointing to mitigation of reference bias by imputation. On the other hand, imputed data show bias towards the reference panel populations as the coverage decreases. Allele frequency calculations show up to 15% difference in low coverage Anatolian Neolithic samples. Overall, it is possible to get reliable results using imputed data for common variants for low coverage ancient genome samples from the region of interest.

Keywords: imputation, lc-WGS, ancient DNA, reference bias,

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Overcoming bias and postmortem damage to improve the accuracy of ancient genome analysis

Dilek Koptekin[1], Etka Yapar[2] , Kıvılcım Başak Vural[3], Ekin Sağlıcan[3], N. Ezgi Altınışık[3], Anna-Sapfo Malaspinas[1], Can Alkan[4], Mehmet Somel[3]

[1] University of Lausanne
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[3]Middle East Technical University
[4]Bilkent University

Ancient DNA (aDNA) contains invaluable information about population history and evolution, but its analysis is plagued by challenges such as reference bias and postmortem damage (PMD). Here, we propose new strategies to address these challenges. First, we show that masking variable genomic positions before alignment or using a graph genome both effectively reduce reference bias in ancient human genome data. However, since quality-filtered BAM files and 1240K capture data retain bias, this solution depends on data availability in FASTQ or unfiltered BAM formats. Second, we evaluate various strategies for removing PMD, including trimming, rescaling base quality, and a new algorithm, bamRefine, that masks polymorphic regions vulnerable to PMD. Compared to trimming and rescaling, bamRefine significantly improves genotyped loci by up to 20% while increasing accuracy. Overall, we advocate for the adoption of graph alignment in conjunction with bamRefine to minimize data loss and bias in aDNA research. Furthermore, our study highlights the importance of publishing FASTQ files for comprehensive analysis. By addressing these technical challenges, our work increases the reliability and depth of information obtained from ancient DNA, which in turn will improve our inference of population history and evolution.

Keywords: ancient DNA, reference bias, graph-reference genome, post-mortem damage, masking

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Keynote Address: Is evolution open-ended?

Eörs Szathmáry

Parmenides Foundation, Center for the Conceptual Foundations of Science

Charles Darwin closed the first edition of The Origin with one of the best-known passages of all biology, beautifully summarizing the two basic pillars of his theory: descent with modification and the power of natural selection to ‘produce higher animals’ and ‘endless forms most beautiful’ from a ‘simple beginning’. Many still feel uncertain about whether the production of higher animals would indeed (even indirectly) follow, simply because a quantitative theory of macroevolutionary change is in its infancy. Despite major advances in evolutionary theories, some aspects of evolution remain neglected: whether evolution: would come to a halt without abiotic change; is unbounded and open-ended; or is progressive and something beyond fitness is maximized. I shall discuss some models of ecology and evolution and argue that ecological change, resulting in Red Queen dynamics, facilitates (but does not ensure) innovation. I distinguish three forms of open-endedness. In weak open-endedness, novel phenotypes can occur indefinitely. Strong open-endedness requires the continual appearance of evolutionary novelties and/or innovations. Ultimate open-endedness entails an indefinite increase in complexity, which requires unlimited heredity. Open-ended innovation needs exaptations that generate novel niches. This can result in new traits and new rules as the dynamics unfold, suggesting that evolution is not fully algorithmic.

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SESSION II: EVOLUTIONARY GENOMICS

Discover the secrets behind the triumph of asexual parasitism from a nematode's point of view

Arda Burak Karagoz[1], Mehmet Dayı[2]

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Sexual reproduction is the dominant method of reproduction among animals, with over 99% of species employing this process. Asexual reproduction, on the other hand, is generally limited to the lower branches of the Tree of Life. Meloidogyne species, however, present an interesting case as they are plant pests that can reproduce both sexually and asexually, with certain species capable of transitioning between both modes of reproduction. These species have undergone diverse evolutionary processes, resulting in varying genome ploidy levels that indicate significant genomic complexity. Asexual species are characterized by polyploid genomes, featuring more than two sets of chromosomes, which enables them to infect a wider range of hosts and inflict greater damage on crops. The existence of specific genomic traits that contribute to their success without sexual reproduction, however, remains unclear. This study aims to compare asexual and polyploid Meloidogyne species with their sexual and diploid counterparts to gain insight into the former's survival strategies and parasitism in the absence of sexual reproduction. The research entails a comprehensive examination of Transposable Elements (TEs), which are known to drive genome evolution in parasitic nematodes. Specifically, the study focuses on three distinct asexual and polyploid Meloidogyne species. Automated TE annotation methods are used to identify and compare the TE content of these species with their sexual and diploid counterparts. The findings reveal that asexual and polyploid Meloidogyne species possess greater TE content in their genomes than their sexual and diploid counterparts. This disparity arises from allopolyploidization events that occur when two species interbreed, leading to the formation of genomic structures that offer adaptive potential and promote the thriving of these species. Furthermore, the TE insertions in asexual and polyploid species are relatively more ancient than their sexual and diploid counterparts, providing unique evolutionary insights into their adaptive potential and ability to flourish in diverse environments. The study findings suggest that TEs play a significant role in the genetic makeup of asexual and polyploid parasites. By harnessing TEs, asexual and polyploid parasites can undergo rapid genetic changes, enabling them to survive and thrive in changing conditions. Therefore, a thorough understanding of TE-mediated genetic change is crucial in comprehending how these organisms adapt to different environments and developing novel strategies for successful parasitic infections.

Keywords: Genome evolution, Parasitism, Transposable Elements.

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Unveiling the Dark Matter of Oyster Genomes: Insights from Satellitomics and Repeatomics

MonicaTunjić Cvitanić[1], Daniel García-Souto[2], Juan J. Pasantes[3], Miroslav Phohl[1], **Eva Šatović Vukšić[1],**

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[2]Centre for Research in Molecular Medicine and Chronic Diseases (CIMUS), Santiago de Compostela
[3]Centro de Investigación Mariña, Vigo

Segments of the genome enriched in repetitive DNA sequences like satellite DNAs (satDNAs) and transposable elements (TEs), are often referred to as the "dark matter" of the genome. These sequences are also acknowledged as important factors in genome architecture, and drivers of its evolution. Consequently, research focused on identifying and characterizing the satellitome (the entirety of satDNA sequences) and repeatome (all repetitive sequences) is expanding. By employing different experimental and bioinformatic methods, we have determined that oysters have unique traits that make them useful organisms for studying repetitive DNAs. We found that the centromeric chromatin of the Pacific oyster Crassostrea gigas lacks uniformity in the composition of DNA sequences, and that the heterochromatin of this species is extremely scarce and predominantly constituted of DNA transposons. In oyster species we have observed novel, highly interspersed patterns of satDNA organization, differing from the conventional concepts. We have characterized the satellitomes of six oysters from the Ostreidae family, revealing not only a substantial number of satDNAs per genome (33 - 61), but also peculiarities in their composition. An extensive number of detected satDNAs was found to be either associated to or derived from TEs. Through comparative satellitomics, we were able to confirm the applicability of the “satDNA library hypothesis” to this set of related species. SatDNAs and TEs were also found to be strongly interconnected in numerous aspects within this organism group. Satellitomics and repeatomics are anticipated to continue playing an important role in advancing our understanding of genome structure and evolution.

Keywords: satellite DNA, transposable elements, oysters, centromere,heterochromatin

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Unveiling the signs of positive selection: What haplotype-based methods tell us about Populus trichocarpa and Populus balsamifera

Çiğdem Kansu[1], Tommy Phannareth[2], Constance Bolte[3], Jill A. Hamilton[3], Matthew C. Fitzpatrick[4], Stephen R. Keller[5], Jason A. Holliday[6]

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Sister species *P. trichocarpa* and *P. balsamifera* are found primarily in temperate coastal and continental regions of western and northern North America, with the Rocky Mountains roughly dividing their ranges and encompassing a hybrid zone. Previous studies suggest that introgression, the transfer of genetic material between species, may play a role in transferring adaptive traits between these two species. We sought to characterize the process by sampling six west-to-east transects that each span putative parental-type P. trichocarpa, the hybrid zone, and end in putative parental-type P. balsamifera. In this study a total of 576 samples were sequenced at ~20X coverage of the whole genome. As a prelude to understanding the role of adaptive introgression in the evolution of these species, we sought to characterize how parallel and non-parallel selection have shaped the genomes of the parental species. From 318 parental individuals, ~25M SNPs were screened with haplotype-based methods: the iHS (integrated Haplotype Score) and the XP-EHH (cross-Population Extended Haplotype Homozygosity). Using genome-wide scans, we aimed to detect evidence of positive selection in widely distributed populations to determine putative genomic intervals undergoing selection in each species. We identified loci potentially under selection with a high-quality dataset of SNP markers across the genome. Our findings highlight those genomic regions that have undergone positive selection in these sister species, providing valuable information for future studies investigating the underlying molecular mechanisms of adaptation.

Keywords: Populus, WGS, SNP, selection signatures, positive selection

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Unveiling Ancient Coastal Biodiversity Through DNA Metabarcoding in the Mediterranean and Aegean Seas

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The Mediterranean and Aegean Seas have been pivotal to the development of coastal civilizations, particularly at notable archaeological sites like Liman Tepe and Çeşme -Bağlararası. These sites offer a window into the cultural and commercial dynamics from the mid-5th Millennium BC to the Classical Age. Our study focuses on overcoming the challenges of ancient DNA (aDNA) analysis, such as degradation and contamination, which are particularly problematic with ancient coastal samples where modern human DNA frequently contaminates the results. To enhance the integrity of species-level identification, we experimented with various bleach concentrations to decontaminate ancient fish bones and crust samples. We refined DNA extraction protocols by testing different kits and pre-incubation methods to reduce modern DNA contamination. Successful optimization allowed us to retrieve high-quality aDNA, which we then analyzed using metabarcoding. This technique employed universal primers specific to fish (12SrRNA) and invertebrates (COI) to amplify DNA, followed by high-throughput sequencing that generated around 1 million reads per sample. Bioinformatics analysis of these reads identified 66 fish and 50 invertebrate species, marking a significant breakthrough in aDNA research from Turkish waters. This study not only showcases the efficacy of aDNA metabarcoding in revealing biodiversity from ancient samples but also highlights the technique's potential to provide insights into historical species distributions and ecological changes. The discovery of species previously unrecorded in ancient DNA studies underscores the rich, yet unexplored, ancient biodiversity of these seas.

Keywords: Ancient DNA, Metabarcoding, Coastal Archaeology, Species-Level Identification

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SESSION III:GENERAL ECOLOGY

Monitoring and biocontrol of the chestnut gall wasp

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Asian chestnut gall wasp (ACGW), Dryocosmus kuriphilus, is the most important insect pest of the chestnut worldwide. It was first recorded in Turkey in 2014 in Marmara Region. This study aimed to monitor its populations in the region between 2019 and 2021. We identified 31 chestnut stands in the region where we first determined the presence and the population size of the pest through collecting and counting galls. For phenological and morphological studies, we additionally identified four intervals on an altitudinal gradient: 0-200, 201-400, 401-600, and 601-800 m. We measured length, width, and weight of the galls, determined their color and complexity classes, and number of adult emergence holes. As a result, by 2021, ACGW had spread throughout Marmara Region, except for Kazdağı. The spread rates were between 20 and 105 km/yr. In the invasion front, we found exponential population growth, while in the invasion core population sizes fluctuated annually. Interestingly, neighboring localities showed negatively correlated fluctuation patterns. Studies on the phenology of ACGW at different altitudes evidenced approximately two-month lag in larval development and adult emergence from 100 to 700 m. These results can be used in planning pest management programs. We also determined morphological characteristics of galls, including color, length, width, weight, complexity, and number of larval chambers. Predominant gall color was green/reddish brown and green. Unilocular galls were significantly shorter than the other gall classes and multilocular galls were significantly wider than the other gall classes. Reddish-dominated galls decreased in frequency towards the end of the sampling period in August. The greater the number of larval chambers, the heavier the gall was.

Keywords: *Dryocosmus kuriphilus, invasion, life cycle, population growth, range expansion*.

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Monitoring Farmland Avian Biodiversity Using Acoustic Indices in an Agro-ecological Context in the Mediterranean Region:The Case of Gödence Village, İzmir, Türkiye

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Ecoacoustics and the use of acoustic indices are emerging tools for comparing the impacts of different farming practices on biodiversity. While this is an expanding field, there is a need for comparative studies across different regions and habitats. In this study, we collected over 340 hours of acoustic recordings in 2022-2023 from two agroecological orchards in the Gödence Village, İzmir. We employed Audiomoths to collect sound data for four seasons, three days for each season, and at least 12 hours continuously from before sunrise until after sunset each day. Recordings were divided into 5-minute files. We used Kaleidoscope Pro for calculating five widely used acoustic indices (Bioacoustic Index, Normalized Difference Soundscape Index, Acoustic Complexity Index, Acoustic Evenness Index, and Acoustic Diversity Index) for each 5-minute file. Bird species richness will be evaluated by manual inspection of acoustic recordings by an expert ornithologist to assess the correlations between acoustic indices and bird species richness. Calculated acoustic indices showed that biophony (vocalizations of sound-producing organisms) was dominant in this agricultural landscape rather than anthropophony (human-generated sounds). However, the strong presence of geophonic sounds, such as rain and wind, biased some of the indices. Moreover, non-avian species such as crickets masked bird vocalizations in summer, further biasing the indices. The study contributes to the ecoacoustics literature by assessing the biodiversity of under-investigated agroecological farmlands in the Mediterranean. The findings point out the potential for the use of acoustic indices for conservation organizations working with farmers in agricultural landscapes.

Keywords: Acoustic Monitoring, Ecoacoustics, Acoustic Indices, Agro-ecology, Avian Biodiversity

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Adaptive Shifts Rather Than Climatic Relicts Hypothesis Explains The Radiation of Improphantes Spiders in Anatolian Subterranean Habitats

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Improphantes is a monotypic genus of tiny spiders from the family Linyphiidae. All known species dwell in damp and moist microhabitats. One species was recorded to occur in shallow parts of caves as well. New subterranean populations of Improphantes spiders have been recently discovered in Anatolia, colonizing various habitats, such as different cave zones and MSS. The adaptive shifts hypothesis implies that functional traits should diverge between epigean and subterranean populations, and adaptive evolution for subterranean niches will give rise to troglomorphic traits. Alternatively, no difference is expected if the niches are conserved or if the geneflow continues as expected in troglophiles, which can effectively colonize both the epigean and subterranean habitats. The aim is to test this prediction using morphological traits at intraspecific and interspecific levels. Morphological data were gathered from two sources: i) compilation from the taxonomic literature with coverage of all known Improphantes and ii) direct measurements on the recently collected specimens, including those collected from epigean and subterranean environments. Ordination and regression analyses successfully identified trait differences between individuals from different habitats at both population and specific levels. Findings indicate that troglophily is more common in Improphantes than previously known, and there are troglomorphic populations showing extremes in trait values of characters associated with troglomorphism. The colonization of subterranean environments in the Palearctic has been traditionally explained by the climatic relicts hypothesis. The observed patterns of trait differentiation imply the adaptive shifts hypothesis and a recent radiation of Improphantes spiders in Anatolian subterranean habitats.

Keywords: Arachnology, Speleobiology, Biodiversity

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Coupling of Morphology & Behavior in Cryptic Grasshopper Species

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Cryptic species lack obvious morphological differences yet maintain reproductive isolation through behavioral cues, which challenges taxonomy and conservation efforts, especially as they may often go unnoticed. Understanding the relationship between subtle morphological traits and behavioral signals is crucial for delineating genetic differentiation between hybridizing species. The Chorthippus biguttulus complex in the Alps provides an excellent system for investigating the role of morphological traits in nonecological speciation. Reproductive isolation within this complex is maintained through the coupling of multiple barriers. However, the presence of a putative hybrid, which exhibits an intermediate courtship song, challenges this pattern. Our study aimed to identify 1) the morphological traits associated with divergent courtship songs that aid in species distinction and 2) determine whether these traits evolve neutrally within a phylogenetic context. Through three morphometric approaches and population-level sampling, we evaluated wing morphological differentiation among five taxa. Linear discriminant analysis effectively distinguished taxa based on wing morphology, particularly wing width and length, highlighting form-function coupling. Our findings suggest a correlation between wing morphology and courtship songs, albeit with discrepancies from genomic data, implying non-neutral evolution. Additionally, the putative hybrid displayed intermediate wing morphology, further emphasizing the coupling of form and function in speciation processes. These results underscore the potential of morphological traits as proxies for behavioral traits and have implications for museum collections, where such traits can be used to infer behavioral characteristics of specimens. Moreover, our study highlights the utility of geometric morphometric approaches for efficiently detecting cryptic species in future high-throughput analyses.

Keywords: Cryptic species, hybridization, behavioural isolation, geometric morphometrics, integrative taxonomy

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Keynote Address: Mutation and selection on tandem repeats promote genetic and phenotypic diversity across species

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Tandem repeats (TRs) are frequent in genomes across the tree of life. TRs contribute to fundamental biological functions and can be associated with virulence, resistance, and human diseases. TR diversity offers a perfect playground for natural selection. However, TR studies are typically non-trivial due to their high mutability. In this talk I will discuss some statistical methods for analysing TRs and present several applications. For example, we analysed TRs with long repeat units (> 15 residues) across eukaryotic proteomes. We found that most TRs are ancient, with TR regions preserved since distant speciation events. In contrast, short TRs (STRs, with units of 1–6 bp) are orders of magnitude more mutable than other well-studied genotypic variants; STRs therefore make major contribution to genetic and phenotypic divergence. Our current work shows that STR mutations might regulate gene expression in colorectal cancer (CRC). We identify putative expression STRs (eSTRs) for which the STR copy number is associated with gene expression in CRC tumors. Linear models describing eSTR-gene expression relationships allow for predictions of gene expression changes in response to eSTR mutations. Furthermore, we found an increased mutability of eSTRs in MSI tumors. This may be an early indication that eSTR mutations confer a selective advantage for some CRC tumors. Our evidence of gene regulatory roles for eSTRs in CRC highlights a largely unexplored way through which tumors may modulate their phenotype.

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SESSION IV: POPULATION GENETICS

Geneticand Morphological Diversity of Botryllus schlosseri on the Turkish Coast

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Botryllus schlosseri is a vital model organism in the botryllid ascidian species. It is a crucial reference point for phylogenetic studies due to its ancestral position within the chordate lineage. Despite its acknowledged significance, research on B.schlosseri along the Turkish coasts is surprisingly limited. The unique features of the Turkish seas make it important to study B. schlosseri in this region as it can help understand potential lineages and adaptive evolution within the species. This study aims to address the gap in knowledge by using mitochondrial COI region sequencing and morphological analyses to identify haplotype groups and morphotypes collected from various locations along the Turkish coastline. Genetic and morphological analyses have already begun on B. schlosseri samples. The COI region was amplified for phylogenetic analysis, and morphological features will be examined using a stereo microscope. Preliminary results based on mitochondrial COI region sequencing have identified 26 distinct haplotype groups for B. schlosseri, ranging from the easternmost Artvin to the westernmost Karaburun stations. The observed haplotype diversity value of 0.8414 indicates a high genetic variation within the populations. Morphological analyses further revealed the presence of more than 20 morphotypes among these samples. Findings indicate that B.schlosseri populations have significant genetic and morphological diversity even within the limited confines of the Black Sea. Sequence and morphological analyses are ongoing for the remaining regions. This research underscores the importance of investigating this unique and valuable model organism in Turkish waters, revealing novel insights into its adaptive evolution and lineage diversification.

Keywords: *Botryllus schlosseri*, mitochondrial DNA, COI region, haplotype, evolution

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A potential hybrid zone between two species of humphead cichlids Cyphotilapia sp. along the east coast of Lake Tanganyika

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The population genetics of Cyphotilapia sp. was investigated using ddRAD-seq along the east coast of Lake Tanganyika. Using a combination of ADMIXTURE, PCA, genome polarization and 2D Site Frequency Spectrum analyses, we confirm the presence of two species, C. frontosa in the north and C. gibberosa in the south as documented in other studies. We also found evidence of a hybrid zone separating the two species, with a sharp genetic cline centered in the middle of the lake and apparent introgression in both directions, but predominantly from 'gibberosa' into 'frontosa'. The highest proportion of introgressed 'gibberosa' ancestry was present in the southernmost populations of C. frontosa: Karilani Island and Cape Kabogo. At the intra-specific level, there was support for between 1-3 populations of C. frontosa, whereas the results indicated only a single homogeneous population of C. gibberosa. The presence of different morphs around the lake despite the low levels of heterozygosity suggests that a small number of loci may be involved in the morphological variation and/or there is more complex interplay between genetics and the environment in different locations.

Keywords: cichlid fish, ddRAD, hybrid zone, Lake Tanganyika

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Comparative demographic analysis of *Cardamine hirsuta* and *Arabidopsis thaliana*

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Understanding the dynamics of populations and their genetic divergence in relation to historical ecological and climatic events is a major goal of evolutionary biology. Comparing the population dynamics and distribution of closely related species can illuminate the roles of common versus divergent ecological parameters in shaping trait and sequence diversity patterns, identifying convergent genetic responses to global ecological changes. Cardamine hirsuta (Cardamine) is a small crucifer related to Arabidopsis thaliana (Arabidopsis), and shares features with Arabidopsis, making it an attractive experimental system. Population genetics analyses of Pan-European Cardamine samples comprising 746 natural accessions revealed that Cardamine from the Iberian Peninsula and the Macaronesian Islands retain considerable genetic diversity, thus resembling Iberian relict populations of Arabidopsis. However, Cardamine strains extend further into mainland Europe than Arabidopsis relicts, suggesting a greater ability to establish beyond glacial refugia. In Arabidopsis, the deepest population splits have been reported to be those between the African populations. The absence of information on Cardamine African diversity leaves many open questions on the comparative understanding of the population dynamics of the two species. In this study, we developed a standardized bioinformatics workflow to generate variation data for two related Brassicaceae species sampled from Europe, North Africa, and East Africa. Next, we joint-analyzed the demographic history of Cardamine from Europe and Africa and compared it to that of Arabidopsis. Our findings shed light on the complex interplay of historical events, geographic influences, and ecological factors in shaping these closely related plant species population history and genetic divergence.

Keywords: Populations, Africa, comparative genomics, Demographic history

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Genetic, epigenetic and morphometric diversity of Pinus nigra populations with differential exposure to air pollution and climatic change

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The effects of pollution and climatic change on genetic, epigenetic and morphometric diversity of black pine (Pinus nigra) were investigated in two sites of western Macedonia and south-eastern Peloponnese respectively, where for decades the largest lignite mining and burning centers of Greece operate, resulting in large amounts of primary air pollutant emissions, mainly SO2, NOx and PM10. P. nigra, a biomarker for air pollution and a keystone species of affected natural ecosystems, was examined in terms of needle and cone morphometrics, genetics (AFLP) and epigenetics (MSAP), using two locations per site (exposed to pollution and "control") to investigate pollution effects, and two populations nested within location (high and low tree limits) to investigate climatic change effects and their interaction with pollution. In Western Macedonia genetic diversity parameters, did not show statistically significant differences between exposed population and "control". Nevertheless, statistically significant differences were detected at the population epigenetic level. Needle and cone morphometric parameters generally showed higher and mostly statistically significant values in control populations over exposed and in low elevation populations over high elevation ones. In the Peloponnese populations, the low elevation "control" populations generally showed statistically significant higher values in morphometric parameters, compared to the high elevation exposed population. This study elucidates phenotypic, genome, and epigenome dynamics in forest tree populations exposed to long term differential atmospheric pollution burden and stresses the importance of detailed studies in order to assess and monitor the complex effects of pollution and climatic change in natural perennial plant populations.

Keywords: *Pinus nigra*, AFLP, MSAP, morphometrics, air pollution, climatic change

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Keynote Address: Gene flow and population structure in a highly mobile species across Eurasia: genome-wide analyses of the gray wolf (*Canis lupus*)

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Large carnivores have a strong capacity for dispersal and have been known to travel several hundred kilometers. In some instances, we nevertheless observe genetic structure across relatively short distances, at times associated with environmental or physical boundaries. Long-term isolation and genetic drift can explain some of the observed differentiation, whereas in other cases there are no clear physical barriers to dispersal. In the western part of Eurasia, gene flow might also be easier east-west than north-south, owing to natural features such as water and mountain ranges. The gray wolf (*Canis lupus*) is among the most widely distributed mammal species, where individuals can disperse over a thousand kilometers. The species may thus be expected to show limited genetic differentiation, with stronger signatures of genetic drift in peninsular populations that have experienced strong isolation during the past centuries. Analyses of over 700 wolves genotyped with the Illumina CanineHD BeadChip with more than 170 000 single nucleotide polymorphism (SNP) loci detected population structure across Eurasia, yet relatively high gene flow in central and eastern Russia. In contrast, populations in the Iberian, Italian and Scandinavian peninsulas showed distinct profiles suggesting protracted isolation and genetic drift. In contrast to recent findings from analyses of mitochondrial DNA, wolves from the Dinaric-Balkan region were clearly divergent from those sampled in the Carpathian Mountains. New genomic methods can help clarify the role of environmental and ecological factors in structuring genetic variation in wide-ranging species, including those that can take advantage of a wide variety of food resources.

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Evolutionary change through developmental endosymbiosis

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Variation and natural selection are two major forces of evolutionary change. Genetic change, epigenetic change, developmental plasticity, canalization, endosymbiosis, and the environment are some of the factors that cause variation in phenotypes. At the same time, developmental bias and niche construction are some of the factors that influence natural selection. Attempts to integrate these concepts into the standard evolutionary theory have recently taken the forefront of evolutionary studies. Our lab has recently established a system of study, using ants and their cellular endosymbionts, in which these factors can be studied in an integrated manner. Ants have acquired cellular endosymbionts at least four times independently during evolution. These independent events have been preceded by genetic changes and developmental alterations that facilitated the acquisition of endosymbionts. More importantly, these changes often appear to be induced by the endosymbionts themselves. Here I will share our lab's attempts to address the question of how developmental endosymbiosis leads to evolutionary change.

Keywords: Eco-Evo-Devo, Developmental Integration

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Gut reorganization during regeneration and asexual reproduction in a freshwater annelid

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Regenerating the whole-body axis upon bisection often leaves organisms with incorrect body proportions that need to be reorganized after regeneration. While there are many studies that have focused on the process of regeneration, the tissue remodeling that takes place during or after regeneration to achieve accurate body composition remains understudied. Here we investigate tissue remodeling in a highly regenerative segmented worm (annelid) Pristina leidyi at the molecular, cellular, and morphological levels. We specifically focus on the gut tissue, which is highly regionalized, and which undergoes extensive remodeling during and after regeneration. For example, bisected worms have to turn intestine tissue into stomach. Using single cell RNA sequencing (scRNAseq), we identified specific molecular markers for different gut cell types and regions that were not easy to distinguish via histological or bulk RNA sequencing techniques. We visualized the localization of these markers using Hybridization Chain Reaction (a multiplexed fluorescent in situ hybridization method), and found that P. leidyi has a complex gut organization along the entire anterior-posterior axis of the body, from mouth to anus. Some of these regions are as specific as 2 segments, with very defined borders where marker expressions do not overlap. We next carried out amputations and analyzed gut reorganization at the morphological level, and we found that gut tissue reorganization takes place over a longer time period (weeks), after regeneration is completed (in 4 days). Future studies will focus on the dynamic changes in cell identity using the molecular gut markers and cell lineage tracing.

Keywords: asexual reproduction, gut, regeneration, post-embryonic development, cell type diversity

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Beyond modern synthesis

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The theory of evolution, when defined as a scientific research program, establishes gene as the focus of its mechanism in a broad sense, and follows whether the variation in that gene can be inherited to the next generation. Every other process in living beings is considered a secondary or proximate factor in the theory. Endosymbiotic relationships, which mean the union of two organisms living together, are seen as rare events in terms of producing evolutionary outcomes. These inter-relationships are mostly examined as ecological and metabolic. Genomic relationships are regarded rarely and are addressed almost exclusively as horizontal gene transfer between the symbiotic partners. Besides, the endosymbiont has the potential to affect gene expression and may become a part of developmental processes. In our study system, the carpenter ants, we observe that gene expression patterns differ from those in closely related ants (Rafiqi, 2020) as well as the model system drosophila. To transmit maternally, the endosymbiont undergoes a segregation of bacteria during embryonic development between gut and germline. A germline capsule contains germline molecules/granules localized in a position unlike their usual position in the posterior. Germline nuclei move to this location, along with some bacteria out of the majority of bacteria. In our model, we predict that there is interaction between these three; germline, germ granules and bacteria. In order to uncover these interactions, we performed differential expression analysis between germline capsule and other tissues. Based on these analysis, we plan to perform knockdown of select genes to figure out the functions of the molecules and interactions among them. The results from this project will provide a new perspective on the mechanism of evolutionary change, because it takes into account interactions between two genomes in the context of organismal biology, broadening the framework of evolutionary theory.

Keywords: endosymbiosis, germline, transcriptome

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SESSION VI: MICROBIAL EVOLUTION

Exploring the Oral Microbiome and Pathogens in Dental Calculus from 13th-Century Crusaders in İznik

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Towards the end of the 13th century, various communities with diverse ethnic backgrounds were residing in İznik. Several excavations have been conducted to understand this complex structure. These include human skeletons obtained from the İznik Roman theater and the İznik Museum Rescue Excavation (IMKK) burials. Archaeological and burial-type analyses revealed that the human skeletons from the interior of the Roman theater were likely Crusader warriors, while those from outside could be a part of the local Muslim population, and the IMKK burials belonged to the local Christian population. Although archaeological analyses provided insights into the everyday life of these groups, limited information is available about the oral microbiome content, possible pathogenic organisms, and diet-related DNA reads in this community. In this study, we analyzed DNA reads from dental calculus material of six different Christian Crusaders to identify (i) the oral microbiota composition, (ii) opportunistic pathogenic organisms in the oral cavity, and (iii) diet-related eukaryotic DNA reads. Our initial results indicate that ancient bacterial DNA from species such as Streptococcus and Neisseria, along with Red Complex species. Additionally, partial genomic sequences of bacteria responsible for meningitis (Neisseria meningitidis) and gonorrhea (Neisseria gonorrhoeae) were retrieved using de novo assembly methods. Furthermore, DNA sequences from foods consumed by the local population at that time, such as sheep and pig, were identified in the dental calculus. These findings suggest that dental calculus analysis can provide valuable insights into the health, lifestyle, dietary patterns and possible health risks faced by these communities.

Keywords: Ancient DNA, Oral Microbiome, Dental Calculus, İznik

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Detecting Biodiversity in Ship Ballast Water Using Environmental RNA Metabarcoding

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Ballast water, transported internationally by ships for structural stability, contains diverse living organisms. These organisms pose significant ecological risks when introduced into non-native marine environments as invasive species. Although many do not survive or adapt post-transit, some can disrupt local biodiversity and establish thriving populations. Utilizing environmental RNA (eRNA) metabarcoding to detect these organisms offers a proactive approach to managing these risks. In this study, we collected 2-5 liters of water from five different fuel vessels in İzmit, Türkiye, filtering each sample through 0.22 µm Sterivex filters. This process was repeated three times per vessel to ensure consistency. Post-filtration, the samples were treated with RNA fixative, transported to the laboratory in a portable cooler, and subjected to RNA extraction using the TRIzol protocol. Subsequent cDNA synthesis included DNase treatment to minimize DNA contamination. Our results confirm the feasibility of extracting eRNA from ballast water, with lower yields observed from ships employing filtration and UV treatment. This preliminary study supports the use of eRNA and metabarcoding techniques for assessing biodiversity in ballast water, indicating a promising method for ecological monitoring and invasive species management.

Keywords: Environmental RNA, Biodiversity, Metabarcoding, Ballast Water, RNA Extraction

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Demographic and Evolutionary Consequences of Damage Dynamics in Single-Cell Ageing

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Ageing plays an important role in evolutionary dynamics by affecting the fitness components of individuals and changing the fate of newly arriving mutations. At the molecular level, ageing is driven by damage accumulation leading to a decline in function over time. This damage accumulation is not only inherently stochastic but also — in the case of damage partitioning at cell divisions — asymmetric. Despite empirical single-cell studies providing quantitative data at the molecular and demographic level, there is not a comprehensive theory of how cellular damage production and asymmetric partitioning lead to demographic patterns and evolutionary consequences. We develop a generic and flexible damage model using a stochastic differential equation approach which can be scaled further to population and evolutionary scales. Our model incorporates stochastic damage accumulation and asymmetric damage partitioning at cell divisions. Our analytical and numeric analyses allow us to show explicitly how stochasticity (noise) in damage production, asymmetry in damage partitioning, and division rate shape lifespans. Interestingly, the lifespan of cells follows an inverse-gaussian distribution whose underlying properties derive from cellular and damage parameters. We apply our model to various empirical E.coli data revealing non-exponential scaling in mortality rates, which cannot be captured by classical models. Furthermore, we analyse how molecular parameters and damage distribution affect the fixation probability of beneficial mutations. Our findings provide a deep understanding of how fundamental processes contribute to cellular damage dynamics and generate demographic patterns, and provide the necessary theoretical framework linking cellular damage processes to demographic, population and evolutionary dynamics.

Keywords: Ageing, Single-cells, demography, population and evolutionary dynamics

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The Future of Western Palearctic Biodiversity Hotspots: Assessing Climate Change Vulnerability

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The Western Palearctic biodiversity hotspots (the Mediterranean, the Irano-Anatolian, and the Caucasus) stand out with high levels of endemism and genetic diversity. These hotspots host the High Biodiversity Importance Ecoregions; however, they are under insufficient protection and categorized as nature-imperiled. Also, they are threatened by anthropogenic climate change compounded by land use changes, which alters species distribution and abundance, as well as degrades habitats and declines ecological connectivity. The Kunming-Montreal Biodiversity Framework addresses these threats and aims to protect at least 30% of the Earth by 2030. To achieve this goal, it is crucial to investigate the effects of anthropogenic climate and land use changes on these areas. Here, we assessed the climatic vulnerabilities of the Mediterranean, the Irano-Anatolian, and the Caucasus biodiversity hotspots. We used the velocity of climate change algorithms and land use changes to assess vulnerability. We quantified the velocity of climate change using spatial climate analogs. We used Coupled Model Intercomparison Project Phase 6 (CMIP6) projections for different Shared Socioeconomic Pathways (SSPs) by the end of the century. We investigated potential shifts in both climate and land use at the levels of hotspots, ecoregions, and key biodiversity areas. We highlighted areas of relatively low and high risk from both species and habitat perspectives. We found that hotspots, ecoregions, and key biodiversity areas differ in climate change vulnerability. Additionally, the current protection network is not sufficient to safeguard these biodiversity hotspots. We discussed how to enhance conservation actions in line with the Kunming-Montreal Biodiversity Framework.

Keywords: climate change, land use change, biodiversity hotspots, biodiversity conservation

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Species diversity, abundance and community composition of Carabidae (Coleoptera) across habitats in north central Anatolia

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Among insect families, carabids (Coleoptera: Carabidae) are noteworthy for their species richness, diverse behaviors and roles in the food web, as well as their habitat specificity, which has led to their use as indicators of habitat change and degradation. We studied carabid diversity across various habitats within a 1000 km2 area north of Ankara, Türkiye. We examined four habitat types dominated the landscape in the region: steppes, field margins, forests, and riparian zones. For each habitat type, we selected three 1-ha sites and conducted four sampling sessions from June to October 2022. Carabids, being ground-dwelling insects, were collected using pitfall traps filled with a vinegar-salt solution. Traps were arranged in a 3 × 3 grid design with a 20 m spacing between each trap. Approximately four weeks after trap establishment, carabid samples were collected monthly and brought to laboratory for identification. We performed generalized linear models assuming binomial and Poisson distributions and calculated the Shannon diversity index to compare the presence and abundance of carabids across habitats. Furthermore, we used principal component analysis to compare community compositions. In total, we identified 27 Carabidae species, with presence and abundance varying significantly across habitats. Species richness was highest in forest and riparian habitats. Additionally, the sampling month significantly affected species richness and abundance, with the highest number of species and individuals recorded in October in each site, regardless of habitat type. Our findings indicate that both habitat type and season are key drivers of the carabid community composition in the study region.

Keywords: Carabidae, habitat preference, insect community, species diversity.

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Keynote Address: Roots, rhizomes, tubers and bulbs: A missing plant dimension

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Half of a plant is hidden belowground. Consequences of this fact are manifold: we have poor knowledge about which organs and which functions are unseen, how much a plant invest to them, how much a plant rely on them when stressed or disturbed, how easily they evolved or how much they affect ecosystem functions. Using examples form Central Europe I will show diversity of belowground organs, their evolutionary history, how they affect plant distribution along environmental gradients and among plant communities, how they shape plant strategies and ecosystem functions, how they relate to plant economic spectrum. I will also introduce activities of our group to promote research focused on plant belowground organs, including free datasets, methodological handbooks, and courses focused on practical assessment on traits of belowground organs.

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SESSION IIX: PALEOBIOLOGY

Grave Matters: Discerning Ancient DNA Profiles from Grave Dirt vs. Skeletal Remains

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Sedimentary ancient DNA (sedaDNA) has become a valuable tool for studying past populations in the absence of human remains. Here, we explore the use of sedaDNA as an alternative to ancient DNA from skeletal elements. We collected skeletal material, along with grave dirt from the skeletal surfaces, at n=3 archaeological sites. We generated mitochondrial and nuclear genome data using target enrichment, and analyzed the differences in sequence profiles from sediments versus bones. In general, we found sedaDNA could be more degraded than the skeletal DNA from the same grave, and contained relatively higher amounts of modern human contamination.Then, we tested for the presence of non-human DNA in grave dirt. In n=3 samples, we identified ancient faunal DNA in addition to human DNA, in all cases belonging to domestic animals such as sheep and dogs. Further, we explore the differences between the two types of data in population genetics analyses. Compared to matched bones, we were able to identify the same or slightly more ancestral haplogroups in sediment samples. particularly We also observed similar clustering patterns in PCA and f-statistics where we assessed the relative affinities to the adjacent contemporary populations. Together with the haplogroup inferences, these results suggest that the human DNA in the sediments primarily originates from the buried individual. Overall, we show that although less DNA is typically recovered from sediments, in some cases it can be possible to achieve a comparable accuracy in genetic studies by sampling sediments rather than the skeletal material itself.

Keywords: ancient DNA, sediment, genetics

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Analyzing social traditions of Neolithic Çatalhöyük based ancient DNA

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The Neolithic site of Çatalhöyük (7100 BC and 5950 BC), located near modern-day Konya, Turkey, is internationally significant due to its well-preserved buildings, size, dense population, and continuous occupation for approximately 50 generations. It is consequently recognized as a laboratory for studying long-term change in the earliest agricultural societies. Here, we present 131 paleogenomes from burials comprising the Early (7100-6700 BC), Middle (6700-6500 BC), and Late (6500-6300 BC) periods to characterize house-based social organization and provide new insights into social traditions. Our results reveal that the Neolithic Çatalhöyük gene pool did not change significantly throughout its occupation and, furthermore, no evidence of patrilocality was observed, in contrast to European Neolithic sites. Studying genetic kinship patterns, we find individuals often buried with close relatives in the Early period, while connections become sparse in the Middle and Late periods, with children from multiple biological families being buried in the same building. Additionally, pedigree and uniparental marker analysis showed skeletons co-buried within the same buildings to be connected mainly maternally, rather than paternally. These findings suggest that maternal kinship networks may have influenced house-based social structure of Neolithic Çatalhöyük, and that this pattern of social dynamics persisted despite shifting social norms.

Keywords: Çatalhöyük, Neolithic, Ancient DNA, Genetic Kinship

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PALEOLIMNOLOGY OF THE LAKES OF BOLKAR AND ALADAĞLAR MOUNTAINS, TURKEY

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Sediments of alpine lakes constitute important chronological archives of climatic signals due to their isolated locations and simple ecosystems. Furthermore, alpine lake ecosystems may exhibit significant shifts in ecosystem structure in response to climate change and other anthropogenic impacts. Anatolia, Turkey hosts large extents of mountainous regions with several Alpine lakes, however no paleoecolgical investigations have been carried out so far. We conducted palaeoecological sampling expeditions to Bolkar and Aladağlar Mountain ranges in South Anatolia between 2019 and 2023. A total of 25 lakes were sampled between 1364-3066 m altitude. Two long cores were collected from Lake Çinili and Çini at Bolkar Mountains (85 and 111 cm). Both lakes were small (2.74 and 2.16 ha) and deep (c. 11.3 and 20.3 m respectively) The lake catchments were small and covered with limestone rocks and alpine vegetation. The long cores were scanned with XRF, sliced for 0.5 cm and analysed for loss of ignition (LOI), C & N content as well as composition of diatom, pigment and polen remains. Preliminary dating based on Pb210, Cs137 and C14 radioisotopes suggested that the long cores may represent a time period 2000-4000 years before present. LOI, Ca/Ti and Mn/Fe stratigraphy of the long cores suggested alternating periods of high and low productivity and water level. Overall, the preliminary data on the cores indicates a dynamic shifts in these alpine lake ecosystems in the recent past, which might have reflected the dynamics in the climatic changes.

Keywords: Paeloecology, Alpine lakes, Limnology

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Cormohipparion cappadocium, a new species from the Late Miocene of Yeniyaylacık, Türkiye, and the emergence of Western Eurasian Hipparion bioprovinciality

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The effects of pollution and climatic change on genetic, epigenetic and morphometric diversity of black pine (*Pinus nigra*) were investigated in two sites of western Macedonia and south-eastern Peloponnese respectively, where for decades the largest lignite mining and burning centers of Greece operate, resulting in large amounts of primary air pollutant emissions, mainly SO2, NOx and PM10. P. nigra, a biomarker for air pollution and a keystone species of affected natural ecosystems, was examined in terms of needle and cone morphometrics, genetics (AFLP) and epigenetics (MSAP), using two locations per site (exposed to pollution and "control") to investigate pollution effects, and two populations nested within location (high and low tree limits) to investigate climatic change effects and their interaction with pollution. In Western Macedonia genetic diversity parameters, did not show statistically significant differences between exposed population and "control". Nevertheless, statistically significant differences were detected at the population epigenetic level. Needle and cone morphometric parameters generally showed higher and mostly statistically significant values in control populations over exposed and in low elevation populations over high elevation ones. In the Peloponnese populations, the low elevation "control" populations generally showed statistically significant higher values in morphometric parameters, compared to the high elevation exposed population. This study elucidates phenotypic, genome, and epigenome dynamics in forest tree populations exposed to long term differential atmospheric pollution burden and stresses the importance of detailed studies in order to assess and monitor the complex effects of pollution and climatic change in natural perennial plant populations.

Keywords: Cormohipparion, Yeniyaylacık, Evolution

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SESSION IX: WILDLIFE ECOLOGY

Seasonal Fecal Glucocorticoid Metabolites Concentration Fluctuations in Captive and Free-Ranging Endangered Mountain Gazelles (*Gazella gazella*)

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Fecal glucocorticoid metabolites (FGM) are known as an indicator of stress in mammalian species. Mammals under short-term stress may simply require reserve biological resources to deal with the stress, and those reserves can be easily restored with the restoration of homeostasis without requiring a lengthy recuperation period. On the other hand, long-term stress can cause serious problems in the well-being of the animals. The aim of our study is to measure FGM concentrations in captive and free-ranging male and female mountain gazelles (Gazella gazella) during their circannual cycle. Fecal samples were collected from the field for the captive and free-ranging populations of the species in Hatay, Türkiye in four seasons of the year. For sex determination and measurement of FGM concentration, in total of 262 samples were collected. After the analysis of sex via the SRY gene in isolated DNA samples, we found 133 females and 129 males. FGM concentrations were measured by ELISA. The analysis results indicated a statistically significant difference in FGM concentrations among seasons, however, the FGM concentrations did not significantly differ between sexes or between captive and free-ranging populations. In animals of both sexes, the highest concentrations of FGM were observed in September, the high numbers of visitors and youngers in the populations may influence the results and the lowest in December we assume that their adaptation processes do not require a significant adrenocortical response in December. The obtained data may be beneficial for the population management and conservation of mountain gazelles.

Keywords: mountain gazelle, stress, large mammals, hormones, fecal analysis

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Seasonal survival of the gray mouse lemur under changing climate

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Tropical ecosystems are characterized by alternating dry and wet seasons. Wildlife populations already adapted to this seasonality via seasonally varying survival rates. However, seasonal patterns of temperature and rainfall are changing under climate change, especially in the tropics, forcing species to adapt their seasonal survival strategies. Therefore, it is important to understand how the survival of tropical species responds to seasonality and recent changes therein. To do so, we studied gray mouse lemurs (*Microcebus murinus*) of Kirindy Forest in Madagascar using three decades of capture–recapture data. We conducted multistate mark-recapture models using a hierarchical Bayesian framework and focused on age and sex-specific survival in response to rain, temperature, and population density. Mouse lemurs had a higher mean survival probability during the dry season than during the wet season. While survival of all groups decreased with increasing rainfall during the wet season, maximum temperature during the dry season affected survival depending on the density-dependence. Males were more sensitive to temperature changes than females. These results highlight the pronounced impact of temperature fluctuations on seasonal survival relative to variation in rainfall, while also emphasizing the influence of population density. This study also underscores the importance of accounting for seasonality in demographic analyses to pinpoint environmental drivers of population parameters and to refine predictions amid changing environmental conditions.

Keywords: Bayesian population analysis, mark–recapture, hierarchical models, seasonality, survival, Microcebus

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Species and Photoreceptor-Specific Quantification of Light

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Light serves as a vital environmental regulator of physiology and behavior, with ecological light pollution disrupting circadian rhythms and impacting animal health and well-being. Proper lighting is crucial for indoor-housed mammals. The commonly used lux measurement, based on human-perceived brightness, lacks suitability for non-visual light effects and cross-species application. We've developed technology for species-specific light quantification in any mammalian species, accounting for evolutionary differences in photoreceptor types, spectral sensitivities, and eye anatomy. We developed a high-throughput, easy-to-use, method to derive spectral sensitivities for recombinantly expressed Opsin proteins and use it to establish the spectral sensitivity of melanopsin from twelve non-human mammals. We also collated pre-receptoral light transmissions of these species. Through phylogenetic comparison, we've assessed ocular and photopigment-related characteristics. Demonstrating the superiority of species-specific light measurements over lux, we show their effectiveness in predicting physiological responses in mice and enabling ecologically relevant photosensitivity comparisons between species. Addressing the need for simple measurement strategies, we've developed an online toolbox and validated a low-cost, multichannel light sensor for easy measurement. Our study demonstrates that measuring light considering differences between species is superior to the existing unit of lux and holds the promise of improvements to the health and welfare of animals, scientific research reproducibility, conservations against ecological light pollution, and energy usage.

Keywords: Light pollution, photoreceptor, lens transmission

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Climate change modulates ecological network of Brown bears across Türkiye

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Broad-scale landscape connectivity is critical to buffer against the adverse effects of habitat loss and fragmentation on wildlife. Brown bears are the largest carnivore living in Türkiye. The current study examined the ecological network of brown bears across Türkiye and climate change effects on their connectivity. Combining circuit and graph theories, prioritized patches and movement routes, their quality, and pinpoint bottlenecks to the movement for current and future conditions. 61 core habitats and 106 linkages were mapped for the present day. Our analysis showed the most essential patches for maintaining landscape-wide connectivity were in the Black Sea and Eastern Anatolia. Barrier mapping showed substantial barriers, especially in central Anatolia. The most ideal areas for restoration were scattered across the central Black Sea, Marmara, and Eastern Anatolia regions. Our findings showed climate change-driven shifts would disrupt brown bears' ecological network across the country.

Keywords: Wildlife, Ursus arctos, Connectivity, Climate Change, Türkiye

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From Hydra to Human: *In silico* Investigation of the Atavistic Model of Cancer

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Cancer manifests as a disruption in the regular functioning of multicellular systems, arising from the malfunctioning of genes responsible for cellular cooperation. Notably, cancer exhibits atavistic characteristics, wherein cancer cells diverge from the conventional Darwinian evolution, highlighting a distinctive trajectory in their development. Atavism refers to the re-emergence of ancestral traits or characteristics that have been dormant or suppressed in a species' evolutionary history. Cancer cells may display traits such as uncontrolled proliferation, evasion of cell death mechanisms, and altered metabolism, which could reflect ancient biological programs related to growth and survival. In this study we employed the basal metazoan Hydra, which is known to have polyps, a type of cancer. We aimed to trace the evolutionary origins of cancer by analyzing tumor-related proteins in Hydra and their conservation across different taxa. To this end, we have employed bioinformatic approaches to investigate the conservation status of protein-coding genes that are differentially expressed in the tumor-bearing Hydra across diverse taxa. Through investigating Hydra's tumor-related proteins, we have traced the ancient evolutionary roots of cancer through the tree of life. We also suggest Hydra as an emerging model organism in cancer research by providing evidence of conservation among cancer related proteins. Our findings position Hydra as a promising model for cancer research, shedding light on the evolutionary underpinnings of cancer and highlighting its relevance in broader biological contexts.

Keywords: Atavism,Cancer, Bioinformatics, Evolution, Phylogeny, Unicellularity, Multicellularity

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Automating the Design of Hybridization Chain Reaction in situ Probes for Big Data Sets

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One major hurdle to achieving biologically-meaningful results from massively-parallel techniques like single-cell RNA-sequencing (scRNA-seq) and SPLiT-seq (separated PCRs of linked templates for sequencing), lies in determining how statistical groupings relate to the original tissues. We have developed a python library to rapidly design mRNA in situ hybridization probes compatible with the multiplexible, fluorescent HCR3.0 system described by Choi et al 2018, expanded by Wang et al. 2020, and modified by Tsuneoka and Funato in 2020.

Keywords: *In situ* Hybridization, Python, Command line, Fluorescent, Probes

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Parasitism in a boiling world: effect of latitude and climatic variables in damselflies parasitism

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The world is experiencing dramatic changes in temperature and rainfall patterns which may facilitate parasitism. However, evidence regarding the effect of latitude and climate on insect parasitism is limited. Therefore, we tested the effects of a) latitude and b) climatic factors on parasitism by comparing the prevalence and intensity of water mite ectoparasite (Arrenurus) on Ischnura heterosticta damselflies (Odonata) across a latitudinal gradient along the Australian east coast. The life history of damselflies is influenced by climate and parasites, making them ideal for studying host-parasite interactions. We sampled 45 different populations spanning tropics, subtropics, and temperate regions, collecting over 1100 individuals. Our results revealed higher parasite prevalence and intensity at lower latitudes, with tropical populations exhibiting the highest infection rates (48%). The outstanding individual was a female from a lower latitudinal population carrying 28 parasites. Bioclimatic analysis indicated a positive correlation between annual temperature and parasite prevalence while only annual rainfall was positively correlated with parasite intensity. We are currently using molecular tools to identify mite species, assess fitness costs, and mating behaviour associated with infection. Understanding the ecology of host-parasite interactions across latitudes and determining the effect of bioclimatic factors are crucial in predicting infection patterns in insects and wildlife in a changing climate.

Keywords: Climate change, disease, aquatic organisms, host-pathogen interaction, spatial variation

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Challenges and opportunities for the assessment of the ecological status in temporary rivers

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Temporary rivers (TRs) make up the majority of the world’s river networks and are known to be hotspots of freshwater biodiversity. They are expected to become more widespread globally and experience longer dry periods due to ongoing climate change. The effects of anthropogenic disturbances on TRs are mixed with the effects of the natural disturbance imposed by flow intermittence. Despite the advances in TRs research, many gaps persist that limit the development of appropriate methodologies for the assessment of the ecological status. In this review, we identify the current challenges for the assessment of the ecological status of TRs and analyze the existing opportunities to address these challenges. These challenges focus on: the differentiation between natural and hydrologically impacted TRs, the differentiation between natural and anthropogenic disturbances, the development of biological indices for disconnected pools and dry riverbeds, the adaptation of hydrogeomorphological indices, and the application of the metacommunity theory in TRs. The opportunities are related to: the use of molecular tools, the existence of alternative indices to the traditional ones, the availability of data to be able to do modeling, and the social implication in the assessment of the hydrological and ecological status. The review focuses mainly on the scientific and management knowledge accumulated since the implementation of the Water Framework Directive in Spain but gathers experiences from TRs around the world to guide conservation and management actions in these unique ecosystems highly threatened by global change.

Keywords: bioindicators; biotic indices; disconnected pools; dry riverbeds; Water Framework Directive; water quality

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Testing evolutionary histories of Weevil families (Coleoptera: Curculionoidea) based on COI sequences

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Weevils (Coleoptera: Curculionoidea) constitute one of the most diverse groups of insects, arranged in seven families (Anthribidae, Attelabidae, Belidae, Brentidae, Caridae, Curculionidae and Nemonychidae) including approximately 62.000 described species. Modern phylogenetic classifications of weevils mostly agree on family level, however; there is still some debate on relations of these seven families. COI sequences i.e. DNA barcodes are widely used in species identification as well as constructing hypothesis of evolutionary phylogenetic relationships. This study aims to suggest and argue evolutionary phylogenetic relationships between seven families of Curculionoidae by using COI sequences available in NCBI database. We randomly chose COI sequences which equally representing weevil family members and constructed two datasets each including 32 COI sequences (five from each family, two from Caridae which has only a few COI sequences in NCBI). We used two Chrysomeloidae members as outgroup. We used MUSCLE algoritm to align sequences and produced phylogenetic trees using Neighbor-Joining and Maximum Likelihood methods in MEGA-X program. In all four phylogenetic trees produced, all families except Caridae constituted monophyletic clades, however relationships of families differed for two datasets and for the methods used. Basal and derived positions of families within Curculionoidea were not identical in the four evolutionary scenarios that resulted from the datasets we used. We argued the internal relationships among families and compared our results with current phylogenies in literature.

Keywords: DNA barcode, cytocrome c oxidase subunit 1 gene, Curculionoidea

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Ecological Context of Zoonotic Helminths: Upcoming Study on Grey Wolves in Türkiye

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Wildlife plays vital roles in ecosystem functioning, maintaining and sustaining balances through fundamental activities such as feeding, breeding, hunting, and migration. These activities support biodiversity and ensure the healthy functioning of ecosystem. However, environmental changes from human activities have increased interactions between wildlife, domestic animals, and humans. Particularly, wild animals belonging to the Canidae family serves as significant sources of parasitic infections commonly observed in humans, playing crucial roles in parasite spread and epidemiology. Gray wolves (*Canis lupus*) within this family harbor numerous endoparasites with zoonotic potential. Therefore, identifying parasitic infections in these wild animals species is critical, especially in rural areas and regions where wildlife habitats are close to human settlements, to prevent parasite transmission from wild carnivores like wolves to domestic animals and humans and implement effective preventive measures. The aim of this research is to collect wolf fecal samples from the populations of Ankara, Burdur, and Antalya Provinces. Fecal samples will be examined both macroscopically (for adult helminths, proglottids, etc.) and microscopically (using flotation, sedimentation, and Baermann-Wetzel techniques), searching for helminth eggs and larvae. This study will provide insights into grey wolf helminth fauna and conduct comparative ecological and epidemiological evaluations among different populations of the species Identification of potential zoonotic parasites through analyses will contribute to biodiversity conservation and safeguarding human health. The findings will hold significance in public health, biology, and One Health fields, thereby enhancing regional awareness on the subject.

Keywords: *Canis lupus*; Helminth; Zoonosis

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Ecological Insights into Helminth Fauna among Eurasian Lynx Populations: An Initial Framework for Future Research

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Wildlife plays a crucial role in maintaining the balance and diversity of ecosystems. However, activities such as deforestation and poaching have increasingly threatening wild habitats over the years. Eurasian lynxes (*Lynx lynx*) are part of these affected habitats and are among populations facing extinction. Factors such as habitat fragmentation, climate change, along with bacterial, viral, and parasitic diseases, impact the health and survival of these species. The water sources, feeding habits, and interactions with other animals in lynx habitats influence parasitic infections, affecting morbidity and mortality rates. The main aim of this study is to thoroughly examine the helminth diversity in Eurasian lynx in Türkiye and understand how these infections affect lynx populations. We collect fecal samples from Eurasian lynx populations of Ankara, Antalya, and Burdur. Macroscopic and microscopic examinations (flotation, sedimentation, Baerman-Wetzel) will be conducted to detect helminth eggs and larvae. The results help determine which three different populations of Eurasian lynxes in Turkey are afflicted by helminth infections, and they additionally allow an evaluation of the chances that these diseases may spread to other predatory animals that inhabit the same area, like wolves, jackals, and hyenas. Parasitological similarities and differences among populations of the same species preferring different habitats are discussed based on ecological principles. Additionally, zoonotic helminths carried by Eurasian lynx are identified, and their potential effects on human health are assessed. The data of the study sheds light upon helminth infections in wildlife.

Keywords: Large mammals, Helminth fauna, *Lynx lynx*

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Bottlenose dolphin offspring in Zonguldak, Turkiye: occurrence pattern and group size of adults-calves units

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It is known that the occurrence and group size of bottlenose dolphins (Tursiops truncatus) in the Black Sea are subject to temporal fluctuations. This study presents the results of the photo-identification surveys of bottlenose dolphins in the adjacent waters of Zonguldak, the southwestern coast of the Black Sea, from 2019 to 2023. The results showed that dolphins were encountered in shallow waters up to a depth of 150 metres and were present throughout the year, with the frequency of encounters and group size varying seasonally (median ranged from 2 to 20). The peak occurrence of immature individuals was in the spring period. The results indicate that the group size of the dolphins increased in February - April (Kruskal-Wallis test =19.2, $p < 0.05$) with median = 3.5; the most abundant group consisted of up to 50 animals. The groups of bottlenose dolphins with calves were significantly larger (median =6) than the groups without calves (median =2, Mann-Whitney test =224, $p < 0.05$). The larger group size with immature individuals, when there are advantages for the protection of young individuals and increased foraging efficiency of nursing females, might be a common feature of bottlenose dolphins. These results contribute to our understanding of bottlenose dolphin population dynamics and mother/calf habitat utilisation and underline the importance of continued monitoring and conservation efforts for this species in the region.

Keywords: Black Sea, bottlenose dolphin, calves, group size

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Revealing gene expression networks involved in development of ovary and straited muscle in teleostei using RNA-Seq method

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Bony fish, comprising half of all vertebrate species, showcase remarkable morphological, anatomical, physiological, and behavioral diversity. From a biotechnological standpoint, understanding key processes in fish reproduction and muscle development holds immense significance. This study investigates hub genes and gene expression networks governing oogenesis and myogenesis in pivotal bony fish species for aquaculture, employing RNA-Seq methodology. Utilizing high-scale RNA-Seq data sourced from the NCBI SRA transcriptomic database, we conducted comprehensive analyses using bioinformatics tools. Our investigation targeted the ovarian tissue, crucial for oogenesis and reproduction, and the striated muscle tissue, pivotal for body mass through myogenesis. Through intricate analyses, we aimed to identify potential master genes regulating these processes across various developmental stages. Key steps in our methodology encompassed species selection, database mining for RNA-sequencing data, data pre-processing using tools such as FastQC and Trim Galore, followed by alignment to the reference genome using HISAT2. Differential gene expression analysis was performed using DESeq2, edgeR, and Limma. Functional annotation involved GO and KEGG analysis, while gene set enrichment analysis (GSEA) identified enriched biological pathways. Orthologous genes were detected using OrthoVenn3, with gene family expansions analyzed via CAFE5. Positively selected genes were identified using PAML and PosiGene, and gene-gene interaction networks were constructed using NetAct, Cytoscape, and String.
Notably, we identified crucial genes for myogenesis (myod, pax3, mstn, tgfb, myog) and for oogenesis (ddx4, nanos, gdf9, wnt4, pgrmc1). In light of our findings, this research advances the broader comprehension of evolutionary ecology and paves the way for precise genetic manipulation in aquaculture practices.

Keywords: *teleostei, RNA-seq, myogenesis, oogenesis, transcriptome*

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Adaptation of Daphnia magna to the fluctuating temperatures

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A growing body of experimental studies demonstrated that an increase of variation of temperature significantly influences the response of several life history traits important for survival, 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 fluctuating temperatures. To investigate evolution under fluctuating thermal environment, we will carry out an experiment with a plankton crustacean, Daphnia magna. We will subject clonal populations of D. magna to a regime where temperatures will fluctuate in irregular 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: Fluctuating thermal environment Daphnia magna

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Adaptation of *Daphnia magna* to the elevated temperatures

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Global warming has been widely considered to pose an unprecedented challenge for survival of many organisms. This is because temperature significantly affects various life history traits of organisms important for survival, such as development time and body size. Moreover, our knowledge about the genomic basis of responses to variable temperature regimes is limited. So, we are in need of experimental studies to understand how will the life history traits respond to global warming and to uncover the genomic basis underlying these changes. To investigate the impacts of increasing temperature on organisms over extended periods, we designed an experiment with the plankton crustacean, Daphnia magna. Clonal populations of D. magna will be subjected to increasing temperatures in regular intervals. Experimental populations will be monitored in a series of common garden experiments to elucidate changes in the life history traits. These traits include somatic growth rate, development time, and adult body size.

Simultaneously, genomic DNA samples will be taken at regular intervals to uncover the genomic basis of observed changes. Whole-genome sequencing will be conducted to identify genes related to life history changes, their roles in thermal adaptation, and their interactions with each other. This project will help us understand how global warming affects the life histories of organisms and, consequently, how organisms adapt to changing environmental conditions. It will enable us to understand the genomic responses of organisms to temperature changes and better grasp long-term evolutionary processes.

Keywords: *Daphnia magna*; Life history traits; Deteriorating temperatures

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Body mass and fat score relations in Willow warblers during the migration at the Eymir Ringing Station in Ankara

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Length of stay during migration varies depending on the availability of food in bird stopover locations. The willow warbler is a long-distance migrant species and is a passage migrant in Turkiye. The weight and fat score changes of Phylloscopus trochilus (Willow warblers) ringed at Eymir in 2022–2023 were examined in this study. In both spring and autumn, weight and fat change increased in parallel. In the spring, the lowest weight was 6.9 g and the highest 12.6 g, and similarly, the lowest weight was 6.9 g and the highest 12.7 g in the autumn. On the other hand, it was discovered that some birds had higher fat scores in the autumn. There is a strong positive correlation between fat score and weight in the autumn. Long-distance migrants need energy to travel long distances. For this reason, they can store large amounts of fat in a very short time during migration with their excessive and fast-feeding characteristics. Birds store large amounts of fat for a single long-distance migration. The duration of this fat storage also affects the duration of the stopover and thus the migration phenology. Fat score and weight gain may vary depending on their feeding characteristics during their stay in Eymir. Lake Eymir is a basin with rich biodiversity in the steppe ecology of Ankara. Ringing studies in Lake Eymir show that this basin is an important stopover and feeding point for migratory birds.

Keywords: Willow Warbler, *Phylloscopus trochilus*, Stopover, Migration, Lake Eymir, Eymir Ringing Station

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Genetic links between Anatolia and the Italian Peninsula during the Roman Imperial period

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Archaeological and historical accounts consistently indicate increased mobility from the Near East into the Italian peninsula during the Roman Imperial period. Multiple ancient DNA studies on Roman-era groups from central Italy have corroborated these narratives, reporting high rates of mobility from the Near East towards the city of Rome and its surrounding. However, the genetic sources of this Near Eastern ancestry, and its degree of spread into the rest of the Italian peninsula are still largely unknown. To address these questions, we generated genome-wide data of 33 individuals from northern Italy and 24 individuals from Anatolia associated with the Roman period. A Principal Component Analysis reveals that the individuals from northern Italy form a cline of genetic ancestry stretching from preceding Iron Age populations to the newly sequenced Anatolian individuals. When the northern Italian group is modeled as a two-way mixture between local Iron Age and coeval Anatolian populations, the results mirror patterns previously observed for central Italy. However, the proportion of Near Eastern ancestry varies considerably. Most northern Italian individuals derive three-quarters of their ancestry from the preceding Iron Age population and one-quarter from Anatolia as the Near Eastern source, which amounts to ~50% of what measured for central Italy. Overall, our findings indicate that Roman-period groups from Anatolia serve as good proxies for the Near Eastern ancestry in Italy and show that contemporaneous northern Italian groups followed a similar but not identical demographic pattern to the one observed for central Italy.

Keywords: Ancient DNA, Population genetics, human demographics, Roman archaeology, palaeogenetics.

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Bibliometric Analysis of Climate Change Effects on Plant Ecology and Conservation

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The adverse impacts of climate change on plant ecology are accelerating and call for the need of increased conservation, which as a prominent mitigation measure influences sustainability. However, the statistical evaluation of the scientific literature regarding the interplay among climatic change, plant ecology, and conservation remains limited. Herein, we evaluated relevant bibliographic data to explore the temporal progress, research collaboration, and trend topics from 1998 until 2023 year using the Bibliometrix package in R software. The publication trend showed fluctuations over the years with sharp increases at a frequency of about five years, in 2005, 2010, 2017, and 2022. The Journal of Ecology dominated publications in these areas, while most research originated from the USA, UK, and Australia. Despite the dominance of the Anglo-Saxon countries in research, the most productive institutions were the Chinese Academy of Sciences followed by the University of Bern. A keyword co-occurrence network analysis displayed three clusters: climate change, conservation ecology, and medicinal plant distribution. Besides climate change and conservation, other prevailing key research themes were: biodiversity, genetic diversity, fire ecology, biogeography, conservation ecology, and forest management. The network analysis demonstrated that most networks consisted of European countries, along with the US, China, Canada, and Australia. Institutional networks mostly reside within countries but have significant international collaborations as well. Our results facilitate future research by detecting trend topics and gaps, as well as supporting policymaking decisions.

Keywords: performance analysis, science mapping, network analysis

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Comparative molecular evolution of most dominant and virulent recombinant Sars-CoV-2 variant (XE), and its parent lineage viruses BD.1 and BA. 2.30

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Sars-CoV-2 is a globally circulating virus chronically infecting tens of millions of people every year. In addition to mutations, with the advance of the Omicron variant novel recombinant viruses are emerging. Similar to mutations' effect on the infection and disease dynamics, recombination has the potential to create dangerous viruses. However, the effect of recombination on the molecular evolution of the viruses is not known. We aimed to compare the molecular evolution of most dominant and virulent recombinant Sars-CoV-2 variant (XE), and its parent lineage viruses BD.1 and BA.2.30 using population genetics and phylogenetic methods. High coverage full genome sequences of XE, BD.1 and BA.2.30 viruses are downloaded from GISAID. The sequences were aligned using the Muscle algorithm in MAFFT (v7.520) . Annotation was performed using whole genome of the Wuhan type virus. Population genetic tests included nucleotide and haplotype diversity, diversification, selection and demographic change tests. Effect of amino acid changes on protein structure and functionality is investigated. BEAST is used for phylogenetics analyses. BD.1, BA.2.30, and XE formed distinct clades in the phylogenetic analyses indicating sufficient diversification of recombinant lineage from the parent lineages. Synonymous and non-synonymous nucleotide diversity, Tajimas D, Fu-Li D, and Fu-Li F test results for genome regions upstream of recombination point were rather similar between XE and BD.1, whereas for genome regions downstream of recombination point the parameter estimates were more similar between XE and BA.2.30. Results suggest that molecular evolution of recombinant lineages genomes' continue as a mixture of parent lineage's evolutionary trajectory.

Keywords: Sars-CoV-2, Recombinant subvariant, Molecular evolution, Selection, Statistical modeling

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Identification of Genetic Variants Determining the Effect of Maternal Age on Offspring Longevity in *Drosophila melanogaster* by Genome-Wide Association Analysis

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Parental age has a decisive effect on the life of the offspring, especially in organisms where sexual reproduction is observed. Maternal age has been studied for years in the context of the interaction between genetics and environment in the field of accumulated mutations. The presence of maternally transmitted hereditary material and non-hereditary factors affect the life span of offspring. Although there are studies showing that offspring from older mothers have shorter lifespans in general, studies in Drosophila melanogaster have shown that this varies within species and from line to line, but the genetic background has not been studied. In this study, we investigated the effect of maternal age on offspring fecundity by genome-wide association analysis(GWAS) with 90 lines from the D.melanogaster Genetic Panel(DGRP) to show the genetic background of the variation in offspring fecundity in relation to maternal age, based on the differences between individuals from offspring of mothers of two different age groups, young (5 days) and old (35 days). Since the studies conducted so far have always been limited to phenotypic differences, it is important to reveal the genetic variants that determine the effect of maternal age difference between inbred lineages in order to pave the way for further studies. In the results, 109 candidate variants associated with maternal age effect on offspring longevity were obtained from GWAS. Gene ontology analyses have shown us that non-genetic variants are as important as genetic variants have effect of maternal age on offspring longevity.

Keywords: Maternal age, offspring longevity, DGRP, GWAS

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Determination Of Genetic Elements Affecting Exercise Physiology Responses of srl Gene In Drosophila melanogaster via Genome Wide Association Study

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Nowadays, with the development of urbanization, industrialization and technology, people have started to have a sedentary lifestyle. Physical inactivity is a global problem and the fourth leading cause of global mortality. In addition to this sedentary lifestyle, hypokinetic diseases have become quite common due to the ease of access to high-calorie foods at any time. The human body develops certain responses and adaptations as a result of physical activity or exercise. These responses and adaptations provide protection against diseases and increase personal well-being. Based on these, in order to understand the genetic basis of exercise physiology and to discover the genetic elements underlying the diseases that occur in the case of physical inactivity, many studies have been conducted with both humans and the model organism Drosophila melanogaster. In order to expand this repertoire, Genome-Wide Association Analysis (GWAS) was performed to identify genes associated with the spargel (srl - human ortholog PGC-1α) gene, which is known to be associated with energy metabolism in both humans and Drosophila. The phenotypic scores used in the GWAS were obtained from Drosophila Genetic Reference Panel strains with known whole genome sequence, srl mutant strains and control strains. The phenotypic scores obtained are the response of Drosophila melanogaster to exercise; the effect of the change in negative geotaxis behavior on climbing ability performance. As a result of the GWAS's performed, 257 genes interacting with the srl gene in pathways that might have associated with exercise physiology were identified.

Keywords: Exercise physiology, Drosophila melanogaster, Genome Wide Association (GWA)

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Parasite-mediated selection targets immune genes based on their molecular function: insights from avian genomes

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Theory predicts that during host-symbiont co-evolution, arms races diversify immune genes. However, it remains unclear whether this applies equally to all immune genes and beyond well studied MHC or TLRs genes. Does positive selection differ based on gene molecular function or cellular localization? To answer these questions, we performed a large comparative analysis of positive selection in 50 avian genomes from TOGA annotation. First, we compiled the unique list of 453 immune genes based the overlap AmiGO (GO: immune system process) and Reactome (immune system) databases. We then manually classified all genes into five different immune catalogues based on their functions and cellular locations. Using three dN/dS-based methods (CODEML, FUBAR, MEME), we revealed positive selection in 363 protein-coding immune genes. While surprisingly no differences in intensity of selection exist between innate and adaptive immunity, core immune genes (i.e. whose function is only in immunity) were subject to stronger selection than peripheral immunome genes, which have also multiple non-immune functions. Effector molecules were also more strongly selected than genes with signalling, enzymatic or recognition functions. Membrane-bound and extracellularly secreted immune genes underwent stronger positive selection than those expressed in the cytosol or nucleus. Our new categorisation of immune genes based on function and cellular location proved to be more powerful than traditional gene enrichment analysis (using GO terms or Reactome pathways) in identifying major trends in immune gene evolution. These results suggest that immune genes whose products physically interact with pathogen structures may be subject to stronger positive selection.

Keywords: evolutionary genomics, evolution, positive selections, immune genes, host-parasite

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The "neighbour repulsion" phenomenon in f-statistics

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Patterson's f3- or f4-statistics use genome-wide allelic correlations between populations to study shared drift and admixture. They have evolved into the workhorses of demographic inference over the last decade but can exhibit unexpected behaviour in certain instances. Several human paleogenomic studies have noted one such pattern: using f3- or f4-statistics, pairs of closely related populations sometimes appear genetically closer to a more "distant" population. We first present another case of this phenomenon using published genomes from Bronze Age Greece and East Anatolia, where East Anatolian genomes systematically show higher f3 values with those from Greece than with other East Anatolians. An explanation for this pattern may be low-level admixture from a genetically divergent source into the neighbours showing "repulsion". We support this a) by using population genetic simulations that reproduce the observed pattern and b) by describing the expected conditions for this behaviour using a mathematical model. Our results underscore how complex demographic histories that include low-level admixture from relatively divergent sources can result in unexpected behaviour in point estimates of allelic correlations.

Keywords: demographic history, Patterson's f-statistics, simulation, admixture

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Anterior Determination in Ants Housing Intracellular Endosymbionts

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Anterior determination is a process that defines the anterior of the animal during embryonic development. In insects, specific genes called anterior determinant genes are known to initiate formation of the anterior during oogenesis and early embryogenesis. Well-known examples of this are: Bicoid in Drosophila, TCF/Pangolin in Anopheles, Panish in Chironomus, Cucoid in Aedes and Culex, Zic/opa in Clogmia, Otd in Nasonia and Tribolium. However, anterior determinants have not been explored in insects, which host intracellular endosymbionts. Here we investigate anterior determination in the carpenter ant, Camponotus floridanus, in which embryogenesis has been shown to be influenced by the presence of endosymbionts. Homologs of the anterior determinant genes from C. floridanus were identified by sequence comparison with known genes from other species. We use transcriptomics, RNAi, qPCR, and in situ hybridization to analyze the candidate genes using criteria that fit the known characteristics of an anterior determinant. The discovery of anterior determinant in these ants will help us understand how anterior determination occurs in the presence of intracellular endosymbionts.

Keywords: Anterior Determination, Endosymbiont, Developmental Biology

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Demographic Analysis and Population Genetics of the Hittite Capital Hattusa (Bogazkoy/Bogazkale)

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Hattuşa (Boğazköy/Boğazkale), with its ruins located near modern-day Çorum, Turkey, is best known for having served as the Hittite capital during the Bronze Ages. Tangible evidence of occupation in the area dates back to the Chalcolithic period (~5000 BC). During the Bronze Age, Boğazkale is thought to have first been inhabited by the local Anatolian Hatti people, later hosted an Assyrian Merchant's Colony, and eventually became the Hittite state's capital in the Middle and Late Bronze Ages. Although the city was destroyed in 1200 BCE, the area experienced human occupation during the Hellenistic, Roman, Medieval and Early Modern periods. Consequently, Boğazköy has been a settlement area for human populations of various cultures for nearly seven millennia. Here we present analyses of 4 published and 17 unpublished shotgun-sequenced paleogenomes from Boğazköy, spanning the Early Bronze Age to the Ottoman period. Our initial results suggest apparent genetic similarity within the Boğazköy sample through the seven millennia, including the time of Turkic migrations. However, we also find a possible genetic outlier from the Roman era with possibly higher Eastern ancestry. We interpret the results in light of demographic change patterns and interregional connections in Anatolia.

Keywords: ancientDNA, population genetics, demography

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fPEDigreeSim: A python tool for calculating expected inbreeding under different demographic and reproductive scenarios

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Inbreeding dynamics in populations reflect population size as well as cultural norms and are vital for understanding past societies. However, while calculating the inbreeding coefficient based on runs of homozygosity (fROH) in a genome is relatively straightforward, it is difficult to calculate expected fROH under different demographic and reproductive scenarios, even without consanguineous marriage. To address this issue, we developed a Python script tailored to simulate large-scale (e.g. including thousands of individuals) pedigrees based on user-defined parameters and calculate the pedigree-based inbreeding coefficient (fPED) for the last generation. Key parameters include female and male effective population sizes, mean offspring per individual, mean offspring per couple, and the number of generations. We used fPEDigreeSim to study fROH values estimated in genomic data produced from various ancient settlements, asking whether empirically estimated fROH distributions would be compatible with random mating in the population (without inbreeding avoidance or consanguinity practices), using archaeologically-informed population size estimates. Our results help understand reproductive behaviour in past societies.

Keywords: inbreeding coefficent, fPED, fROH

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Predicting Relatedness Degree From Ancient Samples Using Deep Neural Networks

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Estimating genetic relatedness among individuals using genomic data from ancient samples is crucial for understanding historical populations. However, existing tools can be limited in their accuracy in predicting familial relationships. This study addresses this gap by developing a Convolutional Neural Network (CNN) model capable of predicting parent-offspring and sibling pairs, alongside second- and third-degree relationships and unrelated and identical pairs, using low-coverage ancient genomes. We started by simulating ancestral founders via "msprime" and "PedSim" tools to generate pairs spanning up to third-degree relatedness under realistic demographic scenarios. Utilizing the mismatch rate, the coefficient of relatedness (r) was estimated across genomic windows comprising 200 SNPs, reflecting the likelihood of shared alleles due to common ancestry. These r values were then subjected to two-dimensional binning, producing fixed-length vectors for each pair, which served as input for training the CNN model. The trained model's performance was evaluated by testing it across various shared SNPs between different relationship categories. The model achieved high macro-average F1 scores of 1, 0.98, 0.89, 0.86, and 0.62 for pairs sharing 50,000, 20,000, 10,000, 5,000, and 1,000 SNPs, respectively. This study showcases the potential of deep artificial neural network models in precisely discerning diverse relatedness categories within low-coverage ancient genomes. Its findings lay a robust groundwork for future research endeavours in this evolving field, promising deeper insights into the genetic dynamics of historical populations.

Keywords: deep learning, ancient dna, kinship

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Studying allele frequency trajectories in ancient Anatolia

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Evolutionary processes, including natural selection, genetic drift, and gene flow, shape the distribution of genetic variants within and among populations. Furthermore, genetic diversity, a hallmark of evolutionary processes, can result in population-specific predispositions to certain disorders. In this project, we aim to analyze the genomic data over a time span of 10,000 years in Anatolia, which is present-day Turkey and investigate the selection patterns of certain diseases by analyzing aDNA sample SNP frequencies. From the selected phenotypes, forward-time simulation scenarios will be created and compared by selection patterns of real data. 34 ancient and 16 modern human genome were analyzed from Anatolia. Allele frequency changes were determined for all genetic variants using a maximum likelihood-based approach for three different periods: Neolithic, Late Chalcolithic and present day. A total of 32 phenotypes and 3728 SNP were analyzed for disease related variants. Forward-time simulation scenarios were created for each phenotype and simulation frequencies were calculated. The results show that 13 SNP frequencies of 9 different phenotypes increased and 6 SNP frequencies of 5 different phenotypes decreased from Neolithic to present day Anatolia. Increased disease phenotypes are associated with age-related traits, anatolia-common, metabolic and physical traits. Decreased ones are associated with age-related traits and metabolic traits which are Age at Menarche, body mass index, osteoarthritis, parkinson's disease and Type-2 diabetes mellitus. Some frequencies increased from Neolithic to Late Chalcolithic and then decreased, or vice versa. This might be due to positive selection, negative selection or migration from the Caucasus hunter-gatherer population to Anatolia.

Keywords: Population genetics, ancient DNA, selection, genetic diseases

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Variation in Positive Selection in Avian Immune Genes

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Host-pathogen interactions are shaped by reciprocal selection that is acting between the two partners. Co-evolution between hosts and pathogens can be predicted to particularly diversify immune genes involved in pathogen detection and clearance. Our study aims to explore patterns of positive selection in 100 protein coding immune genes across 3 key avian clades (Galloanseres, Australaves and Elementaves) and identify footprints of evolutionary convergence across the orthologues. Using a comprehensive immune catalogue, we selected 100 candidate immune genes representing relevant groups of distinct protein features described by a combination of their molecular function and cellular localization. We analysed 100 avian genome sequences from publicly available databases by testing for site-specific positive selection using 3 different methods. Furthermore, convergent evolution was assessed by comparing the consistency of the protein physicochemical feature distances with the phylogenetic relatedness of the avian species. Our preliminary results indicate a high positive selection ratio in the genes that have primary function in the immune system and that are forming direct molecular bonds with pathogenic structures. Notably, we show how a positive selection ratio translates into patterns for molecular convergence. This study enhances our understanding of the evolutionary dynamics that influence immune system variability and selective pressure in response to pathogens in birds. Further analyses will focus on tracing convergence for more immune genes and functional validation of selected genes to elucidate the mechanistic basis of observed evolutionary patterns.

Keywords: immune genes, positive selection, convergent evolution, evolutionary genomics

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Evidence for selfing in a vertebrate from whole-genome sequencing

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A growing number of recent genomic studies report asexual parthenogenetic reproduction in a wide range of taxa, includ- ing vertebrate species from the reptile, bird, and fish lineages. Yet, self-fertilization (selfing) has been recorded only in a single vertebrate, the mangrove killifish Kryptolebias marmoratus. In cichlid fishes, sex determination is notably diverse and can be influenced by the environment, and sequential hermaphroditism has been reported for some species. Here, we present evidence for a case of facultative selfing in the cichlid fish Benitochromis nigrodorsalis, which is otherwise known as biparentally reproducing ovophilic mouthbrooder from Western Africa. Our laboratory observations revealed that a wild-caught individual produced repeatedly viable offspring in absence of a mating partner. By analyzing genome-wide single-nucleotide polymorphism (SNP) data, we compare that individual and two of its offspring to shed light on its reproductive mode. First, our results confirm uniparental reproduction. Second, overall heterozygosity is reduced in the offspring compared with outbred individuals. Retained maternal heterozygosity in the offspring is ∼51%, which is close to the theoretically expected value of a heterozygosity reduction of 50% by selfing. Heterozygosity patterns along individual chromosomes do not point to alternative parthenogenetic reproductive mechanisms like automixis by terminal or central fusion. Facultative selfing may represent an adaptive strategy ensuring reproduction when mating partners are absent and, hence, contribute to the cichlids' enormous evolutionary success.

Keywords: cichlid fish, selfing, whole genome sequencing, automixis

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Co-evolution of gut microbiota and immune cells during ageing in killifish

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Commensal microbes play key roles in multicellular host development, survival, and disease susceptibility. Throughout an organism's lifespan, the composition and metabolic function of microbial communities within the gut undergo substantial shifts, influencing critical phenotypic traits such as nutrient absorption, vitamin synthesis, and protection against pathogens. One of the major factors affecting gut microbiome composition is diet. Despite accumulating evidence of the dynamic evolution of the microbiome within the host, a comprehensive understanding of the ecological and evolutionary processes shaping microbial dynamics over the host's lifespan remains limited. In this study, we aim to investigate whether age-related alterations in host immune functionality, including changes in antibody diversity and inflammatory responses, contribute to and potentially predict the ecological and evolutionary trajectories of host-associated microbial communities, as well as overall host health in later life stages. Additionally, in our pilot experiment, we first aim to examine the effect of diet on the bacterial composition of the fish gut and assess whether stool can be used as a proxy for the gut microbiome.Leveraging the naturally short lifespan of the African turquoise killifish (Nothobranchius furzeri) as a model organism, which possesses a diverse gut microbiota and both adaptive and innate immune systems, we will examine the association between age-dependent variations in immune function and shifts in microbiota composition using large-scale shotgun metagenomics and immune profiling data. In the pilot experiment, we sought to determine optimal experimental conditions for longitudinal microbiome collection in killifish by feeding them four different types of food and collecting stool samples weekly for amplicon sequencing. The pilot experiment revealed a significant effect of diet on the gut microbiome and demonstrated how different diets can alter the similarity between the gut microbiome and the stool microbiome. We selected pellet food for the downstream experiment to investigate microbiome evolution and assessed its impact on fish health using a lifespan cohort. Our preliminary findings highlight the critical role of experimental design in studies of microbiome evolution. Our evolution experiment will deepen our understanding of the ecological and evolutionary dynamics of the gut microbiome during the ageing process.

Keywords: gut microbiome, immune aging, microbiome evolution, host-microbiota interactions

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The evolving regulation of bithorax complex in ants

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Hox genes encode highly conserved transcription factors that define the identity of the segments during embryogenesis in all bilaterian animals including insects. Hox genes of the bithorax complex (BX-C) have been known to regulate hundreds of downstream genes involved in multiple pattern formation processes. In ants, the function of the BX-C has not been completely explored yet. Recent data has shown that BX-C genes are rewired in the Carpenter ant lineage such that they acquired maternal expression influencing posterior, and germline formation. This means that in addition to the homeotic function, this genomic region underwent radical evolution of regulatory elements in a departure from its canonical function. In this project, we explore the expression and regulation of BX-C genes, Ultrabithorax, abdominal-A and Abdominal-B in ants. We selectively target the zygotic genome using CRISPR/Cas9-mediated knockout to test the stage-specific functions of these genes in ants. This study provides a way to understand how BX-C is regulated in ants.

Keywords: Hox genes, Bithorax complex, Carpenter ant

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Analysis of BMP Signaling in Early Development of an Ant that Houses Cellular Endosymbionts

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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 the embryo proper and extraembryonic membranes within the egg correlates with the presence of endosymbionts. This raises the possibility that the endosymbiont interacts with the axis patterning mechanisms in these ants. In order to understand, these processes were characterized in carpenter ant Camponotus floridanus. Bone Morphogenetic Protein (BMP) signaling, which primarily controls DV patterning in animals, was characterized. In situ hybridization and RNA interference were used to examine the expression and function of developmental genes that are particularly involved in DV axis formation. The results indicate that the expression of BMP genes are restricted in the germdisc to form DV axis of the future embryo but not expressed in the extraembryonic membranes like other known insects. The RNAi also confirm that BMP has conserved role in case of DV patterning of the embryo but its role on extraembryonic membrane formation is not clear. Future studies will help us to understand role of BMP signalling in ants and its alteration in the presence of endoysmbionts.

Keywords: ants, BMP, signalling

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Comparative analyses of gut microbiota composition in migrating European blackcap (Sylvia atricapilla) population on the seasonal visits to Eymir Ringing Station in spring and autumn

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This study comparatively investigated the microbiota diversity of Blackcap (Sylvia atricapilla) visiting Eymir Ringing Station, a strategic stopover hotspot on the migratory routes, in the spring and autumn seasons. In order to determine the effects of seasonal changes in diet, habitat and social interactions on microbiota, metagenomic sequencing methods were applied onsamples collected from 18 randomly selected individuals in both seasons. Sequences were analysed to reveal the microbiota composition of each individual and potential functional changes. The data obtained showed that seasonal migration can have significant effects on the gut microbiota of birds and that these changes may be directly related to the health status of the birds. The results provide insights for large-scale ecological and evolutionary studies to better understand the relationships between bird migratory behaviour and microbiota dynamics.

Keywords: avian microbiome, gut microbiota, sylvia atricapilla, 16s rRNA, sequence analysis, population comparation

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Predicting metabolic functioning in extreme microbial communities

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Extreme habitats like deserts impose the most challenging conditions for life, such as, extreme UV radiation, desiccation and thermal stress. Under these conditions, microorganisms are the sole life forms that seek refuge by colonizing the interiors of the rocks (endoliths), forming simple communities composed of Cyanobacteria as the primary producers along with an assortment of heterotrophic taxa. Understanding how these communities adapt and function on the edge of water limitation is crucial for predicting the fate of the ecosystem under increasing desertification and for investigating how life might exist elsewhere. Yet, despite a number of sequencing surveys that have uncovered considerable diversity, we understand very little about the functioning of these communities since it is difficult to link genomic content with metabolic outputs. To address this knowledge gap here our goal was to elucidate energetic pathways potentially used by the endolithic communities in the Atacama Desert, one of the oldest and driest deserts in the world. We used metagenomic data obtained from the different endolithic communities in two locations (KM and MTQ) exposed to different climate conditions. First we described metabolic potential by extracting marker genes involved in main energetic pathways. Then we used a gene-centric biogeochemical model to simulate energy metabolisms under specific environmental conditions. Our study suggests that biogeochemical models, especially when they incorporate microbial diversity, genome-informed metabolism, and gene abundance data can enhance our understanding of the metabolic capacity of extreme microbial communities. Moreover, comparison of simulations with gene abundance data reveals the complex dynamics between metabolisms.

Keywords: biogeochemical modeling, metagenomics, extreme communities

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First Identification of Cathaemasia hians in Black Storks: Unveiling a Novel Trematode Species Through DNA Barcoding

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In this study, we report the first identification of Cathaemasia hians, a trematode from the order Echinostomida, in black storks (Ciconia nigra) in Turkey. Traditional morphological identification methods often fall short due to the cryptic nature of many parasitic species. Overcoming these challenges, DNA barcoding was employed to confirm the presence of this parasite, extracted from the throat of black storks. PCR amplification targeted three gene regions (28S, ITS, and ND1) using four different primer pairs, enhancing the robustness of our genetic identification. The amplified DNA underwent Sanger sequencing, yielding a definitive 100% match for sequences targeting the 28S region with two different primers. In contrast, the ND1 gene region presented an 80% match, underscoring the potential for slight genetic variations among regional populations of C. hians. This multi-gene approach not only enhances the accuracy of species identification but also addresses the limitations posed by sparse reference databases. The discovery of Cathaemasia hians in black storks contributes significantly to the taxonomic categorization of parasites in Turkey and enriches our understanding of host-parasite interactions in this geographic area. The successful application of DNA barcoding highlights its critical role in parasitological research, particularly in ecosystems with diverse and poorly documented parasite fauna. Future studies should focus on the broader distribution, ecological relationships, and potential impact of C. hians on avian hosts to inform comprehensive wildlife management and conservation strategies.

Keywords: trematode, parasite, DNA barcoding, Cathaemasia hians

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Finding Cindirella: A DNA Barcoding Study of Snake Shed Skins

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Snakes generally have a criptic life, and their lifetime still has so many mysteries. Thus, snakes are among the most difficult species to encounter in the field, especially during biodiversity studies. Thanks to DNA barcoding studies that have become widespread in recent years, it is possible to obtain taxonomical identification by using the remains (feather, shed-skin, egg shell etc.) of hard-to-detect creatures such as snakes. The aim of this study was to obtain COI data of Natrix natrix, from two shed skins; 1-collected from a field under direct sunlight; 2- directly collected from the specimen under captivity. A shed skin was found in the field, then stored in a resealable bag, and according to the pholidotic characteristics and marks on the shed skin, it is identified as N. natrix. The other shed skin was collected from a specimen under captivity, and preserved in ethyl alcohol. The DNA extracted with the EURx Tissue & Bacteria Kit underwent PCR amplification using dgHCO-dgLCO primers. Sanger sequences were performed and fragments that were trimmed and quality checked. Nucleotide sequences were aligned and checked for read errors, insertions, and deletions. All analyses were performed using MEGA 11 to measure the proportion of correctly identified queries. As a result of the study, both of the shed skins samples that were amplified successfully were barcoded. In the light of the data obtained as a result, both samples were uploaded to the GenBank database as N. natrix. With this study, it is clearly seen that obtaining COI data from shed skins as a non-invasive method proceeds in parallel with the data under captivity. In this way, we think that DNA barcoding from shed-skin can be used as indirect observation data during the fauna inventory studies. In addition, since we have no idea how fresh or old the skin remains found in field studies are, we believe that it would be useful to increase these studies on how long the structure of the DNA in the skin remains can deteriorate and how it will affect the data obtained.

Keywords: DNA barcoding, Natrix natrix, shed skin, ecdysis

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Revealing the importance of Lake Eymir for the Eurasian Blackbirds (Turdus merula) (Linnaeus, 1758) (Aves: Passeriformes) with ringing studies

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Due to its location and suitable climate conditions, Lake Eymir is used as a feeding and stop-over site for a large number of migratory and resident birds. The Eurasian Blackbird (Turdus merula) is one of the resident species in the Eymir. In this research, we undertook a study to quantify the importance of Lake Eymir for T. merula. Ringing studies were carried out between 2018 and 2023 located at the eastern end of Lake Eymir. T. merula caught with mist-nets, ringed and measured according to SE European Bird Migration Network standards. Between 2018 and 2023, 283 T. merula were ringed, 44 in spring, and 239 in autumn. During the 6-year period, the number of blackbirds ringed and captured in the same season was 27 in spring and 55 in autumn, while the number of birds recaptured in different seasons was 13 in spring and 18 in autumn. A blackbird ringed in 2011 was recaptured exactly 10 years later by Eymir Ringing Station. It has been determined that blackbirds breed in the area between March and June. While approximately 61% of those caught in the spring are immature, this figure rises to 80% in the autumn. This suggests that immature blackbirds have used the area in the autumn and then have dispersed. Understanding such adjustments that the area has suitable habitat and is rich in food resources for blackbirds has important implications for the conservation and management of wildlife in urban ecosystems.

Keywords: Eurasian Blackbird, Turdus merula, Lake Eymir, Eymir Ringing Station

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Casting Light on Fluorescence in Hemidactylus turcicus

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This study focuses on a juvenile Turkish Gecko, Hemidactylus turcicus, a nocturnal species native to the Mediterranean region and the Southern United States. For the first time, we employed advanced microscopy techniques to investigate both iridophore-based and bone- based autofluorescence in this gecko. Utilizing an advanced upright epifluorescence microscope that can be used for imaging large specimens AxioZoom V16 stereo fluorescent microscope (Carl Zeiss, Germany), we conducted our investigations with precise control over the excitation wavelengths. For capturing green- hued images, we employed an excitation wavelength of 488nm and utilized a 520/40 BP filter for emission. Conversely, when examining red-hued images, an excitation wavelength of 561nm was utilized, accompanied by a 610/50 BP filter for emission. Obtained The results unveil the presence of iridophore-based autofluorescent regions on the skin, while simultaneously revealing bone-based autofluorescence within the gecko's transparent dermal structure, thus contributing significantly to the understanding of the enigmatic autofluorescent properties of Hemidactylus turcicus and their potential ecological and physiological significance. Our study unveils the presence of iridophore-based autofluorescence regions on the skin, while simultaneously revealing bone-based autofluorescence within the gecko's transparent dermal structure when subjected to light with varying wavelengths. These findings mark a significant contribution to the understanding of the fascinating autofluorescent properties of Hemidactylus turcicus, shedding light on their potential ecological and physiological significance.

Keywords: Fluorescence, Hemidactylus turcicus, microscopy, advanced microscopy, iridophore

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Investigating the origin of Pamir-Alai shilajit through metabarcoding analysis and biochemical profiling

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Shilajit is a traditional medicine that has been used for over 4000 years. It is derived from sedimentary rock layers in mountainous regions worldwide. Although it has been traditionally used for its potential health benefits due to antioxidant activity, the origin of shilajit is still debated. The aim of this study is to determine the plant origins of shilajit samples obtained from the Pamir-Altai mountain range through metabarcoding analysis and biochemical profiling.The analysis of shilajit samples using metabarcoding detected a diverse range of plant taxa, spanning various taxonomic levels from order to species, that contribute to its composition. Additionally, the identification of bioactive compounds in the identified plant species highlights their potential role in shilajit formation. Comparative analysis with regional flora reveals both similarities and disparities, suggesting historical biogeography and climatic influences. The plant species present in shilajit samples were accurately characterised by using a multidisciplinary approach that includes DNA metabarcoding and biochemical profiling. This sheds light on the biological origins and therapeutic potential of shilajit. The metabarcoding data obtained provides crucial information on the plant composition of shilajit and offers insights into the past and present vegetation of the Pamir-Alai mountain range. This analysis examines shilajit from botanical, genetic, and biochemical perspectives, enhancing our understanding of its implications for human health and ecological studies.

Keywords: Antioxidant, metabarcoding, Pamir-Altai, plant origin, shilajit

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Assessment of Some Triticale (xTriticosecale Wittmack) Cultivars Based on Morpho-Physiological and Biochemical Analysis Under Drought Stress

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Drought stress is one of the most important stress factor that results physiological, biochemical and metabolic damage in the plant phenotype. In this study, 13 different drought (24% PEG-6000) stress applied triticale cultivars mostly grown in Turkiye and Italy by the farmers evaluated by physiological and biochemical parameters and comparatively associated with its parents, wheat (♀) and rye (♂). Following seven days of germination and twenty-one days of seedling development, germination and coleoptile percentage, coleoptile and radicle length (cm), number of radicles, flag leaf diameter (mm), plant height (cm), fresh weight (g), number of leaves, flag leaf area, stem diameter (cm) and proline, lipid peroxidase (MDA), superoxide dismutase (SOD), catalase (CAT) and ascorbate peroxidase (APX) levels were compared. In comparison with the group that was not applied stress, it was found that drought stress had a negative impact on physiological parameters. Based on the germination/coleoptile percentage after 7 days, the genotypes that are mostly resistant to drought stress are Alperbey (70/77), Mikham (66/79), and Karma (69/67), while Trica (50/56) showed the the most sensitive phenotype. In contrast to the control group and parents, Mikham2001 and Tacettinbey were found to possess sensitive genotypes, whereas Trica, Alperbey, and Presto were found to show resistant genotypes depending on the physiological results of the 21-days pot experiments. Once the plant is exposed to the abiotic stress, its levels of enzymes called antioxidants increase. All cultivars under drought stress showed increased amounts of proline, MDA, SOD, CAT, and APX activity in addition to total protein content. In conclusion, Tacettinbey was shown to be the most sensitive genotype after all criteria were assessed. Alperbey, Trica, and Presto is showed the most successful genotypes to overcome the detrimental effects of drought stress.

Keywords: Abiotic stress, antioxidant activity, Climate change, Sustainable agriculture

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Studying the distribution, habitat suitability, and potential impacts of environmental changes on Pipistrellus pipistrellus

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Nearly all organisms, including bats, are impacted by the rapid changes in the global climate. Acknowledging species distribution patterns can help improve the scientific understanding of species and guide management decisions. Habitat Suitability Models (HSMs) are useful tools for modeling species distributions and the impacts of natural and human-caused environmental changes, including climate change. This study analyzed the geographic and potential distribution of the common pipistrelle, Pipistrellus pipistrellus. We used Worldclim databases, topographic variables, night light development index, and land cover maps, covering the entire area of this species' occurrence. We registered 47 692 records from around the world. The developed HSM for the common pipistrelle to predict the influences of climate and landcover changes was combined with the map of the future distribution of wind farms. An ecological approach that allows us to reproduce bat recolonization accurately was produced. Decreasing bat numbers with increasing wind turbine numbers is expected. With the increased number of turbines, spatial overlap between areas where the wind farms will be and areas of suitable habitat is expected.

Keywords: Bats, Species distribution, Wind farms, Habitat, climate, environmental changes

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Exploring Pelagic Biodiversity in the Black Sea through eDNA Metabarcoding

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Environmental DNA (eDNA) metabarcoding is a revolutionary technique for assessing biodiversity, particularly in complex marine ecosystems like the Black Sea. This study employs eDNA to monitor spatial and temporal variations in biodiversity, using physicochemical parameters to understand the ecosystem's health and stressors. The methodology involves collecting water samples during expedition cruises in December 2022 and June 2023 from 16 stations at various depths, representing the surface, suboxic, and anoxic conditions of the Black Sea. The water samples were then filtered through specific filters, and DNA extractions were performed via the Phenol-Chloroform method. In total, 104 filters underwent DNA extraction, all of which were found to be of high quality and sufficient quantity for library preparation. Following library preparation, samples continue to Next-Generation Sequencing (NGS) with markers like 16S, 18S, and 12S to identify prokaryotic, eukaryotic, and fish biodiversity, respectively. A total of 146 libraries from these three markers were selected for sequencing. Several bioinformatic tools and pipelines facilitate the metabarcoding analysis. The results of 16S metabarcoding show that the bacterial biodiversity of summer season is higher than the winter as expected due to increasing temperatures and river discharge. On the other hand, fish biodiversity results showed the reverse trend. However, relative abundances were higher in the summer than winter. These results are also compatible with the literature since some fish species have the migration behaviorto colder waters of the Black Sea. Furthermore, the anoxic part of the Black Sea has the lowest biodiversity in both cases while the surface part has the highest as expected. Finally, the eukaryotic diversity analyses are still under progress. The total results of the study will enable us to discern the Black Sea's ecological stressors and contribute to conservation strategies providing a cost-effective and non-invasive approach.

Keywords: eDNA, Metabarcoding, Black Sea, Marine Biodiversity, 16S, 18S, 12S

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Exploring Population Dynamics and Interregional Interactions in Early Bronze Age Anatolia: Insights from İkiztepe

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The Bronze Age in Anatolia (3300-1200 cal BCE) ushered in significant socio-economic changes, characterized by the establishment of extensive long-distance networks and innovations in agriculture and weaving. Despite considerable attention given to the population dynamics of Anatolia's Neolithic period, research focusing on later epochs, such as the Bronze Age, remains limited, leaving numerous site-specific questions unanswered. To study the fine-scale human population dynamics during this period, we focus on a diverse human population in North Anatolia, consisting of both local individuals and long-distance migrants, with no discernible differences in diet or burial customs. We produce genome-wide data (0.1 X - 1 X coverage) from 23 individuals excavated from İkiztepe, a Late Chalcolithic/Early Bronze Age cemetery, and co-analyze genomic data with strontium isotopes to understand the origins and genetic interactions of both local individuals and migrants in the site i,e. within-population genetic distance and individual mobility patterns, which in turn will enlighten the fine-scale population dynamics in the region as well as the extent and integrity of interregional interaction between İkiztepe and its neighbors, including the Balkan, Caucasus, Iran, and Levant. Preliminary results indicate that the genetic profiles of İkiztepe individuals exhibit similarity regardless of their mobility status, aligning with anthropological data. This finding underscores the complex population dynamics and interactions shaping Anatolia during the Bronze Age.

Keywords: bronze age, ancient dna, strontium isotope, mobility

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Archaeogenomes suggest longstanding interaction between Anatolia and southern Caucasus

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Archaeological evidence indicates that the Neolithization process in the Caucasus region commenced approximately 3-4 thousand years after its initiation in the Fertile Crescent. Analysis of material culture suggests that the origins of Neolithization in the Caucasus lie in Anatolia or Mesopotamia, rather than arising from local Mesolithic hunter-gatherer communities transitioning to agriculture. Moreover, archaeological findings suggest bi-directional population interactions between Anatolia and the southern Caucasus from the Neolithic period onwards. Although limited archaeogenomic studies support these archaeological hypotheses, the precise population dynamics within the Caucasus and its neighboring regions remain to be understood. Here, we analysed 18 newly sequenced genomes from the Neolithic (N=9) and Bronze Age (N=9) periods in Azerbaijan and two Bronze Age genomes from the Alaybeyi settlement in Anatolia (N=2), along with previously published data. Our results confirm earlier findings indicating the genetic affinity of Neolithic populations in the southern Caucasus with Neolithic populations in Southwest Asia, rather than with Caucasus Mesolithic hunter-gatherers. This suggests a replacement of the population during the Neolithization process in the Caucasus. Furthermore, our findings confirm genetic discontinuity between Neolithic and Bronze Age populations in the Caucasus, reflecting changes in population structure due to significant human mobility. Our analyses reveal the clustering of Caucasus Neolithic genomes with Anatolian Bronze Age genomes, refining the direct source of increasing Caucasian ancestry observed in Anatolia after the Chalcolithic period as originating from the southern Caucasus rather than Upper Mesopotamia. Finally, the genetic affinity between Anatolian and Caucasus Bronze Age genomes suggests that interaction between Anatolia and Caucasus continued after the Neolithic.

Keywords: Archaeogenomics, Anatolia, Caucasus, Neolithic, Bronze Age, ancient DNA,

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Rethinking lightning-induced fires: Spatial variability and implications for management policies

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Lightning is the primary natural ignition source for wildfires. Due to the dominance of human activities in igniting wildfires in densely populated regions, there is a common misconception in many countries that fires are solely anthropogenic rather than natural phenomena. Although this may be statistically accurate at the national level for many countries, neglecting the spatial variability of wildfires can lead to ecologically unsound conclusions and forest management policies. Here, we investigated the spatial distribution of lightning-induced fires across Türkiye using national wildfire database. We found significant regional variation in the occurrence of lightning-induced fires across the country. We also observed that lightning-induced fires clustered in areas with frequent lightning strikes, except in Thrace and parts of Northeastern Anatolia. In some years, lightning-induced fires represent over 45% in regional and 75% in local forest management units. Human-caused wildfires dominated the most populated areas, while in some less populated regions including forested areas, lightning was a major source of ignition. Despite increasing human activity, lightning still significantly contributes to wildfires in various parts of the country. Our findings challenge the notion that human activities are the sole ignition source for wildfires by highlighting significant spatial variability in wildfire causes across Türkiye and highlighting the substantial role of lightning. These findings also challenge the century-old, uniform wildfire suppression policy that is inefficient for regions prone to fires. We recommend revising this policy in Türkiye and similar countries, advocating for suppression practices that account for natural wildfire occurrences.

Keywords: wildfire, lightning-induced fires, lightning, anthropogenic fires, Türkiye, fire suppression, forest fire management

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Phylogeography of the Savi's Pipistrelle (Vespertilionidae, Chiroptera) Complex Based on Whole Mitochondrial Genome Analysis

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Investigating the phylogeography of species provides insight into the historical processes that shape their present geographic distributions and also how they evolve and adapt to different environments over time. Savii's pipistrelle, Hypsugo savii, is a vespertilionid bat species with a broad distribution range across various ecoregions in Europe, Asia, and North Africa. Previous studies have identified deeply diverged mitochondrial lineages within H. savii, suggesting it might represent a cryptic species complex. However, these studies were based on relatively few genetic markers and the reconstructed phylogenies were discordant. This study aims to contribute to the understanding of H. savii complex by investigating its phylogeography by whole mitochondrial genomes. Complete mitochondrial genomes were de novo assembled for thirty samples, representing all of the previously identified lineages. Additionally, closely related species, H. stubbei and H. alaschanicus, from East Asia were also included. Mitochondrial genes are annotated on the assembled genomes. All thirty-seven mitochondrial genes which are typical to mammalian mitogenomes detected; two of these are ribosomal RNA, twenty-two of them are transfer RNA, and thirteen of them are protein-coding genes. Non-coding displacement-loop (D-loop) regions of mitogenomes were also identified. The differences between constructed mitochondrial genomes were quantified to show diversification between taxa. The diversification levels between the genetic lineages are presented. Phylogenetic trees were reconstructed to investigate the evolutionary history of the identified mitochondrial lineages. This study provides a comprehensive view of the phylogeography and evolutionary history of the H. savii complex and also contributes to our understanding of bat evolution.

Keywords: Bats, Mitogenome, Phylogenetics, Evolutionary history, Cryptic species

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Mutation load and evolution of ageing in humans

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Although ageing leads to a decline in fitness and increased mortality, it is nearly universal across species, posing an evolutionary paradox. Non-programmed theories of ageing propose the concept of a selection shadow, where natural selection weakens after sexual maturity, offering an explanation for this paradox. The mutation accumulation theory suggests that slightly deleterious germline variants, which exert their effects primarily in later life stages, accumulate in the genome due to reduced selection pressure within the selection shadow. Consequently, ageing is hypothesised to correlate with an elevated mutational burden. While previous research has explored associations between specific genetic loci and ageing, a comprehensive examination of total mutation load and its relationship with decreased selection pressure in human populations remains unexplored. This study aims to investigate the association between total mutation load, selection, and lifespan- and ageing-associated traits in humans. We use extensive genotype and phenotype data from the UK Biobank. We will employ established population genetics pipelines, measures for selection signatures, and methods to calculate the age of mutations within the population to better infer selection dynamics. Additionally, we will introduce an individual-based measure of mutational burden, which can be summarised for cohorts stratified by age-related diseases or comorbidities. Our preliminary analysis of genomic variants associated with 116 diseases in the UK Biobank provided support for the mutation accumulation theory of ageing. We observed higher allele frequencies for diseases associated with later onset compared to early-onset conditions. While our preliminary analysis supported the mutation accumulation theory, we lacked individual-level information through the analysis of genomes. Moreover, we used disease information rather than direct measures of lifespan or other age-related phenotypes. The next steps in our project will directly test evolutionary genomic theories of ageing and elucidate the genetic mechanisms underlying lifespan regulation in humans.

Keywords: evolution of ageing, mutation accumulation, age-related disease, mutation load

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A First Approach to Understanding the Role of Repeat Induced Point Mutation (RIP) Dynamics in Fungicide Resistance Evolution in the *Monilinia fructicola*

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Repeat-induced point mutation (RIP) is a fungi-specific defense mechanism shielding the genome, especially from the transposable elements (TEs) to maintain genome integrity. RIP permanently mutates genetic targets based on shared homology between repeats. Monilinia fructicola is a fungal pathogen that causes brown rot disease in many stone fruits worldwide. Through experimental evolution in our previous studies, we observed that an ancestral Monilinia fructicola isolate, which was sensitive to a DMI fungicide, gained a resistant phenotype, and -insertion of a specific TE was detected upstream of the CYP51 gene, which is associated with fungicide resistance response, in this evolved isolate. We aimed to evaluate the RIP capability of *M. fructicola* species and compare the prevalence of RIP between the ancestral and evolved genomes. The genomes were checked for RIP-related RID and DIM-2 genes and their presence was confirmed in both. Overall RIP profiles of the genomes were evaluated by using the RIPper tool and the total proportion constituting RIP mutations of ancestral and evolved strains were 2,41% and 2,48%, respectively. The higher percentage of RIP in the evolved genome may be associated with the change in TE due to selective pressure. Additionally, when sequences around CYP51 gene regions were specifically analyzed, no RIP effect was detected on the TE near the CYP51 gene in the evolved genome. This may be because RIP is not yet active, so future generations may provide more information. Overall, this study provides perspectives on RIP dynamics that may occur in a stressed organism in fungal species.

Keywords: RIP, genome defense, fungal evolution

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Assessing the Diet of Mountain Gazelle (Gazella gazella) Using DNA Metabarcoding

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The most crucial elements ensuring herbivores' ability to survive and reproduce are their feeding habits and diet. Conservation studies on endangered herbivorous species can greatly benefit from the knowledge of plant species they consume. We studied the diet of the mountain gazelle (Gazella gazella), an endangered species with two isolated populations, one in Hatay province, Türkiye. We used DNA metabarcoding to identify the plant species on which the mountain gazelles feed. We collected 188 fecal samples from the field in four seasons from the captive and free-ranging populations. Bioinformatic analyses of DNA metabarcoding data from fecal samples suggest that the mountain gazelle consumes several native plant species, and the diet composition exhibits seasonal variability. Obtained data could be used for the conservation and management of the mountain gazelle population in the region, and meanwhile may help to identify the carrying capacity of the study area for the population.

Keywords: dietary habits, mountain gazelle, herbivory, metabarcoding, fecal analysis

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The effect of the choice of reference genome in studying the origin of parthenogenetic rock lizards Darevskia armenica and Darevskia dahli

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The Caucasian rock lizards Darevskia, is a remarkably diverse genus, which includes several parthenogenetic species of hybrid origin. The utility of genome-wide ddRAD markers in this group allows to unravel the origin and the genetic structure of parthenogenetic populations in unprecedented details. As a first step in the analysis, the short-read sequences must be mapped to one of the reference genomes available: either maternal or paternal parent, or a distance outgroup Podarcis sp. We investigated the effect of the choice of the reference genome (i.e. ascertainment bias) on the perceived relationship among two parthenogens, D. armeniaca and D. dahli, as well as their parental species D. mixta and D. valentini. We used Stacks 2, RADpainter and IQ-tree to produce genetic co-ancestry matrices, PCA and phylogenies from SNP data, elucidating the proximity of parthenogenetic species to their assumed parental species. Our analysis underscores the impact of reference genome choice on the perceived strength of species relationships. As the availability of genomes grows, so does the risk of biased results, underscoring the criticality of selecting the most suitable reference genome in genomic investigations, especially in cases that focus on interspecific hybrids.

Keywords: Darevskia, ascertainment bias, parthenogenesis, backcrossing

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Investigating Deletions in Ancient Sheep Genomes

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Ancient genome analyses have predominantly focused on single nucleotide polymorphisms (SNPs). However, many copy number variants (CNVs) play a crucial role in both diseases and evolutionary adaptation. In this study, we will be investigating how dispersal and bottlenecks may have shaped temporal and geographic variation in deletion frequencies by analyzing >1kb deletions in ancient and modern-day sheep genomes. First, we will ascertain de novo deletions from 125 high-coverage (>10x) wild and domestic modern sheep genomes. Then, we will genotype these deletions across 9 (>0.5x) ancient sheep genomes sourced from various regions of Eurasia and dated between c.9000 BP to c.2000 BP, as well as modern-day mouflon genomes using CONGA, an algorithm designed to call deletions from low-coverage genomes. In addition to examining the frequency of these deletions in time and across regions, we will further investigate the functions of the genes affected by these deletions. We expect our results to expand our insight into sheep evolution, including the effects of bottlenecks and intense breeding on large deletions.

Keywords: Sheep, CNV, Deletion, Ancient DNA

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Genetic Sex Determination and Biological Kinship Relations of Köşkhöyük Infants

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Köşkhöyük is an archaeological site housing people since Neolithic times. We have analyzed 97 skeletal remains of infants obtained during the excavations between the years 1987-2009 and retrieved ancient DNA from 94. It is impossible to determine the sex of the sub-adults through anthropological analysis; however, genetic data is capable of determining the biological sex of skeletal remains. 70% of the data has sufficient genome coverage for sex determination. Preliminary results show that 83 pairs of individuals have biological kin relations of several degrees such as sibling, half-sibling, uncle, cousin. In 32% of these relations, it is possible to follow father lineage (via Y chromosome) and mother lineage (via mtDNA). Ancient DNA analysis of human remains from archaeological excavations can answer questions about sex determination, biological kinship relations or populations dynamics.

Keywords: aDNA, Köşkhöyük, genetic sex determination, biological kinship

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Development of in vitro Host Mimicry for Different Hosts of Two Prominent Pathogenic Fungal Species of Brown Rot Disease

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Host preference in fungal pathogens provides important data regarding evolutionary biology such as host-pathogen co-evolution and speciation, and is also important in terms of disease management strategies. The alternative in vitro methods to host use is an important need and have the potential to provide convenience, especially in experiments aimed at investigating host-pathogen relationships in plant pathosystems. Following our group's previous first successful in vitro peach host mimicry for *M. fructicola*, it was aimed to develop media that mimic different hosts for both *M. fructicola* and *M. laxa*, two important pathogenic species of brown rot disease. Four different hosts (peach, plum, cherry, and apple) were successfully mimicked in vitro for both species, and the success of the developed method was confirmed by the expression levels of cutinase, one of the effector genes. Data obtained from the experimental designs also provided data on the host preferences of these two pathogenic species. According to current data, while peach is the most preferred host at the species level, differences in intra- and interspecific preferences have been detected according to the virulence level. Thus, this research provided important data on both successful host mimicry options and host preferences for these fungal phytopathogens."This study was supported by TÜBİTAK under the Grant Number 123Z611"

Keywords: host preference, host-mimic, *Monilinia*

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The Rate and Spectrum of Spontaneous Mutations in Leishmania tarentolae

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Background: As the fundamental source of genetic variation, mutations have a central place in biology and thus, understanding the mutation rate is critical in determining rates of molecular evolution, estimating effective population sizes, understanding the impact of mutations on organismal fitness, and evaluating the power of drift, selection, and recombination in shaping genomes. Today, by applying high-throughput sequencing technology to mutation-accumulation experiments, it is possible to generate the most direct and unbiased estimate of the genome-wide spontaneous mutation rate and spectrum of an organism. Previously, genome-wide spontaneous mutation rates have been estimated for various prokaryotes and some eukaryotes. Aim: To understand how environmental and cellular factors cooperate and ultimately determine the genome-wide mutation rate and spectrum, it is necessary to expand previous experimental assays to different organisms. Therefore, we designed a study to determine a genome-wide view of the spontaneous mutations in a trypanosomatid parasite (Leishmania tarentolae). Materials and Methods: We accumulated mutations over ~3.000 in 80 initially identical, mutation accumulation lines of the Leishmania tarentolae and then performed whole-genome sequencing to determine the genome-wide mutation rates and spectrum. Results: Whole-genome sequencing of 31 mutation accumulation lines of L. tarentolae after an average of 3.100 cell divisions yielded a base substitution mutation rate estimate of 3.55×10^{-11} per site per generation, substantially lower than that observed for most eukaryotic and prokaryotic organisms. Conclusion: Like many other microbial eukaryotes, L. tarentolae has unusual life history and genome features. This work enables us to explore evolutionary forces and molecular mechanisms that may have shaped the mutation rate and spectrum of Leishmania tarentolae.

Keywords: Mutation rate, mutation spectrum, trypanosomatid, WGS

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Genome-wide Predictions of Transcription Factor Binding Sites in the Ancestral DMI-Sensitive and Experimentally Evolved DMI-Resistant Isolates of *Monilinia fructicola* Pathogen

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Transcription factors (TFs) are proteins that are crucial in regulating gene expression by binding to specific DNA sequences, thus influencing various biological processes and stress responses. As these proteins are essential in an organism's response to stress factors, it is important to enlighten the changes that occur in the inclusiveness of TFs in the organisms' genomes. Therefore, in this study we have investigated the evolutionary changes that occur in terms of TFs to the pathogenic fungus *Monilinia fructicola*, using the ancestral isolate and the evolved isolate which was obtained in our previous studies by subjecting the ancestral isolate to fungicide stress over ten generations of experimental evolution. The changes in the TF profiles were determined in silico through the genomic sequences of isolates. Notably, higher TF profiles were predicted in the evolved isolate than in the ancestral isolate. This decrease in evolved isolate is likely due to mutations or abnormalities in the DNA binding domains of target genes, potentially driven by selective pressures to optimize gene expression in response to fungicide exposure. Most of the TFs identified in the evolved isolate were also present in the ancestral isolate, suggesting retention of core transcriptional regulators. Additionally, the transcriptional machinery might be giving a survival advantage by reducing metabolic costs or enhancing resistance mechanisms. This study highlights the critical role of transcription factors in evolutionary biology and fungicide resistance.

Keywords: host preference, host-mimic, *Monilinia*

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Transcriptomic Analysis of Postmortem Anterior Cingulate Cortex Tissues in Psychiatric Patients

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Recently, the incidence of psychiatric disorders has increased in all ages and gender due to environmental stressors. These disorders have a complex genetic background that include alterations in both genomic and transcriptomic level, and diagnosis and treatment still lack sufficient knowledge due to the similarities between diseases. In this study, we selected three cases; schizophrenia, bipolar disorder and major depressive disorder to find significantly expressed genes that are mutual in both conditions. To identify these changes, we performed a small-scale transcriptomic analysis using data from the GSE80655 series available in the Gene Expression Omnibus database. This dataset contains RNA sequencing data from postmortem anterior cingulate cortex tissues from the healthy and disease conditions. Differential expression analysis using Deseq2 showed 17 notable proteins with increased gene expression common in schizophrenia and bipolar disorder patients. Interferon-induced transmembrane protein, Solute carrier organic anion transporter and G protein-coupled receptor protein transcripts were selected for further investigation since they were the most commonly encountered in the literature. All three transcripts plays an important role in psychiatric disorders such as Interferon-induced transmembrane proteins have a immunosuppression effect on the brain which is related to psychiatric disorders, Solute carrier organic anion transporters are responsible for the neurotransmitter uptake and G protein-coupled receptor proteins are activated by hormones and neurotransmitters; they are responsible for nearly 90% of brain function. To make this study more comprehensive, more RNA-seq data could be included. Also investigating gene expressions which are specific for each disorder would be more meaningful for this concept.

Keywords: Transcriptomics, Psychiatric diseases, Differential gene expression, RNA Sequencing

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Investigating the Genomic Differentiation Landscape of the Large Mouse-Eared Bats

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Interspecific gene flow is crucial in evolutionary biology, by providing a rich research area for a deeper understanding of the dynamics underlying species evolution. The large mouse-eared bats Myotis myotis and M. blythii, represent a particularly intriguing species complex. Occurring in sympatry in Europe and Anatolia, these species exhibit evidence of gene flow, by a shared mitochondrial lineage indicative of past hybridization, and nuclear markers suggesting recent hybridization. Despite this, the persistence of separate gene pools remains an intriguing question. This study aims to improve the understanding of the evolutionary history of the large Myotis bats through a whole-genome perspective. In this context, genomic differentiation landscapes were selected to investigate nuclear divergences within and between Large Myotis bats. Whole-genome shotgun sequencing data spanning thirty-four samples representing M. myotis, M. blythii, and their closely related species M. punicus were generated. In Principal Component Admixture analyses performed to assess population structure and differentiation levels, distinct clusters corresponding to three large Myotis taxa were identified. A further split was observed in M. blythii, separating individuals from Kyrgyzstan and Mongolia. Genomic differentiation landscapes were assessed based on Fst, nucleotide diversity, and genomic divergence. Fst values supported the nuclear divergence between *M. myotis* and *M. blythii*, and within *M. blythii*. Introgression analyses based on D-statistics did not reveal any evidence of recent hybridization. This study contributes to future studies on greater Myotis bats and other cryptic species complexes, whilst highlighting the importance of whole-genome data in unraveling the complex dynamics that shape species evolution.

Keywords: Interspecific Gene Flow, Genomic Differentiation, Population Structure, Cryptic Species

Complex, Large Mouse-eared Bats, Introgression

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Comparative Analysis of SSR Marker Diversity with Maize Populations and Their Applications to Genetic Studies

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Maize, a critical field crop, garners significant attention in scientific circles owing to its diverse global applications and pivotal role in human and animal nutrition. This study aims to delve into specific indices of studied SSR markers and their implications for genetic studies among maize populations. Twenty SSR primers and six local populations and two commercial hybrid lines of maize were employed to assess key traits such as heterozygosity (h), polymorphic information content (PIC), effective multiplex ratio (EMR), marker index (MI), and resolution power (PR) across various populations. h reflects marker diversity, ranging from 0.32 to 0.86 indicating varying diversity. PIC indicates marker informativeness, ranging values from 0.268 to 0.844; notably, eleven markers indicate high informativeness (PIC>0.5). EMR demonstrates the markers' ability to detect differences, ranging from 0.5 to 3.125. MI offers an overall evaluation of marker system utility, varying from 0.134 to 3.379, while PR measures the markers' capacity to distinguish between different genotypes, with values ranging from 0.667 to 6.25. Moreover, the Fst value (Fst: 0.462) suggests significant population differentiation, supported by Jaccard similarity indices which gives similarity result between two populations based on presence of alleles. Jaccard results, ranges from 0.1712 to 0.274, emphasizing the distinct genetic compositions of each group. As we expected, the comparison of two hybrid lines and local populations showed less similarity compared to local population comparisons. These insights offer valuable guidance for future genetic studies in maize populations. This study is derived from Ezgi Alaca Yıldırım's thesis study.

Keywords: Maize, local populations, commercial lines, SSR, genetic studies marker indices.

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Understanding Human-wildlife conflict on the Iori Plateau

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Human-wildlife conflicts (HWC) are on the rise in areas where they share space. The increase is due to human population growth, agricultural expansion, and other drivers of habitat loss. We investigated HWC on the Iori plateau including Vashlovani, Samukhi, and Chachuna, which are used as winter pastures. Data was collected using semi-structured questionnaires. The study investigated various types of human-wildlife conflicts, focusing particularly on predator-caused conflicts. Additionally, we examined farmer's attitudes toward the reintroduction of goitered gazelle (Gazella subgutturosa). Several risk factors were hypothesized to impact the mean loss while being on the winter pasture on each farm. Since an incident report does not exist, we asked farmers to provide an approximate number of losses since arrival on winter pastures. Logistic regression showed a statistically significant (p-value = 0.0305) positive relationship between the proportion of sheep per dog and the estimated mean loss. In other words, as the proportion of sheep per dog increases, the expected loss also increases. A statistically significant positive relationship (p-value=0.013) was revealed between the amount of sheep and mean loss. We detected mean loss difference by location, specifically, Samukhi and Vashlovani have significantly lower losses (p-value = 0.000576 and 6.07e-05, respectively), compared to Chachuna, which was the reference level in logistic regression. 75% (48) of farmers have a positive attitude toward the reintroduction of goitered gazelles. However, we could not find any significant influential factors on that attitude. The Chi-square test did not reveal any significant influence of location (X-squared = 8.8254, df = 8, p-value = 0.3572), education level (X-squared = 1.4619, df = 6, p-value = 0.962), farmers' age (X-squared = 12.813, df = 10, p-value = 0.2343) and experience of being farmer (X-squared = 3.4697, df = 8, p-value = 0.9015).

Keywords: Human-wildlife conflict, attitudes toward reintroduction

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Investigation of the effect of ciprofloxacin on Escherichia coli population size using fecal-derived in vitro microbiota model

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Antibiotics have a considerably different effect on the gut microbiome's complex, dynamic ecology and alter the gut's delicate microbial equilibrium, allowing resistant bacteria to thrive. Therefore, the ecological environment of the gut microbiome is critical in determining the overall effects of antibiotic use. This study aimed to evaluate the response of E. coli population dynamics to the ciprofloxacin in the fecal-derived in vitro model, which simulates intestinal microbial communities. Materials and Methods: Fecal samples were obtained from two Mus musculus and cultured in BHI medium with and without ciprofloxacin (antibiotic-treated group and control group). DNAs were isolated from the cultures on days 1, 3, 5, and 10. The E. coli population sizes within the microbial community were quantified using real-time PCR with E. coli-specific primers. Statistical analyses were performed using the R. Results: We found significant differences between the control and ciprofloxacin-treated groups ($p < 0.1$). In the samples from the first and third days, the E. coli population sizes were two-fold lower in the antibiotic-treated group than in the control group. On the fifth day, we observed an increase in the population size in the control group, while the population size decreased in the antibiotic-treated group. The E. coli population was five-fold higher in the control group than in the antibiotic-treated group on the tenth day. Conclusion: This study demonstrates that the Mus musculus fecal-derived in vitro microbial communities may effectively serve as a model for the population dynamics of E. coli in response to antibiotic treatment.

Keywords: Population dynamics, culture model, microbiota, antibiotics

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Temporal Activity Patterns of Golden Jackals (*Canis aureus*) under varying human influence

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Understanding the temporal patterns of golden jackal (Canis aureus) activity is crucial for comprehending their ecological dynamics and providing a scientific basis for assessing conflicts with human populations. In this study, we investigated the daily activity patterns of golden jackals in Turkey and Georgia, by analyzing the camera-trap data collected over the years 2019-2020. We compared the activity patterns of jackals in two study sites with similar characteristics such as elevation, vegetation cover, and climatic conditions: Kartdag Wildlife Reserve in Turkey which is a protected area and a recreation area in the surroundings of a large city - Tbilisi in Georgia. We reveal insights into the daily rhythms of jackals, providing valuable information for wildlife management and conservation efforts. The Kernel density showed that jackals were active during 24 hours, but less active from 8 am to 4 pm. The t-test and Wilcoxon test did not reveal a significant difference (p-value = 0.1651 and p-value = 0.3739, respectively) between the activity patterns in both countries. Our findings contribute to a better understanding of jackal's activity patterns and potential interactions with humans in both protected areas and near urban environments, guiding effective conservation strategies. It emphasizes the importance of considering spatial and temporal dynamics in wildlife management and the need to coordinate efforts to minimize human-wildlife conflicts.

Keywords: Jackal, activity pattern, Georgia, Turkey

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Genomic Insights into Atlantic Bonito (Sarda sarda): Assessing Genetic Adaptation and Resilience to Climate Change

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The Atlantic bonito (Sarda sarda), belonging to the family Scombridae, is a pelagic fish extensively harvested by coastal fisheries yet underrepresented in biological research. This study addresses this gap by presenting the first comprehensive whole genome analysis of the species, aimed at understanding its genetic adaptability to changing marine environments. Given the impending threat of global warming to marine ecosystems, acquiring deep genomic insights is crucial for assessing the species resilience and susceptibility to environmental stressors. Using the shotgun sequencing by synthesis approach we conducted 150 bp paired-end sequencing of the Atlantic bonito genome. The bioinformatics workflow included rigorous quality control of raw data, estimation of genome size, and genome assembly followed by annotation. This process has allowed us to delve into the genetic basis of the species adaptation strategies, providing a framework for predicting responses to climate variability.The outcomes of this research not only enhance our understanding of the Atlantic bonito's genetic architecture but also contribute significantly to conservation efforts and sustainable fishery management. By elucidating the genomic underpinnings of its ecological interactions and evolutionary dynamics, this study offers valuable insights into population dynamics and adaptive potential, essential for mitigating the impacts of global warming on this valuable species.

Keywords: Whole Genome Sequencing, Marine Genomics, Climate Change Resilience Conservation

Genomics

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Acoustic Monitoring of Bat Migration Patterns Across Istanbul

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Türkiye has one of the richest bat diversity in the Mediterranean region. However, information about the population sizes, distributions, and migrations is limited due to previous studies primarily focusing on cave-dwelling species and relying on opportunistic surveys, alongside the elusive nocturnal behavior of bats. This study aims to conduct a systematic acoustic ecology study in Türkiye and focus on the importance of Bosphorus as a migratory corridor for bats, particularly the activity of a highly migratory Pipistrellus nathusii. Meteorological parameters were compared with bat activity to assess the relationship between weather conditions and bat migration. Ultrasonic recordings were collected between April and November 2022 at four locations along the Bosphorus, spanning from north to south. Acoustic analysis was performed by selecting days at periodic intervals (4-9 days). The results indicated an increased activity of P. nathusii in mid-August, followed by a decrease towards late-October. The findings suggest that Istanbul serves as a migratory route for bats, especially during the late summer migration period. Nightly averaged meteorological parameters including temperature, precipitation, and wind speed were compared with bat passes per night. Temperature (positively related) and precipitation (negatively related) were identified as the most important factors. In conclusion, this study highlights the importance of acoustic ecology studies to understand the bat migration patterns in Türkiye. The findings show that Bosphorus is an important migration pathway for bats, emphasizing the need for further research and conservation efforts to protect bat species and their migration routes between Europe and Asia.

Keywords: Bioacoustics, Pipistrellus nathusii, Bosphorus corridor, Late-summer migration, Weather

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Conservation Genomics of the Striped Hyena in Anatolia: Insights from Diet and Microbiota Metabarcoding

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The striped hyena (Hyaena hyaena), a key species in the ecosystems of Asia and Africa, is currently facing potential extinction in various regions, including Anatolia, Turkey, where its status remains largely undocumented. The 'Anatolian Beast: Striped Hyena Study' leverages environmental DNA (eDNA) and metabarcoding—a non-invasive approach utilizing biological traces like feces, hair, and bones—to investigate these enigmatic creatures without impacting their natural behavior. This study focuses on two primary aspects: dietary analysis and microbiota profiling of the striped hyena. By examining the eDNA in collected fecal samples, we aim to elucidate the trophic interactions that define the hyena's ecological niche, explore its adaptation to local environmental conditions, and infer its dietary preferences. Concurrently, analysis of fecal microbiota provides insights into the relationship between the gut microbial communities and the hyena's immune system, which remains robust despite frequent exposure to pathogens. Preliminary results indicate a diverse diet a wide spectrum of vertebrate prey, highlighting the hyena's role as a scavenger and predator within its ecosystem. This adaptability may contribute to its resilience against habitat degradation and human-wildlife conflicts, which are prevalent threats in its diminishing habitat. These findings underscore the importance of conservation genomics in understanding and preserving the ecological dynamics and genetic health of endangered species like the striped hyena.

Keywords: Conservation Genomics, Striped Hyena, eDNA Metabarcoding, Trophic Interactions, Wildlife

Conservation

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Advancing Biodiversity Monitoring in Muğla, Turkey: Novel Molecular Protocols for Insect Species Detection

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Recent advancements in molecular biology have significantly impacted biodiversity research, providing tools that surpass traditional taxonomic methods in speed and precision. These techniques, which do not require extensive taxonomic expertise, allow for rapid and accurate species identification. This study focuses on developing and implementing a robust molecular protocol for insect species detection in Muğla, Turkey, a region noted for its rich biodiversity. Malaise traps were strategically deployed in this biodiversity hotspot to collect insects. Captured specimens were carefully photographed and then homogenized for DNA extraction. This study targeted five specific barcode regions for PCR amplification, followed by next-generation sequencing to achieve precise molecular identification. Through five different primer trials, the predominant taxa identified are Orthoptera, Coleoptera, and Hemiptera. A total of 138 distinct species were detected across various taxa. While the taxonomic composition of species identified varied among primers, similar species were observed. Moreover, molecular methods have proven advantageous, as they enabled the detection of a greater number of species compared to those photographed in the project, highlighting the utility of molecular approaches. The establishment of this protocol is of critical importance both nationally and internationally, as it contributes to the accurate formation of species inventories necessary for effective ecosystem management. Furthermore, the study addresses several challenges unique to insect biodiversity, such as the need for enhancing DNA reference libraries and developing tailored molecular techniques. By overcoming these challenges, the protocol not only streamlines the identification process but also enhances the accuracy and efficiency of biodiversity monitoring.

Keywords: Biodiversity, Insect DNA Barcoding, Species Identification

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Whole Mitochondrial Genome Analysis Reveals the Phylogeny of the Western Palaearctic Serotine Bats (genus Eptesicus, Vespertilionidae, Chiroptera)

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Understanding speciation mechanisms is crucial in evolutionary biology to illuminate biodiversity on Earth. Due to their global presence and diversity, the Serotine bats (genus Eptesicus) offer a rich study material for such studies. With over 30 species distributed globally, excluding Antarctica, their complex evolution is influenced by geography, environmental changes, and gene flow, providing further investigation opportunities. The Serotine bat species are categorized into two main lineage groups in the Palaearctic region: bottae and serotinus. Species identification among Serotine bats is challenging due to possible introgression events. This study aims to enhance our understanding of the Serotine bat phylogeny by analyzing the whole mitochondrial genomes of the Western Palaearctic species. We de novo assembled complete mitochondrial genomes of thirteen samples from the Palaearctic region, comprising six species and ten subspecies. To compare the taxonomic identities of the analyzed samples with previously published data we extracted two commonly studied marker genes, Cytochrome b, and NADH dehydrogenase 1 (ND1), and constructed phylogenetic trees. On the assembled mitogenomes, all 37 mitochondrial genes, including thirteen protein-coding genes, twenty-two transfer RNAs, two ribosomal RNAs, and one non-coding displacement loop (D-loop), were identified and annotated for each sample, revealing the diversification levels among taxa. We constructed a whole mitogenome phylogenetic tree excluding the D-loop region. The resulting phylogenetic trees show a correlation between species clustering and their geographical distribution. Our study contributes to the broader understanding of the speciation process within Serotine bat genetic diversity and evolutionary history by integrating analysis of whole mitochondrial genomes.

Keywords: Evolutionary history, Phylogenomics, Mitochondrial DNA, Bats

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Seed germination in *Ptilostemon chamaepeuce*, an eastern Mediterranean shrub, in response to heat shock and smoke treatments

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Seed germination in Ptilostemon chamaepeuce, an eastern Mediterranean shrub, in response to heat shock and smoke treatments Merve Nur Turan1,2, Çağatay Tavşanoğlu1 1 Division of Ecology, Department of Biology, Hacettepe University, Beytepe, 06800, Ankara, Türkiye 2 Department of Molecular Biology and Genetics, Dicle University, Diyarbakır, Türkiye The germination response to fire-related cues in several Mediterranean species remains unexplored. We studied the effects of heat shock and smoke on the germination of Ptilostemon chamaepeuce (L.) Less. (Asteraceae), an eastern Mediterranean shrub. Observation of seedlings in recently burned areas suggest that post-fire germination enhancement is likely in this species. We collected seeds from a natural population in Marmaris, southwestern Türkiye. We applied three heat shock treatments —80°C, 100°C, and 120°C— for five minutes each, and two smoke treatments at 1:10 and 1:100 concentrations. An untreated group served as the control for heat shock treatments, and a distilled water treatment served as the control for smoke treatments. We sowed 25 seeds into each of four replicate Petri dishes containing agar, maintained them at 20°C for incubation, and monitored germination every two days. Seeds tolerated the 100°C heat shock treatment, showing germination levels comparable to the control, whereas the 120°C treatment was lethal. Although smoke treatments appeared to enhance germination, this increase was not statistically significant when compared to the corresponding control. Given the limited research on the post-fire germination of Ptilostemon chamaepeuce, more comprehensive studies involving additional populations, varied smoke treatments, and smoke-derived chemicals are required to elucidate the fire-related germination behavior in this species.

Keywords: Fire-related germination, heat-shock, Mediterranean species, fire, smoke-water.

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Urbanization Impact on Dietary Patterns and Microbiota in Gulls: A Metabarcoding Analysis

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Urban environments significantly alter wildlife feeding behaviors and associated microbiota due to the availability of diverse food sources. This study examines the influence of varying urbanization levels on the diet and microbiota of the Yellow-legged gull (Larus michahellis) in Istanbul. Utilizing environmental DNA (eDNA) metabarcoding, we analyzed stool samples collected from areas with low, moderate, and high urban development and human interaction. Our metabarcoding approach targeted both the 16S rRNA gene to characterize microbiota and the 18S rRNA gene to assess diet composition. This dual-focus analysis enabled us to detect significant variations in the dietary content and microbial communities among gull populations from different urbanization gradients. The results demonstrate distinct dietary shifts and microbiota alterations, correlating with the degree of anthropogenic impact. This research highlights the profound effects of urbanization on gull ecology, providing critical insights into how urban environments can shape wildlife diet and health through alterations in their feeding behavior and gut microbiota. These findings have significant implications for urban wildlife management and conservation strategies.

Keywords: Urban Ecology, Wildlife Metabarcoding, Gull Diet Analysis, Microbiota Diversity,

Anthropogenic Effects

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