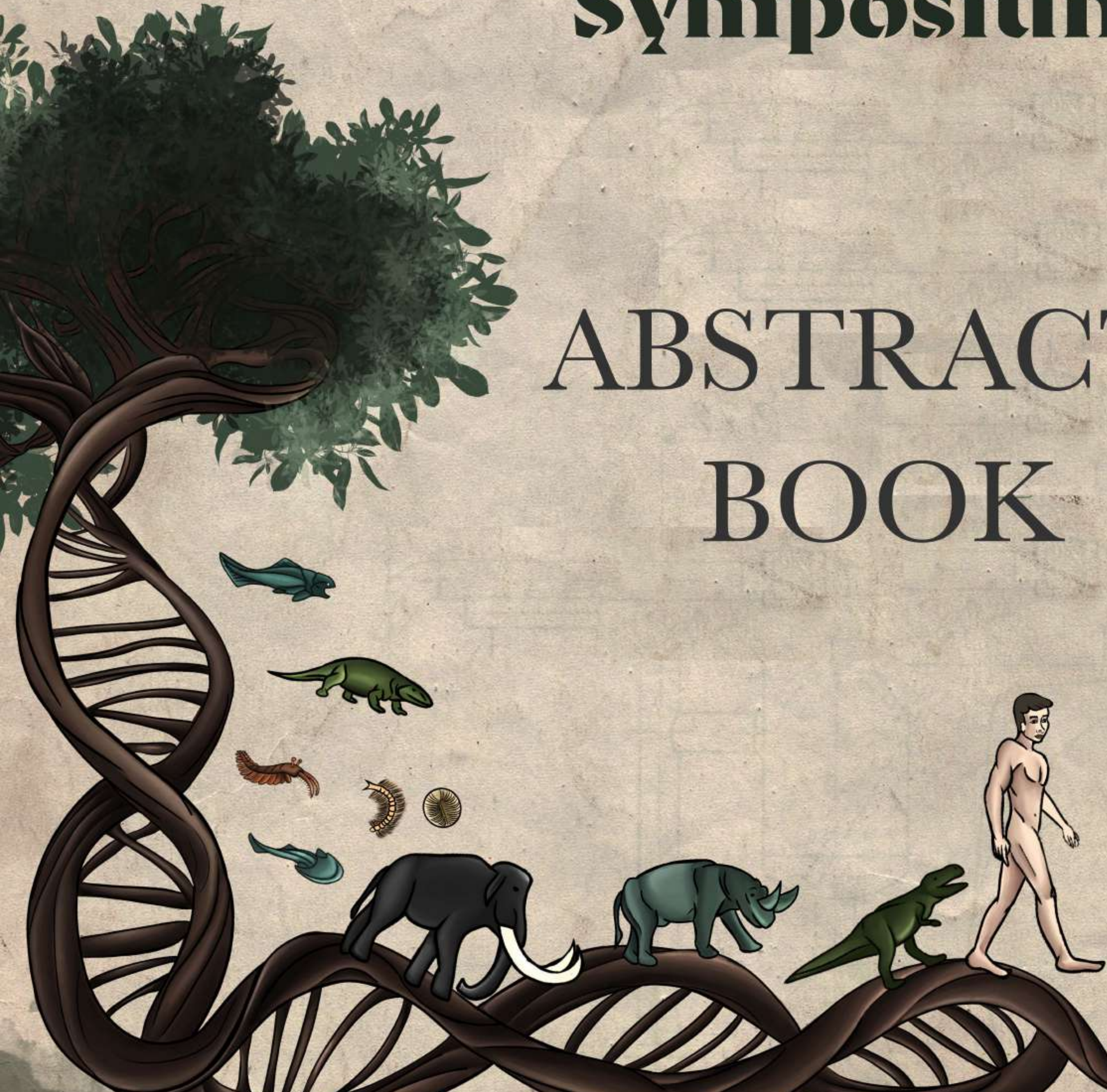
HACETTEPE
ÜNİVERSİTESİ

EEBST 2025

11th Ecology and Evolutionary Biology Symposium

ABSTRACT BOOK



ekoevo
Ekoloji ve Evrimsel Biyoloji Derneği

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Özge Çakmak
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Bünyamin Özdemir
Veli Deniz Ünlü
Selen Kırmızı

11TH ECOLOGY AND EVOLUTIONARY BIOLOGY SYMPOSUM PROGRAM

09.07.2025
WEDNESDAY

08:00 - 09:30	REGISTRATION
09:30 - 10:00	OPENING CEREMONY
10:00 - 11:00	**NATÁLIA MARTÍNKOVÁ - GENOME POLARIZATION: TRACING THE THREADS OF HYBRIDIZATION AND EVOLUTIONARY FLUX**
11:00 - 11:30	COFFEE/TEA BREAK
	SESSION 1: POPULATION GENETICS
11:30 - 11:45	AYŞEGÜL ER GÖKÇE - UNCOVERING THE DIET COMPOSITION AND FORAGING ECOLOGY OF FALCO ELEONORAE USING NON-INVASIVE EDNA-BASED PELLET METABARCODING
11:45 - 12:00	BAHAR PATLAR - MOISTURE MATTERS MORE THAN HEAT FOR EVOLUTION OF REPRODUCTIVE GENES IN DROSOPHILA
12:00 - 12:15	İBRAHİM RAŞİT BİLGİN - THE MITOCHONDRIAL AND DOUBLE DIGEST RESTRICTION-SITE ASSOCIATED DNA SEQUENCING (DDRAD-SEQUENCING) REVEALS ISOLATION AND EXPANSION FROM THE GLACIAL REFUGIA
12:15 - 12:30	KUTLU ŞAFAK ALKAN - DEVELOPING CUSTOM SNP PANELS FOR RAPID AND ACCURATE WILDLIFE CONSERVATION GENETICS APPLICATIONS
12:30 - 12:45	SAHAR JAVAHERI TEHRANI - UNCOVERING HYBRIDIZATION AND SPECIES BOUNDARIES IN PERIPHERAL POPULATIONS OF THE GREAT TIT (PARUS MAJOR) USING HIGH-RESOLUTION GENOMICS
12:45 - 13:00	TONI GOSSMANN - WHY SEX-BASED GENOMIC DIFFERENTIATION SHOULD NOT BE OVERLOOKED IN POPULATION GENETICS
13:00 - 14:00	LUNCH
	SESSION 2: POPULATION ECOLOGY
14:00 - 14:15	BERİL TEZEL - MOLECULAR APPROACHES FOR CONSERVATION: EDNA AND METABARCODING INSIGHTS INTO THE STRIPED HYENA POPULATION IN TÜRKİYE
14:15 - 14:30	NERGİS BİLGE KARABULUT - GENETIC DIVERSITY PATTERNS IN PHENOLOGICAL TRAITS OF QUERCUS ROBUR L.
14:30 - 14:45	KADİRHAN KILINÇ - INFECTED BUT INVESTING: INTERACTIVE EFFECTS OF PARASITEMIA AND FOOD AVAILABILITY ON REPRODUCTION IN GREAT TITS
14:45 - 15:00	NURBAHAR USTA - TROJAN FIR UNDER CLIMATE WARMING: A FACILITATOR SPECIES FACING REGENERATION LIMITS
	SESSION 3: AQUATIC ECOLOGY
15:00 - 15:15	ABDULLAH ÖZ - VARIATION IN AQUATIC FOOD WEBS ALONG THE LONGITUDINAL GRADIENT OF A SOUTHERN ANATOLIAN COASTAL RIVER
15:15 - 15:30	AYLİN AKKAYA - UNSPOKEN DYNAMICS OF SPERM WHALES (PHYSETER MACROCEPHALUS) IN THE EASTERN MEDITERRANEAN SEA OF TÜRKIYE: GROUP STRUCTURE, SPATIAL-TEMPORAL DISTRIBUTION AND BODY LENGTH
15:30 - 15:45	GÜL CANAN YAVUZ - THE EFFECTS OF SALINITY AND HEATWAVE ON ZOOPLANKTON COMMUNITY STRUCTURES, DIVERSITY AND RESOURCE USE EFFICIENCY: SYNCHRONIZED MESOCOSM EXPERIMENTS, TÜRKIYE
15:45 - 16:00	İREM GAMZE ARIK - SALINITY-INDUCED SHIFTS IN ZOOPLANKTON COMMUNITIES: INSIGHTS FROM A GRADIENT-BASED MESOCOSM STUDY

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16:00 - 16:30	COFFEE/TEA BREAK
	SESSION 4: FLASH TALKS!
16:30 - 17:30	ARDA SEVKAR - THE MINI YET MIGHTY STAPES: A SUPERIOR DNA SOURCE THAN THE COCHLEAR POWDER
	ATAKAN YILDIZ - THE ROLE OF SOIL MICROBIOTA IN ECOSYSTEM HEALTH AND SUSTAINABLE TEA CULTIVATION: INSIGHTS FROM EDNA AND METAGENOMIC APPROACHES
	BEDİRHAN AVDANCI - COMMUNITY COMPOSITION AND RESISTANCE LEVELS OF SOIL BACTERIA AND FUNGI IN A MEDITERRANEAN FOREST UNDER VARYING WILDFIRE SEVERITIES
	ELİFNAZ EKER - UNRAVELING ROMAN MOBILITY: ARCHAEOGENOMIC INSIGHTS FROM ASIA MINOR TO THE ITALIAN PENINSULA
	FATIMA NUR OĞUL - INTEGRATED ANALYSIS OF REPRODUCTION AND REGENERATION IN COLONIAL ASCIDIANS
	GENCER YAPRAK - GLOBAL ECOLOGICAL NICHE MODELLING FOR THE BIMACULATED LARK (MELANOCORYPHA BIMACULATE) BREEDING HABITATS AND PREDICTION OF ITS DISTRIBUTION UNDER CURRENT AND FUTURE CLIMATE SCENARIOS
	GÜLCE EDİŞ - DISCOVERY OF TWO NOVEL PARTITIVIRUSES INFECTING THE SAXICOLOUS LICHEN CALOGAYA DECIPIENS
	İLAYDA DUMLUPINAR - EXPLAINING BRASSICACEAE SPECIES RICHNESS PATTERNS IN TÜRKIYE USING SPATIAL STATISTICAL MODELS
	NIKOLA PETKOVIC - THE RESPONSE OF THE LIFE HISTORY TRAITS OF DAPHNIA MAGNA TO THE DETERIORATING TEMPERATURES
	PELİN TAŞ - DIVERSITY DYNAMICS OF AIRBORNE PLANT COMMUNITIES REVEALED BY EDNAIR
	SONGÜL SÖNMEZ - BIODIVERSITY HOTSPOTS AT RISK: PROJECTIONS OF CLIMATE CHANGE IMPACTS ACROSS ECOREGIONS
17:30 - 18:30	**POSTER SESSION 1**
18:30 - 21:00	BIODIVERSITY MUSEUM VISIT & ICEBREAKER COCKTAIL

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10.07.2025 THURSDAY

09:45 - 10:45	**JALIL NOROOZI - PLANT BIODIVERSITY AND BIOGEOGRAPHY OF THE HIGH MOUNTAINS OF THE IRANO-ANATOLIAN BIODIVERSITY HOTSPOT**
10:45 - 11:15	COFFEE/TEA BREAK
	SESSION 5: ANCIENT DNA & PALEOBIOLOGY
11:15 - 11:30	DİLEK KOPTEKİN - OUT-OF-ANATOLIA MIGRATIONS DURING THE NEOLITHIZATION OF WESTERN EURASIA
11:30 - 11:45	FERHAT KAYA - LATE QUATERNARY FOSSIL RODENT ASSEMBLAGES FROM THE MIDDLE AWASH STUDY AREA, AFAR RIFT, ETHIOPIA
11:45 - 12:00	FUNDA ÖZDEMİR DEĞİRMENCİ - RECONSTRUCTING VEGETATION HISTORY OF THE MARMARA LAKE BASIN AND GEDIZ PLAIN USING SEDIMENTARY ANCIENT DNA (SEDADNA)
12:00 - 12:15	HANNAH MOOTS - EARLY 2ND MILLENNIUM CE PEOPLES OF CENTRAL ANATOLIA: AN ARCHAEOGENETIC VIEW FROM YOZGAT PROVINCE
12:15 - 12:30	GÖZDE ATAĞ - ANCIENT HUMAN DNA IN SEDIMENTS FROM OPEN-AIR HOLOCENE SITES ACROSS EUROPE
12:30 - 12:45	ÖZGE KAHYA PARILDAR - PRELIMINARY ASSESSMENT OF LATE MIOCENE HIPPARIONINE ASSEMBLAGE FROM THE SOFULAR LOCALITY (CENTRAL ANATOLIA, TÜRKIYE)
12:45 - 13:00	SEMA YILMAZ - A PRELIMINARY REPORT ON THE TAPHONOMY OF LATE QUATERNARY FOSSIL SMALL MAMMALS FROM THE AFAR REGION, ETHIOPIA
13:00 - 14:00	LUNCH
	SESSION 6: CONSERVATIOUN BIOLOGY & BIOGEOGRAPHY
14:00 - 14:15	ANIL SOYUMERT - DETECTING THE OFFSPRING OF MAMMALS: INDICATORS FOR THE KEY HABITAT PATCHES FOR WILDLIFE CONSERVATION
14:15 - 14:30	BATUHAN ATIF TUNÇ - EXPANDING CLIMATE NICHE FACTOR ANALYSIS BEYOND SPECIES: ECOREGION-LEVEL VULNERABILITY MAPPING UNDER CLIMATE CHANGE
14:30 - 14:45	BİRCAN TAŞKIRAN - ENHANCING GENETIC AND ALTRUISTIC TRANSFORMATION IN AMERICAN CHESTNUTS FOR FUNCTIONAL GENOMICS AND DISEASE RESISTANCE VIA AGROBACTERIUM-MEDIATED APPROACHES
14:45 - 15:00	ÇİĞDEM KANSU - GENETIC DIVERSITY AND PHYLOGEOGRAPHY OF WHITE OAKS (QUERCUS PETRAEA AND Q. PUBESCENS): INSIGHTS FROM THE EASTERN MEDITERRANEAN
15:00 - 15:15	ITRİ LEVENT ERKOL - ECOLOGICAL NICHE MODELING OF RARE TURKISH OLIVE CULTIVARS: A SPATIAL FRAMEWORK FOR AGROECOSYSTEM POLICY AND CONSERVATION
15:15 - 15:30	SADDAM SAQIB - EVOLUTIONARY HOTSPOTS AND ALIEN INVASIONS: INTEGRATING PHYLOGENETICS TO GUIDE CONSERVATION IN THE PAN-HIMALAYA
15:30 - 16:00	COFFEE/TEA BREAK
16:00 - 17:00	**PANEL:** ANTHROPOLOGY IN TÜRKIYE AT ITS CENTENNIAL: PAST, PRESENT, AND FUTURE (IN TURKISH) - FACILITATOR: EZGİ ALTINIŞIK, PANELISTS: FERHAT KAYA, MEHMET SOMEL
17:00 - 17:45	**POSTER SESSION 2**
17:45 - 18:45	**PANEL:** INTEGRATING BIODIVERSITY KNOWLEDGE INTO CONSERVATION PRACTICE (IN TURKISH) - FACILITATOR: NURBAHAR USTA, PANELISTS: C. CAN BİLGİN, UĞUR ZEYDANLI
18:45 - 19:00	SHORT BREAK
19:00 - 20:30	GENERAL ASSEMBLY OF EKOEVO (IN TURKISH)

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09:30 - 10:30 **PARASKEVI KARACHLE - NON-INDIGENOUS SPECIES IN THE MEDITERRANEAN SEA: STATUS, IMPACTS AND PERSPECTIVES**

10:30 - 11:00 COFFEE/TEA BREAK

SESSION 7: MICROBIAL ECOLOGY & EVOLUTION

11:00 - 11:15 EZGİ ÖZKURT - STOCHASTIC DYNAMICS IN THE ASSEMBLY OF THE SEED-BORNE MICROBIOME IN BREAD WHEAT

11:15 - 11:30 IŞILAY ÇELİK - LINKING ENVIRONMENTAL PARAMETERS TO MICROBIAL FUNCTION VIA METAGENOMIC PROFILING

11:30 - 11:45 KEREM GÖKDAĞ - MICROPLASTICS ENRICH PATHOGENIC BACTERIA IN LAKES ACROSS A SALINITY GRADIENT

11:45 - 12:00 SİBEL ALTÜRK KARACA - INFLUENCE OF PHOSPHORUS CONCENTRATION ON GROWTH, PIGMENT ACCUMULATION, AND LIPID PRODUCTION IN FIVE MICROALGAL SPECIES

SESSION 8: ANIMAL BEHAVIOUR & WILDLIFE ECOLOGY

12:00 - 12:15 BEGÜN ERBABA - CORTICAL CELL DISTRIBUTION PATTERNS IN LANGUAGE-TRAINED GORILLAS: IMPLICATIONS FOR NEUROPLASTICITY

12:15 - 12:30 BELCE SU UYKUSUZ - THE EFFECTS OF AFFORESTATION ON THE FUNCTIONAL DIVERSITY OF STEPPE BUTTERFLY COMMUNITIES IN KONYA BASIN, TÜRKIYE

12:30 - 12:45 QAZI HAMMAD MUEEN - ASSESSING BREEDING PERFORMANCE OF A PRECOCIAL BIRD SPECIES USING GPS DATA

12:45 - 13:00 VİLDAN ACAR - ASSESSING COGNITIVE PERFORMANCE AND LEARNING EFFICIENCY IN WILD GREAT TITS: INSIGHTS FROM AN RFID-BASED MULTIPLE REVERSAL LEARNING EXPERIMENT

13:00 - 14:00 LUNCH

SESSION 9 - BIOINFORMATICS & PHYLOGENETICS & EVOLUTIONARY GENOMICS

14:00 - 14:15 ASLINUR AKTÜRK - GENOME ANNOTATION AND ANALYSES OF THE TENEBRIONID BEETLE CARCHARES MACER

14:15 - 14:30 CANSU ÇETİN - UNRAVELING HOST-PARASITE COEVOLUTION IN COMPLEX NATURAL SYSTEMS: INSIGHTS FROM MHC VARIATION IN AMPHIBIANS

14:30 - 14:45 EVA ŠATOVIĆ VUKŠIĆ - EXPLORING THE FUNCTION AND EVOLUTION OF THE "DARK MATTER OF THE GENOME" IN THE ECONOMICALLY SIGNIFICANT BEETLE TENEBRIO MOLITOR

14:45 - 15:00 ILGIN DENİZ CAN - INTEGRATIVE TAXONOMIC REVISION OF HELDREICHIA BUPLEURIFOLIA (BRASSICACEAE) BASED ON MORPHOLOGICAL AND GENOMIC DATA

15:00 - 15:15 PINAR AKBABA - FUNCTIONAL GENOMICS OF MUSCLE AND OVARY DEVELOPMENT IN TELEOSTS: INSIGHTS INTO EVOLUTION AND SPECIALIZATION

15:15 - 15:30 ZAHIDA SULTANOVA -LIFE-HISTORY TRAITS SHAPE THE EVOLUTION OF MAMMALIAN LIFESPAN

15:30 - 15:45 PRESENTATION ON EMBO SHORT-TERM TRAVEL GRANTS

15:45 - 16:15 COFFEE/TEA BREAK

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SESSION 10: COMMUNITY & ECOSYSTEM ECOLOGY

16:15 - 16:30	ANIL BAHAR - EFFECT OF CROWN FIRES ON TEMPERATE MIXED FORESTS OF NORTHEASTERN ANATOLIA: A MODELING APPROACH
16:30 - 16:45	GÜLSELİ KIRGIL - POLLINATOR ASSEMBLAGES AS DRIVERS OF PLANT RANGE: EVIDENCE FROM A MARL STEPPE IN CENTRAL ANATOLIA
16:45 - 17:00	ILGIN ERTAN GÜROL - AVIAN COMMUNITIES OF THE ANATOLIAN DIAGONAL: THE ROLE OF CLIMATE AND LAND COVER
17:00 - 17:15	İSMAİL BEKAR - CLIMATE OR LAND USE? DISENTANGLING DRIVERS OF WILDFIRES IN MEDITERRANEAN NORTH AFRICA
17:15 - 17:30	SELEN AKÇAKOCA - THE EFFECTS OF AFFORESTATION AGE ON THE FUNCTIONAL DIVERSITY OF PLANTS IN THE STEPPES OF CENTRAL ANATOLIA, TURKEY
17:30 - 17:45	ZEYNEP LADİN COŞGUN - CHANGE IN FUNCTIONAL TRAIT STRUCTURE OF PLANT COMMUNITIES ALONG AN ELEVATIONAL GRADIENT IN SOUTHWESTERN ANATOLIA
17:45 - 18:30	CLOSING CEREMONY

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POSTER PRESENTATIONS

- **ABDULLAH ENES GÖKSAL** - OCCURRENCE OF PROTOTHECA SPECIES IN AQUATIC ECOSYSTEMS OF TÜRKİYE
- **AHMET BERKAY DEMİRSEÇEN** - METAGENOMIC INVESTIGATION OF ANCIENT ORAL MICROBIOTA FROM DENTAL CALCULUS: A COMPUTATIONAL FRAMEWORK FOR TAXONOMIC AND FUNCTIONAL PROFILING
- **AHMET CAN TINAZ** - MOVEMENT ECOLOGY OF THE EGYPTIAN VULTURE (NEOPHRON PERCNOPTERUS) BREEDING IN BEYPAZARI: INSIGHTS FROM GSM TELEMETRY
- **AHMETCAN İMBATESEN** - FISH MORTALITIES AND MOLECULAR TRACES: A POST-EVENT EDNA SURVEY IN İZMIR BAY, AEGEAN SEA
- **ALİ KORAY KOÇ** - RIBOSOMAL CISTRON OF TETRIX BOLIVARI (TETRIGINAE, ORTHOPTERA): CHARACTERIZATION OF LINEAR AND SECONDARY STRUCTURE
- **ALİ ONUR SAYAR** - BALANCING ETHICS AND EFFICIENCY: EVALUATING CAPTURE TECHNIQUES FOR WILD GOATS IN RUGGED TERRAIN
- **ALİ SERHAN ÇAĞAN** - MICROPLASTIC POLLUTION AND RISK ASSESSMENT IN SURFACE WATER OF SUSURLUK SUB-BASIN
- **AYÇA YEŞİLBAĞ** - IMPACTS OF AQUACULTURE ACTIVITIES ON MICROBIAL DIVERSITY IN THE EUPHRATES RIVER: AN EDNA-BASED ASSESSMENT
- **AYDA YILMAZ** - ENDOSYMBIONT-ASSOCIATED DIVERGENCE: WOLBACHIA PREVALENCE AND MITOCHONDRIAL PATTERNS IN SAND FLIES OF TÜRKİYE
- **AYŞEGÜL ER GÖKÇE** - NON-INVASIVE MONITORING OF PREDATOR–PREY RELATIONSHIPS AND MICROBIAL DIVERSITY VIA OWL PELLET METABARCODING
- **BAŞAK ESGİN** - INVESTIGATION OF SELECTION PRESSURE ON COHESIN AND CONDENSIN GENES IN NANNOSPALAX XANTHODON
- **BERNA YAVUZ** - VARIABILITY IN SEED MASS, GERMINATION, AND DORMANCY IN STEPPE PLANT COMMUNITIES ALONG A PRODUCTIVITY GRADIENT IN CENTRAL ANATOLIA
- **BÜŞRA KARATAŞ** - GENOME MEETS GRAVE: MOLECULAR IDENTIFICATION OF TUBERCULOSIS IN A BYZANTINE BURIAL
- **CAN ELVERİCİ** - THE SHIFTING MOSAIC: CLIMATE CHANGE IMPACTS ON ENDEMIC VERTEBRATES IN THE MEDITERRANEAN BIODIVERSITY HOTSPOT
- **CEMREAY DEDE** - TAXONOMIC AND FUNCTIONAL DIVERSITY OF MACROINVERTEBRATE COMMUNITIES IN RELATION TO ENVIRONMENTAL VARIABLES IN RURAL PONDS OF ANKARA, TURKEY
- **DOĞAN SÖZBİLEN** - WE ALL LOVE SUCCESS STORIES, BUT WHY IS THE RETURN OF A POPULATION NOT RELIEVING? CONCERNS OVER THE RECOVERY OF THE MEDITERRANEAN SEA TURTLE POPULATION
- **EFE SEZGİN** - NOVEL PROTEIN LANGUAGE MODELS FOR VIRAL ESCAPE PREDICTION
- **ELÇİN EKŞİ** - COMPUTATIONAL METHODS TRANSFORMING PALEONTOLOGY
- **EMİNE BÜŞRA MÜLAYİM** - HOW POND CHARACTERISTICS AFFECT MACROPHYTE DIVERSITY AND COVERAGE IN RURAL PONDS OF ANKARA, TÜRKİE
- **EMRAH KIRDÖK** - ANCIENT SEDIMENTARY DNA REVEALS HUMAN, ANIMAL AND MICROBIAL ACTIVITY IN EL PORTALÓN CAVE
- **EYLEM GÜLAY** - PRELIMINARY ASSESSMENT OF MEIOFAUNAL DIVERSITY AND ENVIRONMENTAL FACTORS IN THE INTERTIDAL ZONE OF THE FILYOS AND SEFERCIK COASTS (BLACK SEA, ZONGULDAK, TÜRKIYE)
- **FERİDE AVCI** - UNDERSTANDING THE FACTORS AFFECTING THE DIVERSITY OF ZOOPLANKTON COMMUNITIES IN A POND METACOMMUNITY
- **G. BİKE YAZICIOĞLU** - A MODELED BIOAVAILABLE STRONTIUM ISOSCAPE (87SR/86SR) OF TÜRKIYE: A RESEARCH TOOL FOR ARCHAEOLOGICAL MOBILITY RECONSTRUCTION
- **GÜLSELİ KIRGIL** - AFFORESTATION ALTERS EPIGEIC BEETLE COMMUNITY IN CENTRAL ANATOLIAN STEPPES
- **HABİB BAKIR** - THE EVOLVING MIND SUBTERRANEAN: MAPPING NEUROANATOMICAL ADAPTATIONS IN SUBTERRAN RODENTS
- **ILGIN DOĞA TEKİN** - ACORN THIEVES: UNCOVERING THE AGENTS BEHIND OAK REGENERATION
- **IŞILAY ÇELİK** - DECODING MICROPLASTIC-ASSOCIATED MICROBIAL COMMUNITIES: EDNA-BASED INSIGHTS INTO DIVERSITY AND ENVIRONMENTAL RISK
- **İLAYDA GÜVEN** - COMPARATIVE ANALYSIS OF $\Delta^{13}C$ AND $\Delta^{15}N$ RATIOS AND TROPHIC POSITIONS IN TWO OMNIVOROUS FISH SPECIES ALONG A DISTURBED URBAN RIVER GRADIENT
- **KAAN YILMAZ** - INTEGRATING CITIZEN SCIENCE AND NON-INVASIVE MOLECULAR TECHNIQUES TO REVEAL THE DIET OF PLANT-MIMICKING MANTISES (MANTODEA: EMPUSIDAE)
- **KANAT GÜRÜN** - KINSHIP ANALYSIS TOOLKIT: A NEW PIPELINE CONSISTING OF IN-HOUSE SCRIPTS TO DETERMINE THE RELATIONSHIP DEGREE AND THE TYPE OF FIRST DEGREE RELATIONS USING LOW-COVERAGE DATA
- **KAYRA CANPOLAT** - THE POPULATION GENETIC HISTORY OF THE HITTITE CAPITAL HATTUSA
- **KEMAL GÖRGÜLÜ** - PHYLOGENETIC RELATIONSHIPS AMONG WEEVIL SUBFAMILIES (COLEOPTERA: CURCULIONIDAE) BASED ON MITOCHONDRIAL COI SEQUENCES
- **KUTAY YÜKSEL** - PYRGOMORPHIDAE (ORTHOPTERA, CAELIFERA) MITOGENOME: CHARACTERIZATION AND PHYLOGENETIC POSITION

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POSTER PRESENTATIONS

- **MEHMET GÖKTUĞ ÖZTÜRK** - MODELING WILDFIRE OCCURRENCE IN TÜRKIYE: THE ROLE OF CLIMATE, PRODUCTIVITY, AND HUMAN INFLUENCE
- **MEHMET SOMEL** - ANCIENT HUMAN GENOMES FROM MEDIEVAL NICAEA (İZNİK)
- **METEHAN KARA** - STOCHASTIC DNA DAMAGE AND REPAIR DYNAMICS AS A DRIVER OF CELLULAR FITNESS UNDER RADIATION
- **MİNA CANSU KARAER** - DUAL APPROACH TO ASSESS GASTROINTESTINAL HELMINTH DIVERSITY IN CAPTIVE AND FREE-RANGING MOUNTAIN GAZELLES (GAZELLA GAZELLA) IN HATAY, TÜRKİYE
- **MUSTAFA SÖZEN** - TRACING THE RELATIONSHIP BETWEEN MORPHOLOGICAL AND CHROMOSOMAL EVOLUTION IN NANNOSPALAX SP. USING THREE-DIMENSIONAL GEOMETRIC MORPHOMETRICS
- **MUHAMMED ARİF DEMİR** - GEOMETRIC MORPHOMETRIC ANALYSIS OF MALE HIND WINGS AND GENITAL STRUCTURES IN MELOIDAE (COLEOPTERA): PATTERNS OF MORPHOLOGICAL DIFFERENTIATION AND THEIR PHYLOGENETIC IMPLICATIONS
- **MUHAMMED ARİF DEMİR** - ENVIRONMENTAL REQUIREMENTS OF MELOIDAE (COLEOPTERA) SPECIES: A CASE STUDY FROM INNER WESTERN ANATOLIA
- **NASTASSIA ULUDÜZ** - TYPES OF SKIN MARKINGS IN DELPHINIDAE OF THE ZONGULDAK REGION, SOUTHWESTERN BLACK SEA
- **NERGİS YASAV** - ECOLOGICAL CHARACTERISTICS AND LIFE TRAITS OF TWO HONEYBEE SUBSPECIES (A. M. CAUCASICA AND A. M. SYRIACA)
- **NİSA DALAR** - MAGNETORECEPTION IN BIRDS AND MAMMALS: A COMPARATIVE PERSPECTIVE FROM QUANTUM BIOLOGY
- **NUR FİLİZ** - EFFECTS OF WET AND DRY PERIODS ON LONG TERM PHOSPHORUS AND NITROGEN BUDGETS AND THEIR RELATIONSHIPS WITH LAKE NUTRIENT AND CHLOROPHYLL-A CONCENTRATIONS
- **NURSEMA AKTEPE** - COMPARATIVE ANALYSIS OF LEAF FLAMMABILITY TRAITS IN FOREST AND SHRUBLAND PLANTS OF WESTERN TÜRKİYE
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- **VELİ DENİZ ÜNLÜ** - ETHNOBOTANICAL PROPERTIES OF GÜLAĞAÇ (AKSARAY), GÜZELYURT (AKSARAY), ÇIFTLIK (NIĞDE) AND ALTUNHISAR (NIĞDE) DISTRICTS
- **YAĞMUR ACER** - UNCOVERING SUBTERRANEAN LIFE: A PILOT EDNA-BASED BIODIVERSITY STUDY ACROSS CONTRASTING CAVE HABITATS
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11TH ECOLOGY AND EVOLUTIONARY BIOLOGY SYMPOSUM PROGRAM

POSTER PRESENTATIONS

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SESSION 1: POPULATION GENETICS

Uncovering the diet composition and foraging ecology of *Falco eleonorae* using non-invasive eDNA-based pellet metabarcoding

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Abstract ID: 118
Keywords: Avian Ecology, Diet Analysis, Falco eleonorae, Non-Invasive Monitoring, Pellet DNA, Predator–Prey Interactions, eDNA Metabarcoding, wildlife

Falco eleonorae (Eleonora's Falcon) is a long-distance migratory raptor native to the Mediterranean basin, where it breeds in colonies on coastal cliffs and islands. Although globally listed as "Least Concern" by the IUCN, the species exhibits a scattered and restricted breeding distribution in Türkiye, rendering it locally vulnerable to habitat degradation, anthropogenic disturbance, and climate change. Understanding its dietary ecology is therefore essential for effective conservation planning.

In this study, we employed environmental DNA (eDNA) metabarcoding to non-invasively investigate the diet composition of *F. eleonorae*. Pellets were collected from a suspected breeding site near the Karareis Dam in İzmir Province. DNA was extracted and amplified using six universal primer sets targeting a range of taxonomic groups: vertebrates (12SV5, MiBird, MiFish), insects (16Sins, 16S), and bacteria (16SV3–V4). High throughput sequencing generated approximately 500,000 paired-end reads per sample.

The results revealed a diverse prey profile dominated by aerial insects, particularly from the orders Orthoptera and Odonata, confirming insectivory as the primary foraging strategy even during the breeding season. Occasional detection of bird, amphibian, and fish DNA suggests opportunistic feeding behavior. Microbial signatures from the pellets also provided supporting data on digestive tract-associated bacteria.

Our findings highlight the ecological flexibility of *F. eleonorae* and underscore the importance of preserving minimally disturbed habitats that support insect biodiversity. eDNA-based dietary analysis proves to be an effective, non-invasive tool for monitoring avian trophic ecology in sensitive breeding areas.

Moisture matters more than heat for evolution of reproductive genes in *Drosophila*

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Abstract ID: 9
Keywords: climatic gradients, latitudinal variation, population genetics, reproduction, sexual conflict, sexual selection

Environmental variation shapes reproductive strategies and sexual selection/conflict, yet the role of specific ecological drivers in the molecular evolution of reproductive genes remains underexplored. Using whole-genome population data from 144 *Drosophila melanogaster* populations worldwide, we investigated how climatic factors influence the evolution of seminal fluid proteins (SFPs), key mediators of postcopulatory sexual selection. Crucially, our Bayesian modelling revealed that humidity and precipitation, rather than temperature, are dominant ecological factors that correlate with molecular variation in SFPs. Notably, the Sex Peptide gene - a central player in sexual selection - exhibited πN/πS ratios suggestive of balancing selection, with allele frequencies strongly linked to precipitation and expression-modulating SNPs showing environmental sensitivity. These findings highlight the overlooked role of moisture-related climate factors in shaping sexual selection, conflicts and reproductive gene evolution in an era of accelerating climatic change.

Developing custom SNP panels for rapid and accurate wildlife conservation genetics applications

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Abstract ID: 124
Keywords: , SNP panel, conservation genetics, wildlife management, wolf-dog hybridization

Wildlife conservation research, including hybrid detection and population structure analysis, relies heavily on direct sampling and observation. Methods such as marking, camera trapping, and invasive sampling are time-consuming and labor-intensive, limiting their efficiency for large-scale studies. Rapid and accurate genetic tools offer significant potential to replace these invasive methods and address conservation challenges, such as wolf-dog hybridization, which threatens gray wolf (*Canis lupus*) genetic integrity. To meet this need, we developed two custom SNP panels (12-SNP and 18-SNP) using multiplex PCR and Illumina sequencing, designed for flexible and scalable detection of genetic variation across species. We validated the panels by sequencing genomic DNA from non-invasively collected wolf and dog samples in Polish Carpathians, aligning reads to a combined wolf-dog reference, and analyzing informative loci after quality and depth filtering. Population structure analysis using STRUCTURE clearly distinguished wolves and dogs, with several individuals showing mixed ancestry, confirming the panels' ability to detect potential hybrids. The flexible design of these SNP panels makes them well suited for diverse conservation genetics applications, enabling precise monitoring of genetic diversity and population structure while reducing time and labor compared to traditional methods.

Uncovering hybridization and species boundaries in peripheral populations of the Great Tit (*Parus major*) using high-resolution genomics

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Abstract ID: 20
Keywords: hybrid zone, introgression, range margins., reproductive isolation, speciation

Hybrid zones at range margins offer unique opportunities to investigate how genetic novelties emerge and persist over evolutionary timescales. Peripheral populations often experience distinct selective pressures and increased genetic drift, facilitating the formation of novel genetic combinations through hybridization—combinations that may drive local adaptation or even the origin of new taxa. In the *Parus major* species complex, which includes four phylogenetic lineages across Eurasia (*bokharensis*, *cinereous*, *minor*, and *major*), secondary contact has occurred since the Pleistocene, resulting in several zones of hybridization. We focus on a proposed three-species contact zone in northeastern Iran involving *bokharensis*, *cinereous*, and *major*, with particular attention to the hypothesized hybrid origin of *Parus major intermedius*. Using high-resolution genomic data, we find evidence of recent introgression between *intermedius* and *bokharensis*; however, *P. m. intermedius* does not conform to the classical definition of a hybrid species. Instead, it displays unique genetic signatures that point to a complex demographic history. Mitochondrial haplotype networks and phylogenetic tree analyses reveal that *P. m. intermedius* is genetically distinct from central European populations. Moreover, its low mitochondrial diversity and high genetic differentiation suggest that it represents a peripheral population. We also detect ongoing gene flow within the contact zone: *bokharensis* individuals exhibit introgression from *major*, while European *major* populations retain signatures of ongoing introgression from *intermedius*. These introgressed genotypes contribute to the genetic diversity of the *Parus major* complex and may serve as a reservoir for adaptive potential. Our findings shed light on the intricate dynamics of hybridization and introgression, offering valuable insights into speciation and the genetic architecture of species boundaries shaped by both ancient and ongoing evolutionary processes.

Why sex-based genomic differentiation should not be overlooked in population genetics

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Abstract ID: 33
Keywords: SNP-based analysis, W chromosome, Z chromosome, evolutionary genomics, genomic variation, local adaptation, population genetics, reference genome, sex-based differentiation, sex-biased selection

Sex-specific genomic differentiation is a crucial yet frequently overlooked factor in population genetics, significantly influencing interpretations of local adaptation. In this study, we leverage the substantial genomic resources available for the great tit (\textit{Parus major}), including population-scale datasets from many European populations, to investigate genomic differentiation between males and females. Unlike in some other species, where high-quality genome assemblies exist but broad population sampling is lacking, the great tit offers a unique opportunity to study sex-based differentiation at both the genomic and population level. We identify significant differentiation at an autosomal locus on chromosome 5, which we hypothesize originates from sex-linked variation present on the sex chromosomes (Z and potentially W). By referencing genomic data from other songbirds with well-assembled sex chromosomes, we illustrate how autosomal loci may exhibit high sequence similarity to sex-linked regions. Our analyses demonstrate that uneven sex ratios in sampled populations can substantially bias differentiation metrics (e.g., FST), potentially resulting in false-positive interpretations of adaptive differentiation. To mitigate such issues, we stress the importance of sex-aware study designs, including balanced sex sampling and explicitly incorporating sex as a covariate. Furthermore, while optimal study designs would include high-quality reference genomes from both sexes, we recommend, as a pragmatic and cost-effective alternative for labs with limited resources, generating a reference genome from the heterogametic sex (females in birds) to ensure both sex chromosomes are represented in mapping and analysis. Finally, we emphasize the need for rigorous validation of candidate loci to ensure accurate and biologically meaningful outcomes in evolutionary genomic studies.

SESSION 2: POPULATION ECOLOGY

Molecular approaches for conservation: eDNA and metabarcoding insights into the Striped Hyena population in Türkiye

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Abstract ID: 121
Keywords: Conservation Biology, Diet Analysis, Hyaena hyaena, Microbiome, Wildlife, eDNA metabarcoding

Hyaena hyaena (striped hyena) is an ecologically significant scavenger species distributed across Africa and Asia. Although historically present in Türkiye, its current population status remains poorly understood due to limited research and increasing anthropogenic pressures. "The Anatolian Beast: Striped Hyena Project" employs non-invasive environmental DNA (eDNA) and metabarcoding methods to investigate the biology, diet, and microbiota of *H. hyaena* in arid and semi-arid regions of Türkiye, aiming to support conservation planning through molecular ecological data.

Fecal samples were collected across all four seasons from three distinct regions and analyzed using multi-marker metabarcoding to reconstruct dietary profiles and characterize microbial communities. Results revealed a predominantly scavenger-based diet, including DNA from *Canis lupus*, *Vulpes vulpes*, *Gallus gallus*, *Bos taurus*, and *Ovis aries*. Microbiota profiling identified immune-associated bacterial taxa such as *Blautia hominis*, *Blautia glucerasea*, *Acinetobacter beijerinckii*, and *A. kyonggiensis*, suggesting links between diet, environmental exposure, and host health.

This study is among the first to apply non-invasive molecular approaches to assess the health and ecological interactions of *Hyena hyaena* in Türkiye. It contributes critical baseline data for national conservation strategies targeting this elusive and threatened scavenger.

Genetic diversity patterns in phenological traits of *Quercus robur L*.

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Abstract ID: 26
Keywords: Quercus robur L., adaptive traits, climate chang, genetic variation, phenology, plasticity

Oaks are among the most adaptable temperate tree species, and this makes them especially valuable in the context of climate change. Phenological traits such as bud burst and bud set are critical indicators of a tree's response to climatic conditions and have important implications in local adaptation. This study investigates genetic variation in bud phenology—specifically the timing of bud burst and bud set, as well as growing season length (GSL)—in *Quercus robur* L. (pedunculate oak) saplings from different populations and mother trees across four different countries in Central Europe. We examined how much of the observed variation could be attributed to population-level differences versus among mother trees within populations through a common garden experiment and nested ANOVA models. Our findings reveal significant mother tree effects on most of the phenological traits studied, while the effects of population were only significant for terminal bud burst. Lateral phenological traits exhibited weak differentiation among populations and minimal mother tree influence, indicating that they are less affected by inherited genetic differences and more responsive to local environmental variation. This trend could be a consequence of greater phenotypic plasticity in lateral shoots that might allow individual saplings to adjust their growth according to microclimatic variation. These results show how complex phenological adaptation is and how both genetic and environmental factors must be included in when evaluating trait variability and resilience under climate change. It seems that phenotypic plasticity regarding phenological traits is important factor for oak trees to adapt to uncertain environmental conditions.

Ecological characteristics and life traits of two honeybee subspecies (*A. m. caucasica* and *A. m. syriaca*)

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Abstract ID: 52
Keywords: Apis mellifera caucasica, Apis mellifera syriaca, colony development, honeybee, life traits

Honeybees are essential pollinators, valued for both their ecological and economic roles. During plant visits, they contribute to pollination; the collected nectar is used for honey production, while pollen serves as a protein source for brood development. Turkey, the world's third-largest honey producer, hosts five native subspecies, including *Apis mellifera caucasica* and *A. m. syriaca*. These two subspecies differ in geographical range, as well as in behavioral and morphological traits, reflecting adaptations to local climates, floral resources, and environmental threats. We aim to compare the ecological traits of *A. m. caucasica* and *A. m. syriaca* using a common garden experiment at the METU campus apiary. Five colonies from each subspecies were monitored from March to October 2024 to assess colony development, brood production, foraging activity, and defensive behavior. The number of total and capped brood frames are recorded weekly to investigate the colony development. Foraging activity is quantified by counting the number of forager bees, weighing the pollen and annual honey yield. Lastly, the defensive behavior is evaluated by disturbing the colony and recording the number of stings in a piece of suede leather. Results indicate that *A. m. caucasica* invested less in colony development but produced significantly more honey (19.6±4.5 kg) compared to *A. m. syriaca* (3.78±0.72 kg), despite the same floral access. This may be correlated with the fact that Syrian bees are native to scarcer and more ephemeral flora. Additionally, *A. m. syriaca* displayed significantly higher aggression, with four times more stings on average than *A. m. caucasica* during the spring—consistent with previous studies linking defensive behavior of this subspecies to protect limited resources from predators and parasites. Our results show how two honeybee subspecies differ in reproduction, survival, and honey production as they have evolved under different environments, floral composition, and threat levels.

Trojan fir under climate warming: A facilitator species facing regeneration limits

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Abstract ID: 61
Keywords: Abies, Trojan fir, climate change, facilitation, germination, seedling establishment, seedling growth, temperature

Trojan fir (*Abies nordmanniana* subsp. *equi-trojani*) is a coniferous tree endemic to northwestern Anatolia (Türkiye), restricted to high mountain ranges and increasingly threatened by perturbations like mining, intensive forestry, and climate change. Despite these threats, its demographic responses, especially at early life stages, remain poorly understood, limiting effective conservation planning.

We investigated germination and seedling growth under five constant (10°C to 30°C) and two alternating (15/25°C and 20/30°C) temperature regimes, with and without cold stratification treatment (4°C, 35 days). We also explored adult-seedling relationships in Trojan fir and accompanying tree species through fieldwork and recruitment network analysis across six sites in the Kazdağları region, western Anatolia.

Our results showed that without stratification — simulating the absence of winter — germination increased with temperature, while stratification significantly improved germination at nearly all temperatures. In contrast to germination patterns, seedling survival declined sharply at higher temperatures especially at 30°C suggesting divergent seed and seedling responses indicate a climate-induced demographic bottleneck: warming- enhanced germination may not translate into successful establishment.

Recruitment network modeling revealed that in most sites, adult Trojan firs facilitate recruitment of other species' seedlings more than their own; while other species (e.g. *Castanea sativa*, *Quercus petraea*) negatively affect other species' seedlings. These patterns suggest Trojan fir may serve as a key structural species in the region's mixed forests, contributing to broader forest diversity.

Our findings highlight the ecological importance and climate sensitivity of Trojan fir, emphasizing the need for conservation measures addressing its life-stage-specific vulnerabilities. Protecting this species is vital not only for its survival but also for maintaining ecological balance and resilience in the unique mountain forest ecosystems it anchors.

SESSION 3: AQUATIC ECOLOGY

Variation in aquatic food webs along the longitudinal gradient of a Southern Anatolian coastal river

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Abstract ID: 11
Keywords: Aksu river, fish, fluvial systems, land use, river continuum, stable isotope

According to the River Continuum Concept, the availability of food and predatr-prey relationships are expected to change along the longitudinal gradient of river sytems. In these systems, understanding the transfer of energy that supports consumers is of great importance for ecosystem conservation. In this study, we analyzed the carbon an nitrogen stable isotope ratios of basal carbon sources, and assemblages of invertebate, and fish (consumers) along the longitudinal gradient of the Aksu Stream (Antalya) t examine the aquatic food web structure and evaluate how the flow of energy and atter varies among food webs. Furthermore, our study area provided a unique opportunity to test whether the δ^{15}N values of producer and consumer assemblages in the Aksu Stream, hich is under intense land use pressure, particularly in the middle and lower basins, reflect watershed impacts. Overall, the isotopic ratios of basal carbon sources and consumer assemblages varied significantly among sites, with high parallelism identified between the isotopic patterns of the sources and those of the consumers. As expected, the δ^{15}N values of basal sources and consumers in areas under intense land use pressure were higher compared to values from other areas. Assimilation of material derived from in-stream sources was greater for invertebrates and fish assemblages along the downstream gradient of the river. However, in the middle reaches of the river, invertebrates were primarily supported by allochthonous production sources, whereas, conversely, the importance of autochthonous sources increased for fishes. In the reservoir, seston was the main source, while detritus dominates in the tributary. The findings are generally consistent with the predictions of the River Continuum Concept; however, the presence of the impoundment disrupts the natural gradient of the river, and the food webs reflect the impact of land use in the stream system.

Unspoken dynamics of sperm whales (*Physeter macrocephalus*) in the Eastern Mediterranean Sea of Türkiye: Group structure, spatial-temporal distribution and body length

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Abstract ID: 7
Keywords: Deep diving cetaceans, group structure, marine mammals, social behaviour

Sperm whales have been assessed as endangered with an estimation of around 200 individuals in the Eastern Mediterranean. Although they showed residential patterns, sperm whales remain unspoken in the Eastern Mediterranean. Visual and acoustic data were collected using a sailing boat between 14th April, 2018, and 3rd August, 2024 in the Eastern Mediterranean Sea of Türkiye. A total of 222 days were spent at sea, covering 19 seasons. Sperm whales were encountered on 69 occasions. The species were predominantly observed between the easternmost extension of Rhodes Basin, Finike Canyon, and Antalya Canyon, with no records further east. Seasonal patterns were evident, with the highest visual encounters occurring in summer, followed by spring. No visual encounters were recorded in winter. However, winter and autumn still recorded four detections each, suggesting year-round sperm whale presence in the region. Group composition analysis revealed that social units were the most frequently observed, followed by solitary males and bachelor groups. Mean group size holds three individuals (SE = 0.6 ind), while the largest aggregation recorded consisted of 17 individuals, including social units and mature males. Interpulse interval (IPI) analysis estimated a mean body length of 9.5 m (SD = 1.4 m), ranging from 7.7 m to 12.73 m. Social units had a mean length of 8.98 m, while bachelor groups and solitary males measured 10.2 m and 12.1 m, respectively. No large bulls were recorded.. This study suggest the presence of foraging, nursing, and potential breeding habitats in the Eastern Mediterranean Sea of Türkiye and highlights small group sizes, smaller body sizes, and varied group structures within a concentrated area, with a notable emphasis on summer distribution and occasional large aggregations, providing critical baseline data for contributing to the global understanding.

The effects of salinity and heatwave on zooplankton community structures, diversity and resource use efficiency: Synchronized mesocosm experiments, Türkiye

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Abstract ID: 88
Keywords: heatwave, mesocosm, salinization, zooplankton

Zooplankton are integral components of aquatic food webs, playing key roles in energy transfer, nutrient cycling, and overall ecosystem stability. In the context of global climate change, freshwater salinization and increased frequency of heatwaves emerged as pervasive stressors,and those are mainly driven by anthropogenic activities such as urban runoff, agricultural irrigation, and industrial discharges. These change the ionic composition of water bodies and intensify thermal stress, potentially pushing aquatic organisms beyond their physiological limits. To investigate the individual a nd combined impacts of these stressors on zooplankton communities, we conducted syncronized mesocosm experiments in two climatically distinct regions of Türkiye: Ankara, chracterized by cooler conditions, Mersin, known for warmer ambient temperatures. I each site, 16 mesocosms were deployed and assigned to a factorial design comprising two salinity treatments—4 ppt representing low salinity conditions and 40 ppt represeting high salinity conditions—and a simulated heatwave treatment that raised the temperture by 6 °C above the ambient temperature. This experimental approach allowed u to compare the effects of salinity and thermal stress under regional climates. Results indicate that elevated salinity is the dominant driver of community shifts. In high-saliniy mesocosms, zooplankton communities became increasingly dominated by small, salt-tolerant rotifers, whereas cladocerans and copepods prevailed under ambient salinity condiions. The application of a heatwave further exacerbated these patterns, leading to a significant reduction in species richness and average body size. These effects were partiularly pronounced in the warmer Mersin site

where the combined ionic and thermal stresses more limited the range of species able to persist. These findings suggest that as climate change continues to drive freshwater salinization and the frequency of extreme thermal events, the combined pressures will induce further alterations in zooplankton community structure and size dynamics with clear differences emerging across climatic regions.

Salinity-induced shifts in zooplankton communities: Insights from a gradient-based mesocosm study

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Abstract ID: 67
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Keywords: Biodiversity, Community structure, Functional diversity, Zooplankton

Freshwater ecosystems are increasingly threatened by salinization driven by climate change and anthropogenic pressures such as water abstraction. These changes can affect ecosystem functioning, processes, and biodiversity. To better understand these impacts, we conducted a salinization mesocosm experiment at METU Mesocosm System II, Ankara, Turkey from September 2021 to May 2022. Our study focuses on how zooplankton communities respond to increasing salinity.

We implemented a salinity gradient with 16 different salinities, from 0.5 to 50 g/L. Each mesocosm contained 30 cm of natural sediment mixed with washed sand and was filled to a 120 cm water column. Mesocosms were inoculated with plankton, fish, and macrophytes

sourced from both freshwater and brackish lakes with varying salinities. Salinity was manipulated using sodium chloride and sodium sulfate. The experiment had three phases: a one-month salinization phase with gradual increases to target salinities, a five-month stable phase, and a two-month desalinization phase.

This study focuses on the salinization and stable periods to evaluate changes in zooplankton community structure and biodiversity. Preliminary results show that increasing salinity results in pronounced declines in zooplankton richness, biomass, body size, and resource use efficiency (RUE). Functional diversity is also expected to decrease. These responses are nonlinear, with threshold effects observed around 12 g/L salinity potentially caused by the absence of fish at higher salinities, altering trophic interactions.

Our findings highlight the vulnerability of zooplankton communities to salinization and underline the broader ecological risks caused by climate change and water management practices. By identifying community-level tipping points, this research contributes to a deeper understanding of resilience and regime shifts in freshwater ecosystems facing salinization under future global change scenarios.

SESSION 4: FLASH TALKS

The Mini yet mighty stapes: A superior DNA source than the cochlear powder

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Abstract ID: 57
Keywords: ancient Anatolia, ancient DNA, auditory ossicles, paleogenomics, petrous, stapes

Ancient DNA (aDNA) studies provide critical information about demographic history. The petrous bone —specifically the otic capsule— is widely regarded as the most reliable aDNA source due to its compact structure, high density of osteocytes, and early ossification with minimal remodelling. However, sampling of petrous bone results in the irreversible loss of valuable bioarchaeological information. This limitation has led researchers to explore alternative skeletal elements for aDNA retrieval, triggering a broad search for viable substitutes. Among several candidates (e.g., teeth, calcaneus, talus, femur), the auditory ossicles —stapes, malleus, and incus— have recently emerged as promising alternatives despite their small sizes and limited availability. However, the aDNA yield of ossicles has not been systematically tested, and existing studies remain limited in both sample size and scope.

In this study, we investigated 29 individuals from ancient Anatolia (9000—300 BP). We prepared double-stranded DNA libraries (n=61) for each individual from petrous and non-petrous bones. To test the efficiency of ossicle bones against tooth and petrous bones, we compared key sequencing metrics: i) endogenous human DNA content, ii) modern human contamination estimates, and iii) post-mortem damage indicators (cytosine deamination rates and average fragment lengths). Overall, ossicle libraries yielded significantly higher nuclear ($p=0.002$) and mitochondrial ($p=0.011$) human DNA content than petrous and tooth libraries. Although ossicle libraries also showed lower fragmentation, less post-mortem damage, and reduced modern human contamination, these differences were not statistically significant. Notably, most ossicle libraries originated from the stapes and incus, outperformed other sources across most metrics. The malleus produced results comparable to the petrous bone, while teeth consistently yielded the lowest-quality data.

These findings support the stapes and incus as efficient alternatives to the petrous bone for aDNA studies and highlight the potential of auditory ossicles in future paleogenomic research.

The role of soil microbiota in ecosystem health and sustainable tea cultivation: Insights from eDNA and metagenomic approaches

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Abstract ID: 104
Keywords: Ecosystem function, Metagenomics, Microbial diversity, Soil microbiota, Sustainable agriculture, Tea agroecosystem, eDNA

Soil microbiota are foundational to ecosystem functioning, driving nutrient cycling, organic matter decomposition, and plant-microbe interactions that support soil resilience and health. In tea agroecosystems, preserving microbial diversity is essential not only for sustainable crop production but also for maintaining long-term ecological balance. This study investigates the composition and functional potential of microbial communities in tea- cultivated soils using environmental DNA (eDNA) metabarcoding and metagenomic techniques.

These molecular tools allow for culture-independent profiling of microbial taxa and their ecological roles across diverse soil environments. Our results revealed that Firmicutes, Proteobacteria, Actinobacteriota, Acidobacteriota, and Chloroflexi were the dominant phyla in tea soils. Seasonal comparisons showed that winter soils had significantly higher relative abundances of Proteobacteria and Actinobacteriota compared to summer samples, indicating temporal shifts in community structure. These changes reflect microbial responses to environmental conditions and possibly management practices.

By focusing on native microbial assemblages, we demonstrate how local microbiota contribute to the stability, resistance, and recovery of soil systems under environmental stress. The data underscore the ecological value of integrating microbial diversity into land management strategies, particularly in regions where sustainable agriculture is critical. This work contributes to a broader understanding of how belowground biodiversity supports aboveground productivity and resilience in cultivated ecosystems.

Community composition and resistance levels of soil Bacteria and Fungi in a Mediterranean forest under varying wildfire severities

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Abstract ID: 120
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Keywords: Bacterial and fungal diversity, Fire prone ecosystems, Microbial resistance, Soil microbiome, Wildfire, eDNA metabarcoding

Soil microbial communities, particularly bacteria and fungi, play essential roles in nutrient cycling, plant interactions, and post-disturbance ecosystem recovery. However, our understanding of how these communities respond to wildfires remains limited, especially under different fire severity levels. This knowledge gap is critical in fire-prone Mediterranean ecosystems, where rising temperatures and prolonged droughts are increasing the frequency and severity of wildfires. Given the central ecological functions of belowground microbes and the growing need to understand their dynamics under global change, we investigated the impacts of wildfire severity on soil microbial diversity, composition, and resistance. This study was conducted in a Mediterranean forest in Western Anatolia, Türkiye, following a large wildfire event in August 2023. We selected unburned, moderately burned, and severely burned sites based on satellite imagery and field indicators. From each site, soil samples were collected at two depths (0–5 cm and 5–10 cm), totaling 180 samples. DNA was extracted, and high-throughput sequencing targeting the bacterial 16S rRNA (V3) and fungal ITS2 regions was performed. Using eDNA metabarcoding, we assessed microbial alpha, beta, and gamma diversity, community composition, and taxon-specific resistance indices. Differences were found in microbial diversity and community composition depending on wildfire severity and soil depth. These results suggest that fire severity plays a significant role in shaping belowground microbial assemblages, with implications for post-fire soil recovery and ecosystem functioning. The study underscores the importance of considering both fire intensity and soil depth in microbial ecology and highlights the value of eDNA metabarcoding as a tool for monitoring

biodiversity in fire-affected ecosystems. Understanding these responses is crucial for developing effective ecosystem restoration strategies in Mediterranean regions increasingly threatened by severe and frequent wildfires.

Unraveling Roman mobility: Archaeogenomic insights from Asia Minor to the Italian Peninsula

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Abstract ID: 63
Keywords: Roman Empire, ancient DNA, human mobility, population genetics

The Roman Empire, one of the largest state entities of the ancient world, spanned three continents surrounding the Mediterranean Sea for nearly 1,000 years. As it expanded, the Empire connected distant populations through trade, migration, and military service. These significantly influenced the demographic structures of local populations. The establishment and decline of the Roman Empire have been well-documented in political and cultural as well as population history for most parts of the Western Mediterranean. However, there has been little focus on the possible demographic transition in Anatolia following its occupation.

This study addresses this gap by investigating patterns of intra- and inter-regional mobility in Anatolia during the Roman Era. We co-analyzed previously published ancient genomes from western and eastern wings of the Empire alongside newly generated individuals from Anatolia. Our demographic analyses—including PCA, qpAdm, and f-statistics—indicate that the Anatolian gene pool remained largely stable throughout the Roman period, despite extensive cultural and economic integration with Western Eurasia. In contrast, the genetic profile of Central Italy shows a marked shift following the onset of the Imperial period.

Additionally, f-statistics revealed a rise in genetic diversity within Anatolia that was not captured by PCA or qpAdm analyses. These findings suggest that while Anatolia did not experience a major demographic transformation comparable to that of Central Italy, it was not entirely isolated. The region may have experienced small-scale migration events from neighboring areas such as the Caucasus, the Levant, or Europe. Alternatively, it is possible that gene flow occurred from Central Italy—where individuals had admixed with Eastern populations—yet these events did not result in a detectable shift in the Anatolian gene pool.

Integrated analysis of reproduction and regeneration in colonial ascidians

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Abstract ID: 22
Keywords: adaptation, development, gene expression, regeneration

Colonial ascidians stand out among invertebrates for their capacity to regenerate entire bodies from small tissue fragments and to reproduce both sexually and asexually. Their close evolutionary relationship to vertebrates makes them valuable models for exploring fundamental biological processes such as regeneration, reproduction, and environmental adaptation. These features provide insight into how organisms respond to environmental stress while maintaining growth and reproductive capacity.

This integrative study investigates two Mediterranean colonial ascidians, Botryllus humilis and Botrylloides niger, using ecological, cellular, histological, and molecular approaches to understand how these organisms coordinate asexual reproduction, whole-body regeneration (WBR), and environmental responses. Experimental exposure to varying salinity and temperature levels, in both aquaculture systems and natural habitats, revealed species- specific environmental preferences and adaptive strategies, indicating distinct ecological niches and potential mechanisms for coexistence.

Cellular and histological analyses provided a detailed characterization of the blastogenic cycle and regenerative processes. Ten distinct hemolymph cell types were identified, and dynamic changes in these cells were observed during both blastogenesis and regeneration. Immunohistochemical staining revealed expression of markers such as Piwi, PL10, and cadherin, linked to progenitor cell maintenance, differentiation, and tissue remodeling. Notable differences between the species were observed, including faster regeneration and higher hemoblast activity in B. humilis.

At the molecular level, transcriptomic analyses in B. humilis identified key genes and pathways involved at different stages of regeneration. These included stress response, cytoskeletal reorganization, apoptosis, and cell differentiation, as well as signaling pathways such as Wnt, Notch, and TGF-β.

Together, the findings highlight the intricate balance between regeneration, reproduction, and environmental adaptability in colonial ascidians, and contribute to a broader understanding of stress resilience, evolutionary strategies, and the molecular basis of regeneration in early chordates.

Global ecological niche modelling for the Bimaculated Lark (*Melanocorypha bimaculate*) breeding habitats and prediction of its distribution under current and future climate scenarios

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Abstract ID: 107
Keywords: Bimaculated Lark, Climate Change, Ecological Niche Modelling, SDM, Steppe Birds

Understanding how global climate change affects habitat suitability is essential for conserving habitat specialist species. This study focuses on modeling the bioclimatic niche of the Bimaculated Lark (Melanocorypha bimaculata), a key indicator species of steppe ecosystems, using ecological niche models (ENMs) under both current and projected future climate conditions. Species occurrence records were primarily obtained from the Global Biodiversity Information Facility (GBIF) and supplemented with regional datasets. Bioclimatic predictors were selected from the CHELSA Bioclim+ dataset, emphasizing ecologically relevant variables such as temperature extremes and precipitation patterns during the breeding season. After multicollinearity analysis, a reduced set of uncorrelated variables was retained for model calibration. The accessible area (M) was defined based on significant biogeographical barriers. Five algorithms (GLM, GAM, RF, Maxent, MaxNet) were used to build the models, which were evaluated through cross-validation and AUC metrics. Preliminary results indicate that climatically suitable breeding habitats are primarily concentrated in Central Asia, Asia Minor, and parts of the Middle East. However, future projections under various climate scenarios suggest considerable habitat contraction up to 40% and shifts to the north. According to variable importance tests, BIO14 (Precipitation of Driest Month) and BIO15 (Precipitation Seasonality) are the most prominent bioclimatic variables. All models have high statistical accuracy ($AUC > 0.9$). Regions predicted as suitable but outside the known breeding range, such as Spain and North-West Africa, are discussed in the context of interspecific competition. We hope that these findings provide insights into the sensitivity of steppe specialist species to climate change and offer a framework for understanding potential impacts on steppe birds at a global scale.

Discovery of two novel Partitiviruses infecting the Saxicolous Lichen *Calogaya decipiens*

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Abstract ID: 54
Keywords: Partitiviridae, dsRNA, lichens, whole genome

Lichen-associated mycoviruses represent a poorly characterised component of the fungal virome, with only a few studies addressing their diversity, ecological roles, and evolutionary placement. Mycoviruses associated with lichens remain poorly characterized. Given their ecological significance, metabolic complexity, and multi-partner structure, uncovering the viral associations of lichens is crucial for understanding hidden dimensions of fungal virus ecology and symbiosis-driven evolution. In this study, we characterised the complete genome sequences of two novel bisegmented partitiviruses infecting *Calogaya decipiens* (Arnold) Arup, Frödén & Søchting, a saxicolous lichen species from the family Teloschistaceae. Samples were collected from the Ankara University 10th Year Campus and subjected to high-throughput sequencing (HTS) and RNA ligase-mediated rapid amplification of cDNA ends (RLM-RACE) to reconstruct full-length viral genomes. The identified viruses, named Calogaya decipiens partitivirus 1 (CdPV1) and Calogaya decipiens partitivirus 2 (CdPV2), showed 77.59% and 86.02% amino acid identity in their RNA- dependent RNA polymerase (RdRp) regions to Xiaogan partiti-like virus 1 and Lichen partiti- like RNA virus sp., respectively, according to BLASTp analysis. Phylogenetic analyses placed CdPV1 within the alphapartitivirus clade and CdPV2 within the betapartitivirus clade. Both RdRp sequences retain the conserved A, B, and C motifs and the catalytic palm-domain GDD motif characteristic of *Partitiviridae*. This is the first report of viruses infecting *C. decipiens*, expanding the current database of lichen-associated viral genomes. Our findings provide new insights into partitivirus diversity in symbiotic fungi and offer a reference point for future studies targeting the viromes of lichen holobionts. Whether these viruses are restricted to the fungal partner or also interact with algal or bacterial symbionts remains an open question.

Explaining Brassicaceae species richness patterns in Türkiye using spatial statistical models

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Abstract ID: 103
Keywords: Biodiversity patterns, Brassicaceae, spatial autocorrelation, spatial statistical models, species richness, topographic heterogeneity

Understanding biodiversity patterns requires models that incorporate both environmental and spatial components. This study presents the first comprehensive analysis of species richness at a national scale in Türkiye for a major angiosperm family, integrating a broad suite of spatial statistical models. We examined species richness of the Brassicaceae across Türkiye using a 50 × 50 km grid. Richness data were compiled over 1.5 years through an exhaustive review of herbarium records and literature. To explain richness patterns, we considered environmental predictors representing bioclimate, paleoclimatic stability, productivity, drought, and topographic heterogeneity. Ordinary Least Squares (OLS), Spatial Autoregressive (SAR), Spatial Error (SEM), and Spatial Autoregressive Combined (SAC) models were fitted across predictor sets (defined using Variance Inflation Factor, VIF) and multiple neighborhood structures based on K-nearest neighbors. Model performance was evaluated using the Akaike Information Criterion, and spatial autocorrelation in residuals was tested using Moran's I. Spatially varying relationships between richness and predictors were further examined using Geographically Weighted Regression (GWR), revealing locally distinct biodiversity drivers. The best-performing model was significant ($p < 0.05$), with residuals showing no spatial autocorrelation ($p > 0.05$), indicating that spatial structure was effectively captured. Topographic heterogeneity emerged as the strongest predictor of richness ($p < 0.05$). The explanatory power of GWR varied across the study area, underscoring that environmental drivers of richness are not spatially uniform. Variance partitioning showed that predictors explained a meaningful portion of the variation in richness. Partial Redundancy Analysis confirmed the robustness of predictors after accounting for spatial structure ($p < 0.05$), while pure spatial effects were negligible and non-significant ($p > 0.05$). Collectively, these findings highlight the importance of environmental filtering in shaping Brassicaceae richness in Türkiye, as well as the critical value of spatial statistical models in macroecological studies.

The response of the life history traits of *Daphnia magna* to the deteriorating temperatures

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Abstract ID: 64
Keywords: Temperature Deterioration Global warming adaptation Daphnia magna

The adverse anthropogenic impacts on the Biosphere have produced environmental change at a rate unprecedented in the Cenozoic, shifting the environmental conditions outside of the physiological tolerance range of many species. Predicting the patterns of species' response to climate change requires tracking the variation in fitness-related traits (i.e. life histories) during exposure to thermally changing environments, because these traits may strongly correlate with the probability of survival.

A growing body of experimental studies demonstrated that an increase of mean temperatures significantly influences the response of several life history traits, namely reduction of development time and body size at maturation. However, there are still significant gaps in our understanding of how species respond to temperature change, as 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. Moreover, 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.

To investigate evolution under deteriorating thermal environments, respectively, we carry out the two experiments with a plankton crustacean, *Daphnia magna.* We subjected the clonal populations to a regime with continuous increase of temperature in regular intervals. To provide insight into the underlying mechanisms of the change of life history traits, the experimental populations are monitored in a series of reciprocal transplant experiments by measuring five life history traits.

After 30 generations of selection, we detected a significant clone-by-treatment interaction underlying the response of most life history traits monitored. Our results indicate significant genetic basis as potential for the adaptation to the global warming related changes of thermal regimes.

Diversity yynamics of airborne plant communities revealed by eDNAir

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Abstract ID: 113
Keywords: Airborne eDNA (eDNAir), Environmental DNA, High-Throughput Sequencing, ITS2, Metabarcoding, Phenology, Plant Biodiversity

Plant communities are foundational to the structure and function of terrestrial ecosystems. As such, accurate and efficient monitoring of plant biodiversity is essential for conservation and ecosystem management. Traditional observation-based methods, however, are often limited by logistical constraints, particularly over large spatial and temporal scales. This study presents an innovative approach to plant biodiversity assessment using airborne environmental DNA (eDNAir)—a novel application of eDNA techniques that enables the capture and identification of plant genetic material directly from the air.

Between June and September, a total of 13 air samples were systematically collected and analyzed. DNA was extracted and amplified using primers targeting the plant-specific ITS2 barcode region, followed by high-throughput sequencing on the Illumina NovaSeq6000 platform. Taxonomic assignments were conducted using a hybrid reference strategy, combining NCBI databases and a custom-curated local plant barcode database.

The results revealed temporal variation in airborne plant diversity, with July exhibiting the highest taxonomic richness—likely reflecting phenological shifts and seasonal changes in vegetation. Dominant taxa across samples included *Populus nigra*, *Salix babylonica*, and *Quercus petraea*. The clear differentiation between sampling periods highlights the capacity of eDNAir to detect dynamic biodiversity patterns over time.

This study underscores the power of eDNAir as a sensitive, rapid, and non-invasive tool for terrestrial biodiversity monitoring. Its application can significantly enhance temporal resolution and spatial coverage in ecological studies, offering a scalable and cost-effective complement to traditional plant survey methods.

Biodiversity hotspots at risk: Projections of climate change impacts across ecoregions

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Abstract ID: 78
Keywords: Biodiversity Hotspots, Ecoregions, Key Biodiversity Areas, Protected Areas, Velocity of Climate Change

Anthropogenic climate change significantly threatens biodiversity by shifting species distribution and assemblages. These climatic shifts can outpace species' ability to adapt or migrate, disrupting ecosystem structure and function. Anticipating where such changes will occur is key to guiding climate-smart conservation planning. Here, we examine climate change vulnerability of the Mediterranean Basin, the Caucasus, and the Irano-Anatolian biodiversity hotspots. Using the velocity of climate change approach, we calculated forward and backward velocities under the worst-case emission scenario by the end of this century. Additionally, we analyzed potential climate-related changes across 38 ecoregions within the biodiversity hotspots, focusing on key biodiversity areas and protected areas, which are critical for biodiversity conservation. We found that forward velocities are generally higher in key biodiversity areas and protected areas, while backward velocities tend to be lower in these regions. Nearly 80 percent of the ecoregions show higher forward and lower backward velocities in key biodiversity areas and protected areas. Forward velocity is highest in the Mediterranean High Atlas Juniper Steppe ecoregion and lowest in the Cyprus Mediterranean forests ecoregion. Similarly, backward velocity is highest in the Crimean Submediterranean forest complex and lowest in the Corsican montane broadleaf and mixed forests. High forward velocities indicate greater exposure to climate change, suggesting that species in these ecoregions will need to migrate longer distances to track their suitable climatic niches. In contrast, lower backward velocities highlight the potential of these areas to serve as colonization habitats for species migrating from nearby regions. This study supports Sustainable Development Goal 15: Life on Land, and the Kunming-Montreal Global Biodiversity Framework, Target 3, aiming to conserve 30% of key terrestrial areas for biodiversity. This study is funded by the Istanbul Technical University Scientific Research Projects Coordination Unit (Project Number: TGA-2023-43945).

SESSION 5: ANCIENT DNA & PALEOBIOLOGY

Out-of-Anatolia migrations during the neolithization of Western Eurasia

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Abstract ID: 125
Keywords: Anatolia, Neolithic, ancient DNA

Western Anatolia was a key centre in the Neolithization of Western Eurasia, serving as a bridge for spreading farming and social innovations from the Fertile Crescent into Europe. Using 30 new palaeogenomes from Anatolia (c. 8000–6000 BCE), we trace the genetic and cultural dynamics of Neolithization. Our analysis reveals genetic continuity from late Upper Pleistocene hunter-gatherers in the region, together with significant admixture with incoming populations from Central Anatolia. This admixture contributed to the formation of populations that later played a role in the Neolithic expansion into Southeast Europe. We further co-analyze genetic and cultural similarities across Southwest Asia and the Aegean villages using 58 material cultural traits. While material culture exhibits notable diversity among Aegean Early Neolithic communities, this diversity does not correlate with genetic differences, highlighting a decoupling of cultural and genetic dynamics. The absence of a correlation between genetic and cultural distances suggests that sociocultural affinity patterns may have changed at a different speed and following different processes when compared to the genetic affinities captured by ancient DNA data.

Late Quaternary fossil rodent assemblages from the Middle Awash study area, Afar Rift, Ethiopia

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Abstract ID: 62
Keywords: Afar, Ethiopia, Evolution, Fossils, Quaternary, Rodentia

The Afar Depression in eastern Ethiopia is a region of major biogeographic and paleontological significance due to its unique geological and paleoanthropological history. This study presents newly recovered fossil rodent assemblages from the Late Pleistocene deposits of the Faro Daba and Chai Baro Beds of Halibee Member of the Dawaitoli Formation in the Middle Awash research area of Ethiopia. The assemblages range between 100,000 and >155,000 years ago—a time period with scarce fossil records in eastern Africa. The studied assemblages comprise 1,150 cranial and dental specimens and include representatives of *Thryonomys*, *Tachyoryctes*, *Hystrix*, *Heterocephalus*, *Arvicanthis*, *Acomys*, *Mastomys*, and *Gerbilliscus*. Notably, *Thryonomys* and *Tachyoryctes* are not found in the Afar lowlands today, and the timing and causes of their local disappearance over the past 100,000 years remain unclear. Comparative biogeographic analysis suggests that although the Afar region is geographically close to the broader Somali biogeographic zone, its Late Pleistocene rodent fauna is distinct. These findings support the presence of a temporally persistent and spatially unique center of small mammal endemism in the Afar.

Reconstructing vegetation history of the Marmara Lake Basin and Gediz Plain using sedimentary ancient DNA (sedaDNA)

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Abstract ID: 108
Keywords: Marmara Lake Basin, metabarcoding, rbcL gene, sedaDNA, vegetation history

Situated at the intersection of the Aegean coast and the central Anatolian Plateau, the Marmara Lake Basin and Gediz Plain have long served as key corridors for settlement, agriculture, and ecological exchange. This study investigates the vegetation history of this archaeologically rich region over the last 11,000 years, using sedimentary ancient DNA (sedaDNA) analysis as a molecular tool to identify plant species that existed in the past. Five sediment cores, ranging from 10 to 20 meters in depth, were extracted from around the dried Lake Marmara. sedaDNA was extracted, targeting the chloroplast rbcL gene via PCR- based metabarcoding. High-throughput sequencing was conducted using Illumina platforms, and taxonomic identification was performed using QIIME2 with a customized rbcL reference database. A total of over 130 plant genera were identified, revealing distinct spatial and temporal patterns in vegetation composition. Core GM1 (20m) showed strong vertical variation, with early layers dominated by forest taxa such as Quercus, Pinus, and Salix, and upper layers reflecting increasing anthropogenic impact through the appearance of ruderal and cultivated genera like Papaver, Solanum, and Phaseolus. GM2 and GM3 cores, near the ancient shoreline, yielded the highest plant diversity and a stable mix of woodland and herbaceous species, suggesting long-term ecological richness in ecotonal zones favorable for human settlement. In contrast, GM4 and GM5—located farther inland—revealed lower diversity and drought-tolerant taxa such as Astragalus and Juniperus, possibly indicating more marginal environments affected by seasonal dryness or overgrazing. These findings show that sedaDNA metabarcoding can detect both natural and human-modified vegetation signatures, providing high-resolution insight into land use, ecological shifts, and settlement dynamics over time. The persistence of woody and herbaceous taxa across all cores underscores the long-standing mixed vegetation structure shaped by climatic and cultural factors.

Early 2nd Millennium CE peoples of Central Anatolia: An archaeogenetic view from Yozgat Province

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Abstract ID: 32
Keywords: Ancient DNA, Central Anatolia, Mobility, Seljuk

The early second millennium CE was a dynamic and transitional period in Central Anatolia, marked by significant shifts in mobility, cultural interaction, and political power. As maritime connections that had long underpinned Roman and Byzantine administration began to wane, overland caravan routes and trade roads, many of which had ancient origins, were revived and increasingly used. This period also witnessed major movements of people, including the westward expansion of Central Asian nomadic groups and the rise of the Seljuk Empire, as well as intermittent incursions by Roman Catholic Crusaders from the west. These movements created a complex mosaic of cultural and genetic exchange across the region.

To better understand the population dynamics of this period, we employed archaeogenetic approaches to analyze individuals from four neighboring archaeological sites - Alişar Höyük, Uşaklı, Çadır Höyük, and Kerkenes - located in present-day Yozgat Province, Türkiye. We used a multidisciplinary approach to learn about the lives of these individuals, including archaeogenetic, isotopic, and paleopathological analyses. We generated genome-wide data from 41 individuals, with 20 of them having sufficient preservation for population genetic analyses, such as PCA and admixture modeling. This dataset also allowed us to reconstruct a multigenerational family, revealing ongoing admixture across four generations. Additionally, we documented evidence of long-range mobility into the region from diverse geographic sources, highlighting the cosmopolitan nature of medieval Central Anatolian communities. These findings, integrated with the region’s rich archaeological and historical record, offer new perspectives on biological ancestry, population dynamics, and the entangled histories of the people who inhabited this frontier zone during a period of profound transformation.

Ancient Human DNA in sediments from open-air Holocene sites across Europe

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Abstract ID: 14
Keywords: ancient dna, population genetics, sediments

Sedimentary ancient DNA (sedaDNA) can provide a novel means of learning about past societies - with samples taken directly from living spaces. While the majority of existing research has concentrated on cave environments, the performance of sedaDNA from more recent human-made settlements has not been tested thoroughly. Here, we present data from n=13 open-air Holocene settlements across Europe, spanning the Neolithic to the Medieval times. Our n=183 sediment samples taken from different domestic contexts -such as alleys and houses- were processed with mammalian and human mitochondrial DNA capture. We identified a variety of both ancient domestic and wild taxa, with distributions that did not always parallel the zooarcheological record. In more than half of the n=45 samples containing ancient human DNA, we were able to resolve haplotype mixtures or infer single mitochondrial haplotypes. In samples with high amounts of human DNA, we also retrieved sufficient nuclear DNA for population genetics analyses. Our findings show that it can be possible to contribute to the growing body of archaeogenetic research using sediment- derived sequences alone. Given the scarcity of preserved skeletal remains contrasting the abundance of sediments, we highlight sediments as a promising resource for genetic studies especially at archeological settlements lacking graves or human remains.

Preliminary assessment of Late Miocene Hipparionine assemblage from the Sofular Locality (Central Anatolia, Türkiye)

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Abstract ID: 92
Keywords: Hipparion, Sofular, Turolian, paleobiogeography

This study reports newly discovered hipparionine fossil assemblages from Early Turolian sediments in the Sofular study area, located in Central Anatolia, Türkiye. The Sofular fossil locality has been recently dated using radioisotopic methods to 8.42 ± 0.34 Ma and is correlated with the early MN11 biochronological zone (Early Turolian) (Tholt et al., 2025). The large mammal fauna of Sofular includes representatives of artiodactyls, perissodactyls, proboscideans, carnivores, primates, turtles, birds, and aardvarks. Equid fossils include the newly described species *Cormohipparion sofularensis* (Kahya Parıldar et al., 2025), accompanied by three additional hipparionine taxa: *Hippotherium brachypus*, *Hipparion dietrichi*, and *Cremohipparion moldavicum*. Comparative biogeographic analysis indicates that *Cormohipparion sofularensis* represents the youngest known member of its genus in Eurasia and Africa. Morphologically, it exhibits more derived cranial characteristics than the older *Cormohipparion cappadocium* from Yeniyaylacık, Türkiye (Bernor et al., 2024). The Late Miocene is marked by high equid species diversity within the Subparatethys bioprovince, likely driven by the expansion of open habitats. However, this diversity declined sharply toward the end of the Miocene, as part of the broader disappearance of the Old World Savanna Paleobiome.

A preliminary report on the taphonomy of Late Quaternary fossil small mammals from the Afar Region, Ethiopia

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Abstract ID: 106
Keywords: Taphonomy, eastern Africa, small mammal fossils

This study presents a preliminary taphonomic analysis of small mammal fossil assemblages from upper strata of the Dawaitoli Formation (Late Pleistocene, Afar Region, Ethiopia), focusing on the Faro Daba and Chai Baro Beds of the Halibee Member. The assemblage comprises over 1,400 specimens dominated by murids such as *Arvicanthis*, *Mastomys*, and *Gebillinae*. These taxa were selected for analysis according to their small size, while larger rodents like *Thryonomys*, *Hystrix* and *Tachyoryctes* were excluded. The primary goals were to reconstruct predator behaviour and infer paleoenvironmental conditions.

Microscopic examination was conducted following established taphonomic protocols (Andrews, 1990; Andrews and Fernández-Jalvo, 1992). Quantitative analysis included zooarchaeological measures (NISP, MNI and MNE) supplemented by fragmentation and breakage indices. Multivariate methods, including principal component analysis (PCA) and k-means clustering, helped detect internal patterning. Particular attention was given to predator-related modifications, such as digestion marks and bone breakage, to infer the most likely accumulator.

Our analysis reveals a strong cranial bias, with approximately 170 mandibles and 130 maxillae representing the majority of the taxonomically identifiable elements. In contrast, postcranial elements are scarce, suggesting significant taphonomic filtering. Notably, over 98% of all specimens show no visible digestive marks, indicating accumulation by a predator with minimal digestive impact, most likely the barn owl (*Tyto alba*). Multivariate results confirm that over 90% of specimens form a homogeneous cluster with low digestion levels but high fragmentation. The assemblage is dominated by cranial elements, particularly mandibles, while nearly complete specimens are rare. Postcranial bones are underrepresented, and most fragments are heavily broken. This consistent taphonomic pattern likely reflects similar accumulation and preservation conditions. Low digestion and cranial dominance align with pellet-derived assemblages, and the fossils' good preservation suggests low-energy deposition.

This study highlights the value of small mammal taphonomy and multivariate analysis for understanding site formation and accumulation processes in paleoanthropological contexts.

SESSION 6: CONSERVATIOUN BIOLOGY & BIOGEOGRAPHY

Detecting the offspring of mammals: Indicators for the key habitat patches for wildlife conservation

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Abstract ID: 24
Keywords: mammalia, protection, reproduction, wildlife ecology

Reproductive success is crucial for the viable populations of mammals, as is the case for all organisms. The breeding sites and seasons vary among the mammalian species, but they all need safe areas for nursing and protecting their offspring. Therefore, the sites where we spot the species with their young indicate the region's importance for the population's survival. Camera-traps are valuable tools for monitoring mammalian populations and detecting young individuals. We analysed our camera-trap captures to reveal the areas inhabited by the offspring of large mammal species. Camera-trapping surveys were conducted in different parts of Turkey between 2007 and 2022, with 274 camera-trap stations and 16 target species were detected. Among these large mammals we had 1942 cam-trap records in total for the offspring of 11 species with the highest record numbers for brown bear (n=401; *Ursus arctos*), grey wolf (n=168; *Canis lupus*), Eurasian lynx (n=116; *Lynx lynx*), red deer (n=171; *Cervus elaphus*), roe deer (n=331; *Capreolus capreolus*) and wild boar (n=660; *Sus scrofa*). The distribution of these records emphasises several habitat patches that host the offspring of the focus species. Considering these sites as the core areas for breeding periods, and giving priority in wildlife conservation plans, will ensure significant improvement in maintaining the viability of these mammalian populations.

Expanding climate niche factor analysis beyond species: Ecoregion-level vulnerability mapping under climate change

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Abstract ID: 68
Keywords: Ecoregions, Global Change Ecology, Niche Theory, Spatial Ecology

Climate change drives the ongoing biodiversity crises, with impacts projected to intensify. Current approaches to assessing biological responses to climate change offer partial perspectives and are insufficient alone in practical applications. We adapted Climate Niche Factor Analysis(CNFA), a species-specific method for calculating vulnerability to environmental change, and scaled it to higher biological levels utilizing ecoregions. CNFA identifies the niche axes on which biological systems specialize and compares the spread of values along these axes to the spread of the global distribution on the same axes. This comparison quantifies sensitivity to environmental change. The method incorporates exposure(measured as change in environmental conditions) with sensitivity to calculate vulnerability values, following the widely used sensitivity-exposure-vulnerability framework. We treated each biome's climate as global reference distributions and assumed that the ecoregions within each biome represent sets of organisms that share similarities in their climatic niches. These modifications enabled spatial vulnerability mapping for all 14 biomes, covering nearly all of Earth’s terrestrial surface, under different climate scenarios. Results reveal considerable variation in climate change vulnerability across ecoregions and biomes. Very small ecoregions exhibit disproportionately high vulnerability, although this vulnerability-area relationship weakens substantially as area increases. We evaluated vulnerability estimates for protected areas and Key Biodiversity Areas(KBAs). In 4 of 14 biomes, protected areas were significantly more vulnerable than the biome overall; in 5 biomes they were less vulnerable; 5 showed no statistically significant differences. KBAs exhibited significantly higher vulnerability in 9 biomes, lower vulnerability in 4 biomes, with 1 showing no significant difference. Our study provides a novel approach for biologically meaningful, broad-scale spatial assessments of climate change vulnerability, addressing important methodological gaps. It integrates complementarily with current approaches and, when used in conjunction with them, offers a powerful framework for guiding conservation and protection efforts.

Enhancing genetic and altruistic transformation in American chestnuts for functional genomics and disease resistance via *Agrobacterium*-Mediated Approaches

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Abstract ID: 81
Keywords: Altruistic transformation, Chestnut, Developmental Morphogenic genes, Disease resistance, Forest biotechnology

The American chestnut (*Castanea dentata*) once dominated eastern North American forests but was decimated by chestnut blight (*Cryphonectria parasitica*) and root rot (*Phytophthora cinnamomi*). Restoration of this ecologically important species requires modern tools that enable precise genetic modification and functional gene analysis. Although successful transformation of *C. dentata* has been demonstrated using various methods, our study focuses on improving transformation efficiency and significantly reducing regeneration time, which remain key limitations for broader application.

We are developing and optimizing both conventional and altruistic *Agrobacterium*-mediated transformation protocols for *C. dentata*. Altruistic transformation utilizes *Agrobacterium* strains engineered to express developmental (DEV) genes without integrating them into the host genome, thereby enhancing regeneration without permanent genetic alteration. Key morphogenic regulators—including *BABY BOOM (BBM)*, *WUSCHEL (WUS)*, and the chimeric *GRF-GIF* transcription factor—are co-introduced with binary vectors carrying visible and selectable markers (GFP, DsRed, RUBY).

Internodal stem segments and leaf discs are wounded and co-cultivated with *Agrobacterium tumefaciens* or *A. rhizogenes*, then cultured on callus induction medium with appropriate antibiotics. A resting phase precedes selection on media with escalating spectinomycin concentrations. While transgenic callus formation and fluorescent marker expression have been achieved, consistent shoot regeneration has not yet been realized. Current efforts focus on optimizing hormone regimes, DEV gene expression, and co-culture conditions to promote shoot induction.

This research highlights the potential of altruistic transformation as a practical strategy to improve genetic engineering in *C. dentata*. The approaches developed here aim to support future functional genomics, disease resistance studies, and ultimately contribute to the long-term restoration of this iconic species through precision biotechnology.

Genetic diversity and phylogeography of White Oaks (*Quercus petraea* and *Q. pubescens*): Insights from the Eastern Mediterranean

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Keywords: Eastern Mediterranean, Genetic diversity, Haplotypes, Microsatellites, Quercus petraea, Quercus pubescens, White oaks

The Eastern Mediterranean region harbors a complex evolutionary history for European white oaks, shaped by glacial refugia, postglacial recolonization, and interspecific hybridization. This study examines the genetic diversity and population structure of *Quercus petraea* (sessile oak) and *Quercus pubescens* (downy oak) across 36 populations from Greece and Türkiye using 15 nuclear and 10 chloroplast microsatellite loci. High levels of nuclear genetic diversity were observed in both species, with *Q. pubescens* showing greater allelic richness and admixture, particularly in Turkish populations. A total of twenty chloroplast haplotypes were identified, three of which correspond to previously characterized Balkan lineages, while three others exhibit characteristics indicative of ancestral origins. Bayesian clustering of genetic structure identified six primary gene pools for the two species. A high level of admixture was observed in *Q. pubescens*, with distinct differentiation in the Greek mainland populations, while *Q. petraea* populations showed stronger geographic structuring. These findings, together with the observed intraspecific haplotype diversity, strongly support the hypothesis that the Eastern Mediterranean, particularly northern Türkiye and northern Greece, served as a glacial refugia for white oak populations. Moreover, the study highlights the region as a center of genetic and haplotypic diversity, shaped not only by historical isolation but also by ongoing hybridization and gene flow, with important implications for the evolutionary resilience of these species.

Ecological niche modeling of rare Turkish olive cultivars: A spatial framework for agroecosystem policy and conservation

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Abstract ID: 19
Keywords: Türkiye, agroecology, ecological niche modeling, in-situ conservation, olive cultivars

Local knowledge, historical cultivation practices, and distinct environmental conditions shape Türkiye's traditional olive-growing regions. Among the many regionally adapted olive cultivars, *Sarıulak*, *Çöp Aşı*, and *Dilmit* are three rare varieties identified through morphological traits and local farmer knowledge in the southern Anatolian Peninsula. This study applies ecological niche modeling (ENM) to assess their current climatic suitability and to support agroecosystem policy, in situ conservation, and climate adaptation planning.

Occurrence data were compiled through field surveys and participatory documentation. To reduce multicollinearity and enhance ecological interpretability, only four bioclimatic variables were used: maximum temperature of the warmest month (BIO5), minimum temperature of the coldest month (BIO6), annual precipitation (BIO12), and precipitation seasonality (BIO15). We implemented MaxEnt models via the R Wallace GUI, testing 15 candidate models per cultivar by tuning feature classes and regularization multipliers. Model performance was evaluated using AUC, omission rate, continuous Boyce Index (CBI), and AICc.

All cultivars yielded high-performing models. The best model for *Çöp Aşı* had an AUC of 0.995, omission rate of 0.20, and CBI of 0.086, with the lowest AICc among candidates (w.AIC = 0.78). *Dilmit* achieved an AUC of 0.991, omission rate of 0.20, and CBI of 0.356 (w.AIC = 0.95), while *Sarıulak* showed an AUC of 0.991 and CBI of 0.394, although AICc metrics were not available. The selected models reveal spatially distinct suitability patterns, primarily reflecting known traditional cultivation zones.

By integrating ecological modeling with community-based cultivar identification, this study provides a science-based and participatory framework to support the conservation of rare olive varieties. The spatial outputs can guide localized adaptation strategies, policy development, and agroecological zoning in Türkiye's changing Mediterranean landscapes.

This study is conducted within the framework of the Anatolivar Project, which is implemented by Proje Evi Cooperative, the National Olive and Olive Oil Council, and SlowFood Italy, and supported by the EU.

SESSION 7: MICROBIAL ECOLOGY & EVOLUTION

Stochastic dynamics in the assembly of the seed-borne microbiome in bread wheat

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Abstract ID: 10
Keywords: ecological assembly, microbiome, plant microbiome

Plants harbor diverse microbial communities that play crucial roles in their health and development. A subset of these microbes is transmitted vertically among generations of plants through seeds, influencing early-stage plant growth. Although it is known that seed microbiota composition is shaped by environmental conditions, host genetics, and random processes, the specific factors driving variation within and between individual plants of the same species from the same environment remain poorly understood. Moreover, the dynamics of the vertically-transmitted microbes during plant development are not well characterized.

In this study, we examined the bacterial communities of individual seeds from the same spike of adult wheat plants and found a high degree of compositional uniformity. To track how these microbes colonize the host, we grew wheat seedlings under sterile, controlled conditions. Surprisingly, despite the relatively uniform bacterial composition of seeds, the microbiomes of early-stage seedlings—particularly in developing leaves—showed substantial variability, even among seedlings derived from seeds of the same spike. Using a neutral model of community assembly, we found that while seed-to-seedling microbiome transmission is driven primarily by selective forces, the subsequent microbial assembly in seedlings is largely shaped by stochastic processes.

Overall, by analyzing highly replicated seeds from the same wheat plants grown in the same field, we provide novel insights into the ecological forces that shape seed-associated microbiome transmission in wheat.

Linking environmental parameters to microbial function via metagenomic profiling

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Abstract ID: 28
Keywords: functional metagenomics, microbial adaptation, shotgun metagenomics

Microbial life adapts to its environment according to stimuli such as temperature and chemical composition. Understanding these adaptations could reveal insight into how life processes information and changes these processes according to the environment they adapt to. In this study, we have performed functional metagenomic profiling with samples collected from four different thermal spring sources in Türkiye. These sources varied in their chemical composition and temperature. Shotgun metagenomic sequencing data were previously obtained and assembled using MEGAHIT. Gene prediction and annotation were conducted with Prokka, and amino acid sequences were subsequently uploaded to the GhostKOALA web server to retrieve KEGG orthologs. Based on these functional annotations using prokaryotic and virus databases, we quantified and compared the top ten enriched metabolic pathways across environments. Principal Component Analysis (PCA) was used to explore the correlation between environmental parameters and functional profiles. By performing this analysis, we showed which pathways were enriched in the overall microbial community to compare them in terms of the changing parameters. It was revealed that in the environments where temperature was higher, environmental information processing pathways were more enriched compared to lower. On the other hand, genetic information processing pathways were more enriched in the relatively lower temperature environments. These findings suggest that microbial life prioritizes certain cellular pathways over others according to its environment and to these stimuli. This study contributes to our understanding of microbial adaptive strategies in extreme environments and highlights the utility of functional

metagenomics in ecological inference.

Microplastics enrich pathogenic bacteria in lakes across a salinity gradient

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Abstract ID: 128
Keywords: Microplastic, pathogen, plastisphere, saline lakes, salinization

Microplastics in lake ecosystems act as vectors for pathogenic bacteria, compounding environmental risks posed by salinization, eutrophication, and climate change. This study examines cultivable bacterial biofilms on MPs across 11 lakes in Türkiye spanning a salinity gradient (0.25–192.69‰). MPs were primarily fibers and fragments (50 µm–5 mm), hosting biofilm communities dominated by *Proteobacteria* and *Firmicutes*. *Pseudomonadaceae* accounted for 94.7% of MP-associated bacteria, followed by Enterobacteriaceae (1.2%). High-salinity lakes favored halotolerant pathogens (*Proteus* spp. in Lake Bolluk (95.7‰); *Alcaligenes* spp. in Lake Tuz), while the halophile *Shewanella putrefaciens* dominated alkaline Lake Salda. Ubiquitous genera (*Staphylococcus, Comamonas, Enterobacter*) occurred at all salinities, with CVB densities consistently higher on MPs than in water. These findings underscore MPs' role in enhancing pathogen persistence and dispersal, elevating ecological and public health risks in vulnerable lake ecosystems.

Influence of phosphorus concentration on growth, pigment accumulation, and lipid production in five microalgal species

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Abstract ID: 79
Keywords: BG11 Medium, Biomass Production, Carotenoids, Chlorophyll, Microalgae, Phosphorus, Pigment Accumulation

Microalgae are valuable in biotechnology due to their rapid growth and production of pigments, lipids, and bioactive compounds These organisms are cultivated for various applications including biofuels production, aquaculture, pharmaceuticals, and natural pigments extraction.Phosphorous, particularly its availability, is a critical factor determining microalgal productivity.Essential for growth, phosphorus helps in synthesis of pigments and storage of lipids.The role is to understand its part in detail so that we can develop microalgae cultivation systems with maximal potential for biotechnological use.

This study explored the effects of three levels (0.5X, lX, and 2X) of phosphorus on growth performance, pigment accumulation, and lipid production in five species of microalgae (*Chlorococcum hypnosporum, Stichococcus bacillaris, Chlorella vulgaris, Chlorolilaea pamvotia, and Desmodesmus opoliensis)* reared in BG11 medium for 12 days.During this period, the growth rate of each species was observed optically at 680 nm.At the end of this trial, concentrations of chlorophyll a, b, and carotenoids were determined spectrophotometrically at 665 nm, 645 m, and 470 nm, respectively; levels of total lipid content then were measured gravimetrically.

The study demonstrates that phosphorus availability has a significantly positive effect on both biomass and pigments of microalgae.Reduced phosphorus levels resulted in lower biomass and pigment densities. It also shows the species-specific nature of responses to phosphorus availability and underlines the need for optimize nutrient conditions to drive higher microalgal productivity.

This research sheds light on how phosphorus plays a pivotal role in the development of microalgae and its determination of pigment and lipid production. The results are very useful for biotechnological endeavors, such as biofuel production, where maximizing biomass and lipid yields is critical, and for extracting natural pigments and bioactive compounds commercially.

SESSION 8: ANIMAL BEHAVIOUR & WILDLIFE ECOLOGY

Cortical cell distribution patterns in language-trained Gorillas: Implications for neuroplasticity

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Abstract ID: 36
Keywords: brain evolution, language training, neuroplasticity, non-human primates

Investigating how language exposure shapes brain structure in nonhuman primates offers insights into the neural basis of complex communication. American Sign Language (ASL)-trained gorillas, Koko and Michael, uniquely enable exploration of neural adaptations linked to symbolic communication. This study compares their cortical architecture to untrained controls, assessing neuroplastic changes in frontal cortical regions.

Postmortem brains from ASL-trained Western lowland gorillas, Koko (female, 46) and Michael (male, 27), were analyzed. Koko used approximately 1,000 signs and understood 2,000 words, while Michael used about 500 signs and understood 600 words. Histological analyses quantified cell profile area fractions across cortical layers of the left inferior frontal gyrus (IFG), anterior cingulate cortex (ACC), middle frontal gyrus (MFG), and frontoinsula (FI), comparing these to 13 untrained controls. Immunohistochemistry assessed proportions of neurons (NeuN), microglia (Iba1), astrocytes (S100b), and oligodendrocytes (Olig2) in the IFG compared to eight controls.

Language-trained gorillas exhibited higher cortical cell profile area fractions compared to controls. Koko and Michael ranked in the 69th and 62nd percentiles in ACC, 93rd and 87th in MFG, 80th and 60th in IFG, and 92nd and 77th in FI, respectively. Immunohistochemical analyses of IFG revealed decreased neuronal proportions in layers II–III and increased microglial proportions in layers II–III and white matter. Astrocytic proportions were elevated in deeper layers (V–VI), suggesting enhanced astrocyte involvement linked to symbolic training. These findings suggest that extended symbolic communication exposure is associated with microstructural alterations in frontal cortical organization, particularly in cell distribution and composition. The data support a model of activity-dependent neuroplasticity driven by communicative behavior in great apes, with potential parallels to human language-related brain specialization. This work contributes to our understanding of how cognitive and behavioral enrichment can shape brain structure in lineage-specific ways and underscores the neurobiological relevance of symbolic training in nonhuman primates.

The effects of afforestation on the functional diversity of steppe butterfly communities in Konya Basin, Türkiye

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Abstract ID: 89
Keywords: afforestation, butterfly communities, functional trait, steppe

Arid regions in Türkiye have a rich biodiversity with diverse steppe ecosystems. Afforestation is commonly practiced in these areas to fight erosion and climate change. Despite its common use, there is limited knowledge on how afforestation affects steppe biodiversity.

Our study focuses on the butterfly communities in the Konya Closed Basin and examines how their functional diversity is affected by afforestation. Six sites were selected; in each of them, transects were placed in different-aged plantations (young (1–10 years), intermediate (11–25 years), and old (25+ years) afforested sites, alongside natural grasslands. Fieldwork was conducted in 2024, with surveys carried out seven times at three-week intervals from April to September, and a total of 65 species were recorded. The functional traits included were overwintering stage, voltinism, ant association, host plant type, host plant growth form, egg-laying type, flight months, and wingspan. Functional Richness (FRic), Functional Evenness (FEve), and Functional Dispersion (FDis) indices were calculated, and Principal Coordinates Analysis (PCoA) was performed to map species in functional space.

Functional trait analyses showed that different afforestation age classes significantly affected the functional structure of butterfly communities. In intermediate-aged plantations, different functional traits were represented more evenly, while older plantations showed a decline in functional evenness. Control sites offer a balanced functional structure but the functional diversity is limited. This study shows that plantations provide different ecological niches at different ages, influencing the functional composition of butterfly communities.

Assessing breeding performance of a precocial bird species using GPS data

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Abstract ID: 97
Keywords: GPS data, avian biology, movement ecology, nesting success, spatial ecology, waders

Assessing bird breeding performance is essential for understanding population dynamics and informing conservation strategies. Logistic and environmental challenges in fieldwork monitoring during bird breeding can be overcome by remote tracking of studied birds. We used GPS tracking data from multiple projects to evaluate the breeding performance of the Eurasian Curlew (*Numenius arquata*), a declining precocial shorebird. We analyzed movement patterns to identify potential nesting sites based on high revisit frequencies during the breeding season. Parameters for nest detection were informed by the species' breeding biology, and recursion statistics helped distinguish true nests from foraging sites. The efficiency of the methods were also validated by comparison with methods used to identify nesting sites from the same dataset. Nesting success was estimated using a Bayesian hierarchical model applied to visitation patterns, assessing nest survival probability throughout the breeding cycle. Model outputs were manually validated to account for false positives and negatives. While field observations of nest status were limited, our GPS-based assessment showed strong agreement with available validation data. Identification of breeding periods and breeding grounds was facilitated by a custom MoveApp we developed to delineate annual cycles.

Our results demonstrate that high-resolution GPS tracking, combined with recursive movement analysis, provides an effective method for assessing breeding performance in cryptic precocial birds. The integration of automated detection with manual validation improved accuracy in nest site identification and success estimation, while the MoveApp facilitated precise delineation of breeding phases. This approach offers a scalable framework for studying breeding behaviours in other species, particularly where traditional monitoring is challenging. Overall, our methodology advances the use of biologging data in avian ecology, providing valuable insights for conservation management of declining species like the Eurasian Curlew.

Assessing cognitive performance and learning efficiency in wild great tits: Insights from an RFID-based multiple reversal learning experiment

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Abstract ID: 102
Keywords: RFID, animal cognition, behaviour, cognitive flexibility, great tits, learning bahaviour, wild experiment

Understanding individual variation in cognitive performance is critical for uncovering the ecological and evolutionary significance of cognitive flexibility and learning in wild animals. I investigated learning behaviour in great tits (Parus major) using an experimental setup with RFID equipped feeders, incorporating an initial and multiple reversal learning phases over two consecutive years. In total, 106 individuals participated in at least one learning phase throughout the experiment. Participation patterns showed strong individual engagement consistency across learning phases that supported the robustness of the experimental design. I analysed learning speed, defined as the negative log-transformed number of visits required to reach a learning criterion (80% correct in 20 consecutive visits), using linear mixed models incorporating demographic variables (age, sex), feeder malfunction durations, and previous experience metrics. Repeatability analyses revealed moderate individual consistency in learning speed when examined across consecutive reversal phases and after adjusting for confounding factors, which suggests there are stable individual differences present in cognitive abilities in our experiment. However, repeatability estimates were low or non-significant without adjustment and when considering multiple phases, highlighting potential limitations of learning speed as the sole metric of learning performance through multiple learning phases. This limitation proved a need to refine learning measurements by grouping visits into discrete foraging bouts or attempts, which may better capture cognitive flexibility and learning efficiency by accounting for variation in visitation patterns over time within and between individuals. Current analyses further exploring behavioural patterns in foraging and their ecological correlates are ongoing. Preliminary results underscore the importance of considering both individual variation and methodological factors in cognitive ecology studies. This research contributes to understanding how intrinsic cognitive differences manifest in natural populations and shows the need for improved experimental approaches for assessing animal learning. Full results will be presented at the symposium.

SESSION 9: BIOINFORMATICS & PHYLOGENETICS & EVOLUTIONARY GENOMICS

Genome Annotation and Analyses of the tenebrionid beetle *Carchares macer*

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Abstract ID: 29
Keywords: Evolution, Genome, Tenebrionidae

We report here the results of whole genome sequencing, assembly and annotation of the non-model organism *Carchares macer* (Coleoptera), a tenebrionid beetle endemic to southern Africa. Tenebrionids in general are well known for their successful adaptations to very diverse habitats, including the extremely arid regions of the Atacama or Namib deserts. Using an assembly strategy which combines long and short read sequences we constructed a draft genome, predicted coding genes and compared the results with the closely related species *Tribolium castaneum* and *Zophobas atratus*, also tenebrionids. While genome size (about 175Mb), GC- and repeat content are very similar among these species, we find a few remarkable differences regarding transcription factors, gene family size of odorant receptors, and in the complement of genes involved in metabolism, immunity and neurogenesis. We speculate that they may be important targets for environmental adaptation.

Unraveling host-parasite coevolution in complex natural systems: Insights from MHC variation in Amphibians

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Abstract ID: 44
Keywords: amphibians, coevolution, immunogenetics, major histocompatibility complex, wildlife disease

Major Histocompatibility Complex (MHC) genes play a main role in adaptive immunity, yet the evolutionary processes shaping MHC diversity in natural populations remain poorly understood. Ecological communities with multiple co-occurring host species and pathogens create complex selective environments, posing challenges for testing evolutionary hypotheses such as heterozygote or divergent-allele advantage in the wild. Amphibians provide a perfect model for exploring these questions as their disease-driven declines make understanding host–pathogen coevolution an urgent conservation priority. Notably, previous studies have identified associations between specific MHC alleles and disease resistance in amphibians, implicating the potential role of immune-gene diversity on their populations' survival. Here, we apply a multi-scale approach to link MHC variation with pathogen infection across amphibian species. We assembled a comprehensive dataset of MHC class I and II genotypes from multiple populations of evolutionarily distinct amphibian species spanning broad geographic regions of Europe. These genetic data are integrated with field measurements of infection prevalence and intensity for multiple parasite taxa. Using phylogenetically informed analyses, we tested predictions at both individual and population levels, examining how MHC diversity at different scales and specific alleles correlated with infection status and intensity. By integrating genetic and infection data across multiple taxa and scales, our study provides the first comprehensive insight into the functional variation and evolutionary processes shaping immune diversity in wild amphibian communities.

Exploring the function and evolution of the "dark matter of the genome" in the economically significant beetle *Tenebrio molitor*

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Abstract ID: 13
Keywords: evolution, insect, molecular biology, phylogeny, satellite DNA, transcription

The insect yellow mealworm, *Tenebrio molitor* has become an important model organism for various studies in biology, biotechnology and medicine. Additionally, expanding our knowledge about this organism is a necessity following the European Commission's approval of *T. molitor* for human consumption. Repetitive DNA sequences, also called the "dark matter of the genome", are recognized more and more as key builders of genome architecture and drivers of its evolution. Transcription of tandemly repeated satellite DNA (satDNA) was shown to be involved in processes crucial for the cells. The substantial portion of the mealworm genome is composed of a single satDNA that accounts for approximately 50% of its total genetic material. Utilizing the Tandem Repeat Analyzer, we have identified 10 additional satDNAs, and examined their distribution within the mealworm genome. SatDNAs exhibit variations in terms of monomer grouping, array length, and chromosomal placement, with some being exclusively associated to Y chromosome. We have investigated the transcriptional activity of satDNAs across different developmental stages (eggs, larvae, pupae, and adults) finding a significant increase in transcription levels in male pupae and adults. NCBI searches across insect genomes revealed the presence of these satDNAs in both closely and distantly related species. By juxtaposing the distribution of 11 satDNAs against the phylogenetic tree of insect species, we were able to estimate their evolutionary trajectories and determine their minimal age, ranging from 310 - 380 MYA. We have generated the divergence profiles of satDNA monomers, which provided insights into the processes of sequence turnover and homogenization for each satDNA. The unequal crossing-over, transposition, and extrachromosomal circular DNA formation are considered as potential contributors to the spread of satDNAs within the genome. We have confirmed the existence of six satDNAs in the extrachromosomal circular DNA fraction, highlighting its role in the propagation of these sequences.

Integrative taxonomic revision of *Heldreichia bupleurifolia* (Brassicaceae) based on morphological and genomic Data

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Abstract ID: 55
Keywords: Anatolia, Heldreichia bupleurifolia, RAD-seq, phylogeny

Heldreichia bupleurifolia Boiss. (Brassicaceae), as the only member of its monotypic genus, exhibits a predominantly Anatolian distribution, occurring mainly in the alpine zones of the Taurus Mountains and the Anatolian Diagonal -two major biogeographic corridors of the region- with a disjunct record from Lebanon. Currently, the genus is divided into six infraspecific taxa, consisting of five subspecies and one variety. However, significant morphological and distributional overlap, especially between populations in the Central Taurus and Anatolian Diagonal, complicates the clear delimitation of taxa due to similarities in key traits such as basal leaf shape and fruit morphology/size. To address these issues, we used an integrative approach combining morphological analyses with genome-wide molecular data. We analysed 45 populations, using morphological data and high-throughput RAD-seq data encompassing thousands of SNPs and loci.

A multivariate framework was applied to assess morphological differences, including Factorial Analysis of Mixed Data (FAMD) and Canonical Discriminant Analysis (CDA). An Admixture analysis of molecular data was conducted to investigate the genetic structure of populations. Phylogenetic analyses were performed on two datasets, incorporating both single nucleotide polymorphisms (SNPs) and loci (including SNPs and invariant sites). Maximum Likelihood (ML) analysis and SNAPPER species delimitation were applied on the SNP dataset. For the full loci data, both ML and Bayesian methods were used on concatenated sequences, along with a gene tree–species tree approach to clarify subspecies relationships.

Consequently, concatenated data analyses indicated five monophyletic subspecies, whereas the gene tree–species tree method did not support this structure. Instead, the SNAPPER species delimitation analysis supported a three-subspecies model, consistent with both morphological patterns and Admixture analysis.

Functional genomics of muscle and ovary development in Teleosts: Insights into evolution and specialization

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Abstract ID: 40
Keywords: RNA-Seq, adaptation, gene regulation, myogenesis, oogenesis, teleostei, transcriptomics

Teleostei, the most species-rich clade of vertebrates, display remarkable morphological and physiological diversity. Among their most critical adaptations are striated musculature, enabling efficient locomotion and ecological versatility, and highly fecund ovaries supporting diverse reproductive strategies. Understanding the gene expression programs underlying these tissues offers insights into both evolutionary processes and aquaculture potential.

Here, we present comparative transcriptomic analyses of muscle and ovary tissues from 35 ecologically and economically significant teleost species. Differential expression and gene ontology analyses revealed both conserved and lineage-specific patterns shaping tissue specialization.

In muscle, enriched processes included sarcomere organization, energy metabolism (glycolysis, ATP biosynthesis), and mitotic activity. Molecular functions such as oxidoreductase activity, ATP binding, and creatine kinase function were prominent. Key genes like *myod1*, *myog*, *pax3*, and *mstn* were highly expressed, indicating conserved developmental roles with species-specific expression dynamics.

In ovary tissue, genes involved in transcriptional regulation, protein biosynthesis, and early embryonic development were enriched. Notably, *ddx4*, *nanos2*, *gdf9*, and *pgrmc1* were expressed alongside genes related to immune modulation and cilium function—critical for oocyte maturation and signaling. Enriched cellular components included ribosomes, RNA-protein complexes, and nuclear machinery, reflecting high biosynthetic demand.

Our findings suggest that while core developmental pathways are broadly shared, adaptive divergence underpins tissue-specific regulatory complexity across teleosts. Current analyses focus on gene interaction networks to identify regulatory hubs and inform gene panel development for muscle and ovary ontogeny. This work contributes to our understanding of functional evolution and provides genomic resources for applied and comparative biology.

Life-history traits shape the evolution of mammalian lifespan

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Abstract ID: 43
Keywords: ageing, brain, life-history, lifespan, reproduction

The evolution of organismal lifespan is underpinned by the fast-slow continuum, where species exhibit either fast (rapid development, high reproductive rate, short lifespan) or slow (slow development, low reproductive rate, long lifespan) life-histories. However, the relationship between different factors is not well understood. Here we combine machine learning and phylogenetic path analysis to understand the determinants of maximum lifespan based on biological and ecological factors across 970 mammalian species. By using CatBoost Gradient Boosting, we were able to predict maximum lifespan with a mean absolute error of 3.12 years. Our results indicated that life-history traits, rather than ecological and behavioural factors, were the most significant determinants of maximum lifespan, representing 85% of the total importance of features. Longer development, larger body size and larger brain size were correlated with longer lifespan, while higher reproduction was correlated with shorter lifespan. We applied phylogenetic path analysis on the best predictors and revealed that brain size plays a central role in the evolution of maximum lifespan. Larger brain size influences the evolution of longer lifespan both directly and indirectly via gestation length and generation time. These results indicate that the evolution of cognitive function plays an outsized role in mammalian lifespan evolution.

SESSION 10: COMMUNITY & ECOSYSTEM ECOLOGY

Effect of crown fires on temperate mixed forests of northeastern Anatolia: A modeling approach

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Abstract ID: 115
Keywords: Anatolia, fire, forest succession, modeling, temperate mixed forests, vegetation dynamics

Climate change is expected to increase fire frequency and severity in temperate mixed forests, making it crucial to understand vegetation dynamics under altered fire regimes. We studied long-term vegetation dynamics in temperate broadleaf and mixed forests of northeastern Anatolia using FATELAND, a spatially-explicit and trait-based vegetation model. We employed five vegetation types: Euxine Mountain, Colchic mountain, subeuxine, lowland submontane forests, and relict Mediterranean forests and shrublands. Species traits were retrieved from the TRY database and classified into four functional groups: broadleaved trees, conifers, resprouting shrubs, and resprouting herbs. Initial abundances of functional groups were determined using vegetation plot data from the Forest Vegetation Database of Türkiye. Fire-response traits for seeds, juveniles, and adults were represented as binary values across five resource levels. We simulated vegetation dynamics for 120 years under high-severity crown-fire and no-fire scenarios. Broadleaved trees recovered within 25 years post-fire and ultimately became dominant, whereas conifers experienced significant, sharp declines. Shrubs and herbs showed slight post-fire increases but remained minor components. Under the no-fire scenario, broadleaved trees gradually outcompeted conifers in all forest types, with relict Mediterranean forests approaching complete broadleaved dominance. Fire scenarios maintained broadleaved dominance while further reducing conifer resilience, highlighting that crown fires critically shape community composition in these regions. Our findings suggest increasing crown fires due to climate change may favor resprouting broadleaved species over obligate seeder conifers, altering successional patterns in temperate mixed forests. The slower recovery of conifers emphasizes their vulnerability to frequent or severe fires. Effective management should consider species' fire-related traits and diverse fire regimes to ensure conifer persistence. Future modeling should incorporate varied fire frequencies and other disturbances to produce realistic projections and guide adaptive conservation strategies.

Pollinator assemblages as drivers of plant range: Evidence from a marl steppe in Central Anatolia

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Abstract ID: 59
Keywords: insect pollinator, marl steppe, plant distribution, pollination., pollinator diversity, visitation frequency

Pollination is a key plant-insect interaction that ensures the maintenance of biodiversity in terrestrial ecosystems. Insect-mediated pollination affects the colonization capacity of plant species due to direct influences on seed production. Pollinator behavior, such as low visitation rates or avoidance of certain plant species, can lead to pollen limitation through biotic interactions. Thus, insect pollinators may become critical determinants of plant distributional range. In our study, we investigated pollinator diversity and composition, and also the visitation frequency of pollinators among plant groups with different distributional range patterns (rare and endemic, widespread and endemic, widespread and non-endemic) in a marl steppe habitat located in Central Anatolia, Türkiye. We conducted fieldwork between June and July 2024. Five individuals from three plant species from each distributional range group were observed for 10 minutes for insect visitation in two sampling periods. The samples were pinned, identified, and classified as either pollinators or other flower visitors. Taxon richness and visitation frequency were analyzed using generalized linear models with a Poisson distribution, while diversity was assessed using the Shannon index. Non-metric multidimensional scaling analysis (NMDS) was performed to assess taxon composition, and Jaccard index values were used to quantify similarity rates between pollinator assemblages of plant species. Widespread and non-endemic plants had significantly higher taxon richness, diversity, and visitation frequency compared to other distribution range groups. However, taxon composition did not differ among distributional range groups, as Jaccard index results indicated low overall interspecific similarity, although the number of shared taxa was relatively higher in plant species with a broader distributional range. Our findings provide evidence for a positive association between pollinator visitation and plant distributional range, offering empirical support for a widely accepted theoretical framework from an understudied grassland habitat.

Avian communities of the Anatolian Diagonal: The role of climate and land cover

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Abstract ID: 96
Keywords: Clustering, Community structure, Functional traits, Indicator species, Land use, Ordination

Avian diversity is facing severe decline primarily attributed to global change, leading to a drastic erosion of ecosystem functioning and human well-being. Anatolian Diagonal, an endemism hotspot and distribution barrier for many taxa, is poorly explored regarding its avifauna. The objective of the research was to evaluate bird community compositions along the Anatolian Diagonal, and their associations with environmental variables and functional traits. Standard surveys were implemented by DKM along a total of 782 transects in 10x10 km UTM grids, chosen through stratified random sampling. Additionally, 12 environmental variables were extracted via GIS, and 14 functional traits were compiled from avian trait databases. Hierarchical clustering resulted in seven different avian communities. Indicator species analysis confirmed 14 birds as important indicator species. Non-metric multidimensional scaling (NMDS) exhibited that bird species were principally shared between the communities; nevertheless, we identified notable signals of environmental features and functional traits, including bioclimate, land cover, habitat preferences, or avian morphology influencing the divergence of communities. For instance, the community of steppic landscapes was shown to be correlated to lower precipitation levels and greater mean diurnal ranges and were predominantly composed of birds displaying larger body mass and expanded hand-wing index. Conversely, the forest community was associated with higher productivity (NDVI) and it harbored forest-dwelling smaller passerines. Homogeneous highlands corresponded to cooler temperatures with reduced precipitation seasonality. Highly modified agricultural landscapes exhibiting intense human footprints hosted a relatively distinct avian community. The community of habitat mosaics with riparian vegetation was aligned with greater habitat diversity and it sustained avian assemblages with distinct functions, among which *Luscinia megarhynchos* and *Oriolus oriolus* emerged as indicator species. The findings highlight the importance of ensuring the incorporation of a variety of different habitats in the conservation network, prioritizing steppes and riparian zones to represent bird communities and their functions.

Climate or land use? Disentangling drivers of wildfires in Mediterranean North Africa

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Abstract ID: 91
Keywords: climate change, land use and land cover, modeling, wildfires

Wildfires are becoming increasingly important in the context of global environmental change. Climate change influences fire activity by altering temperature patterns, precipitation dynamics. Moreover, there is also impact of land use and land cover (LULC). Although many studies have examined historical interactions between wildfires and LULC projections of future interactions at broader scales remain limited. This creates a gap in understanding how future LULC changes may influence wildfire activity under changing climatic conditions. In this study, we used XGBoost modeling approach and newly available LULC projections from the LUCAS dataset to model wildfire dynamics in Mediterranean North Africa (Algeria, Morocco, and Tunisia) under various LULCC and climate scenarios. To isolate the effects of climate change and LULC, we developed six scenarios in which either climate or LULC was held constant, along with two scenarios where both varied simultaneously. Our results indicate that distinct LULC patterns emerge under different scenario combinations, highlighting complex interactions between anthropogenic and climatic drivers of wildfires. The most pronounced impact was observed under the RCP 8.5 scenario, even when LULC was held constant, with the strongest increase in Fire Proneness Index in Algeria and relatively weaker responses in Morocco and Tunisia. We also observed notable differences across the three countries, despite their geographic proximity. This underscores the importance of comparative analysis in fire-related LULC research, as national-scale variations can produce divergent wildfire outcomes even under similar climate trajectories. Moreover, the influence of climate is more pronounced than that of land use in certain LULC groups. These insights contribute to a better understanding of how land use, land cover, and climate change interact to shape future wildfire risks. While our results focus on Mediterranean North Africa, this approach can be applied more broadly to generate comparative insights across regions.

The effects of afforestation age on the functional diversity of plants in the steppes of Central Anatolia, Turkey

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Abstract ID: 42
Keywords: LDMC, grasslands, grazing, growth form, leaf traits

To mitigate the negative effects of erosion and climate change, afforestation work has been carried out in the arid and semi-arid lands of the world. Yet there is no information about the effect of widespread afforestation activities on the functional diversity of plants. To compare afforested and adjacent non-forest sites in Konya Closed Basin in terms of plant functional diversity, we sampled 77 plots from young (0-10 years), intermediate (11-25 years), and old (26-50 years) age groups and control sites. A total of 443 plant species were identified. Plant height was measured per species per plot in the field. A total of 2023 leaf samples were collected from the field, and leaf traits were measured. Leaf thickness, specific leaf area, and leaf dry matter content (LDMC) were calculated using measurements. In addition, growth form, palatability, life span, cloning ability, dispersal mode, and subsoil storage status data were extracted from the literature. All traits were used to calculate several functional diversity metrics. We found that LDMC was smaller in control plots, leaf thickness was higher in control and old afforestation plots, and SLA was higher in old plots and smaller in control areas. Plant height was smaller in control areas due to grazing pressure. We found that legume and malacophylls had higher cover in control areas, while grass cover was lower in old plots. In addition, annual species were abundant in young and intermediate areas, while perennials had higher cover values in controls and lower in old plots. Overall, control sites and old ages had significantly different in terms of plant functional groups. We recommend the implementation of sustainable grazing management in control sites and the prevention of completely closed canopies in old plantations to conserve plant functional diversity. This project was funded by TÜBİTAK under the project no: 123Z054.

Change in Functional Trait Structure of Plant Communities Along an Elevational Gradient in Southwestern Anatolia

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Abstract ID: 123
Keywords: Mediterranean mountain ecosystems, altitude gradient., community ecology, community weighted averages, functional diversity, plant functional traits

Understanding how plant functional traits vary across environmental gradients is essential for predicting community responses to environmental change. Functional traits—measurable features affecting species' survival, reproduction, and adaptation—offer key insights into ecological strategies and evolutionary history. Despite Anatolia's exceptional biodiversity, few studies have explored trait-based community structure in this region.

This study investigates changes in the functional trait composition of plant communities along a continuous elevational gradient (65–3007 m) in southwestern Anatolia, including all Mediterranean vegetation belts. Fieldwork was conducted across 18 plots positioned along this gradient. For each plot, key plant functional traits—including specific leaf area (SLA), leaf thickness, plant height, stem density, and leaf dry matter content (LDMC)—were measured from collected leaf and stem samples using standardized protocols.

Trait–environment relationships were analyzed using basic statistics, generalized additive models (GAMs), and linear models. Results indicate that most traits do not change linearly with elevation but rather exhibit non-linear, oscillating patterns, reflecting complex ecological and climatic interactions across vegetation zones. Functional trait diversity and community-level trait composition shifted significantly with elevation, with clear distinctions between growth forms (herbaceous vs. woody) along the gradient.

These findings highlight the importance of incorporating functional trait analyses in Mediterranean mountain ecosystems, where environmental gradients are steep and diverse. The study provides novel insights from an underexplored yet ecologically significant region, offering baseline data for future ecological and conservation-focused research in Anatolia and the broader Mediterranean Basin.

POSTER PRESENTATIONS

Occurrence of *Prototheca* species in aquatic ecosystems of Türkiye

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Abstract ID: 93
Keywords: , Pathogenic algae, cytb gene, environmental DNA, qPCR

The genus *Prototheca* comprises free-living microscopic green algae that have lost their ability to photosynthesize in the course of evolution. Although they lack chlorophyll, they still contain plastids. These algae are typically found in moist and nutrient-rich environments and have been isolated from diverse sources such as soil, water bodies, plant surfaces, milk, mastitic udders, feces, and sewage. Their thick cell walls confer high resistance to various environmental stressors. *Prototheca* species, which can cause opportunistic infections in humans and animals, have attracted increasing global attention. However, studies on the environmental distribution of *Prototheca* in Türkiye are limited, and to date, no research has investigated their presence in aquatic ecosystems within the country.

In this study, muddy water samples were collected from various locations to investigate the presence of *Prototheca* species in environmental water sources. DNA was extracted from these samples, and the mitochondrial cytb gene region was amplified using a *Prototheca*- specific primer pair via conventional PCR. Samples that tested positive by PCR were further analyzed using SYBR Green-based quantitative PCR (qPCR) to confirm the results. The qPCR analysis supported the findings obtained through conventional PCR and confirmed the presence of *Prototheca* DNA in the aquatic environmental samples.

This study provides the first molecular data on the presence of *Prototheca* species in water sources in Türkiye. The findings revealed the presence of *Prototheca* DNA in muddy water samples. These results highlight the need for broader sampling and molecular characterization to better understand the distribution and ecological roles of *Prototheca* species.

Acknowledgement: This study is part of the MSc thesis of A. E. Göksal, entitled “Isolation and Characterization of *Prototheca* sp. from Environmental Samples” (2025), conducted under the supervision of İ. Tuney.

Metagenomic investigation of ancient oral microbiota from dental calculus: A computational framework for taxonomic and functional profiling

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Abstract ID: 98
Keywords: Ancient DNA, Ancient Metagenomics, Dental Calculus, Oral Microbiome, İznik

Studying ancient oral microbiota provides a unique perspective on the health, diet, and cultural practices of past societies. Dental calculus provides an important access to this archive, as its mineralized structure that preserves microbial and eukaryotic DNA reads from environmental degradation. Microbial abundance profiles generally provide valuable information for drawing conclusions, but deeper insights can be gained by examining functional profiles such as presence of antibiotic resistance and virulence genes to extend the interpretation of health and disease.

Here, we aim to maximize information recovery from dental calculus samples by testing and integrating several computational workflows. Our case study focuses on the Middle age İznik (ancient Nicaea) city, which is a culturally diverse site where Crusaders, local Muslims, and local Christians coexisted. Those communities left behind distinct burial contexts that offer a rare opportunity to explore the interplay of culture, religion, and health in a shared environment.

Our approach has focused on two main objectives: We will combine *k*-mer based tools (e.g., KrakenUniq) and similarity-based methods (e.g., MALT, bowtie2) to identify and authenticate ancient bacterial and eukaryotic reads. This combination balances between false positive and false negative identifications providing robust microbial abundance profiles that will be used to draw conclusions on cultural differences and patterns of health and disease.

Moreover, we will use metagenome assembly methods that include binning tools, to create metagenome assembled genomes and extend our analysis. This workflow will enable to create longer contiguous sequences, facilitating the prediction of functional markers such as gene abundances, virulence factors and presence of antimicrobial resistance.

This integrative approach will help reconstruct a detailed picture of the oral microbiome and dietary components across İznik's diverse populations, offering new insights into how culture, health, and microbiomes were interconnected.

Movement ecology of the Egyptian Vulture (*Neophron percnopterus*) breeding in Beypazarı: Insights from GSM telemetry

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Abstract ID: 127
Keywords: Egyptian vulture, GSM-GPS telemetry, habitat use, migration route

The Egyptian vulture (Neophron percnopterus) is a globally endangered scavenger species that faces various anthropogenic threats along its migratory route, as well as in its breeding and wintering grounds. To better understand the movement ecology, habitat use, and conservation needs of this species, a monitoring study was initiated in 2022 in Beypazarı (Ankara, Turkey), one of its most important global breeding sites. As part of the study, three adult individuals were equipped with GPS-GSM transmitters. These devices provided high- resolution spatial data enabling the analysis of habitat preferences, migration routes, and seasonal areas. In total, 2,691 individual tracking days were analyzed, covering 265,359 kilometers. Core spatial analyses included Kernel Density Estimation (KDE) and Minimum Convex Polygon (MCP) methods. Migration routes, elevation profiles, and stopover sites were evaluated using analytical frameworks of animal and movement ecology. Behavioral states were estimated through non-parametric Bayesian models, based on guidelines for behavioral inference. All tracked individuals successfully completed migrations between Turkey and Sub-Saharan Africa. Notable variation was observed in migration routes and stopover durations. Semi-natural agricultural areas and waste sites were key foraging habitats, while high-risk zones such as wind farms and power lines were mapped. The results underline the necessity of international cooperation and targeted strategies to reduce mortality along migratory corridors. They also provide a basis for land-use planning and policy development to protect this endangered species.

Fish mortalities and molecular traces: A post-event eDNA survey in İzmir Bay, Aegean Sea

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Abstract ID: 101
Keywords: Fish mortality, Polykrikos hartmannii, eDNA

İzmir Bay is hydrographically divided into three regions: inner, middle, and outer bay. The inner bay is considered hypertrophic due to its shallow depth, limited circulation, and high nutrient input, whereas the outer bay exhibits oligotrophic characteristics under the influence of the Aegean Sea. This study was conducted on 23 August 2024 in the inner bay, where mass fish mortalities were first observed on 19 August 2024.

Environmental parameters including temperature, salinity, dissolved oxygen, and pH were measured in situ using a portable multimeter. Nutrient concentrations (NO_3^-, NO_2^-, PO_4^{3-}) and chlorophyll-a were determined spectrophotometrically. Satellite monitoring was performed using processed Sentinel-2 imagery. Surface water samples were collected for environmental DNA (eDNA) extraction, and the V9 region of the 18S rRNA gene was amplified and sequenced to assess eukaryotic diversity.

During sampling, temperature was 29.5°C, salinity 39, DO 2.27 mg/L, pH 8.35, and chlorophyll-a 88.3 µg/L. Nutrients measured: PO_4^{3-} at 2.48 µM, NO_3^- at 0.24 µM, NO_2^- at 0.105 µM. Based on environmental observations, the fish mortality event was observed in a shallow area (2–3 m), where relatively high nutrient concentrations, rising temperatures, and minimized circulation caused a Harmful Algal Bloom (HAB) event characterized by high chlorophyll concentrations, heterotrophic activity, and hypoxia.

Molecular analyses revealed that about 40% of the reads were assigned as "uncultured eukaryotes," reflecting both regional and global gaps in reference databases. The dinoflagellate *Polykrikos hartmannii*, first reported to bloom in İzmir Bay in November 2023, was detected at a high relative abundance (12%), suggesting its continued presence and potential dominance in the plankton community. The diatom *Cyclotella choctawhatcheeana* (6%) was also relatively abundant.

These findings show the potential of eDNA as a tool for detecting harmful species and exploring biodiversity in coastal areas. This study is also the first molecular report of *Polykrikos hartmannii* from Türkiye.

Ribosomal cistron of *Tetrix bolivari* (Tetriginae, Orthoptera): Characterization of linear and secondary structure

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Abstract ID: 73
Keywords: Characterization, Orthoptera, Ribosomal Cistron, Tetrix bolivari

The order Orthoptera, the most species-rich lineage within Polyneoptera (class *Insecta*) with more than 30,000 species, comprises two suborders: Caelifera and Ensifera. Within Caelifera, the family Tetrigidae (pygmy grasshoppers) has a cosmopolitan distribution and is classified into 27 subfamilies. Among them, Tetriginae remains poorly represented in molecular studies, and no research has focused on its nuclear ribosomal cistron yet.

The ribosomal cistron—composed of ETS, 18S, ITS1, 5.8S, ITS2, and 28S genes—is a highly informative genomic region commonly used in molecular systematics and evolutionary biology. In this study, we generated the complete nuclear rDNA sequence of *Tetrix bolivari*, a representative species of Tetriginae, using Next-Generation Sequencing (NGS) data. We determined the gene order, lengths, AT/GC composition, and gene-specific boundary motifs. Additionally, we predicted the secondary structure of the ITS2 region, focusing on conserved helices and potential compensatory base changes (CBCs) to assess phylogenetic signal. Given its conserved secondary structure and sequence variability, ITS2 is also evaluated as a potential secondary DNA barcode for Tetrigidae and possibly for Orthoptera and insects in general.

As no complete ribosomal cistron has yet been characterized for Tetrigidae, this study provides the first full structural annotation from this group. Our findings address a significant gap in insect ribosomal genomics, where most available data remain partial or genus-specific.

Comparative analyses with other *Orthoptera* species and available insect cistrons will allow testing of the universality and evolutionary conservation of known structural patterns. The results will inform whether rDNA features defined in other taxa are applicable to Orthopterans and insects at large, offering valuable insights into the ribosomal cistron and its taxonomic utility.

Balancing ethics and efficiency: Evaluating capture techniques for Wild Goats in rugged terrain

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Abstract ID: 27
Keywords: Animal welfare, Capra aegagrus, Live capture methods, Mountain wildlife research, Wild goat

Efficient and ethical capture of large mountain ungulates remains a significant challenge for wildlife researchers, particularly in topographically complex and remote habitats. This study presents a comparative field assessment of two commonly used live capture methods—drop net and clover trap—for the Near Threatened wild goat (*Capra aegagrus*) in the Taurus Mountains of Türkiye. Over a two-year period, nine individuals were successfully captured and monitored using GPS collars. Both methods were evaluated in terms of cost, operational effort, capture success, animal behavior and welfare, habituation time, and adaptability to steep, forested terrain. The clover trap was found to be more cost-effective, less technologically demanding, and logistically simpler to implement in areas with network connectivity. However, the drop net allowed for targeted, multiple captures with lower habituation periods. No injuries or mortalities were recorded for either method, although behavioral observations indicated potential differences in stress levels. These findings provide practical insights for researchers planning field-based ecological or behavioral studies involving live capture of mountain ungulates, and offer guidelines for selecting appropriate capture methods under varying field constraints and ethical considerations.

Microplastic pollution and risk assessment in surface water of Susurluk Sub-Basin

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Abstract ID: 80
Keywords: Bursa, CORINE, Hazardous Index, Microplastics, Pollution Risk Index, Susurluk Sub-Basin

Microplastics are an emerging global pollutant of growing concern, commonly found in freshwater ecosystems, which play a crucial role in transporting land-based microplastics to marine environments. This study utilizes diverse pollution assessment indices to investigate seasonal variations and anthropogenic impacts, particularly land use, on microplastic pollution in the surface waters within the Susurluk Sub-basin in Bursa province. Microplastic sampling was carried out seasonally at 11 sites grouped into three main areas: Nilüfer Stream, Kocaçay Stream, and Uluabat Lake areas. Among these, Nilüfer Stream—flowing through Bursa's industrial zone—showed the highest microplastic concentrations, with values reaching up to 6660.35 MPs/m^3 Conversely, lower microplastic densities were observed around Lake Uluabat, an area characterized by regulated urban development. Seasonal variations in microplastic abundance were apparent, peaking in winter and declining in summer, correlated with precipitation changes. The most commonly identified type was fibers, typically ranging in size from 0.11 to 5 mm. FTIR analyses showed that polyethylene (PE), polypropylene (PP), and polystyrene (PS) were predominant polymers. Pollution Load Index (PLI) values exceeding 1, notably in winter, indicated heightened anthropogenic impacts in areas like Nilüfer Stream. Variation in polymer distribution influenced the Hazard Index (H), highlighting elevated risks where high-risk polymers such as polyurethane (PUR), polyacrylonitrile (PAN), and polyvinyl chloride (PVC) were prevalent. Pollution Risk Index (PRI) results highlighted Nilüfer Stream as the most critical hotspot for microplastic pollution, posing substantial threats to marine ecosystems due to its direct hydrological connection to the Marmara Sea—a key conduit between the Black Sea and the Aegean. These findings highlight an urgent need for pollution mitigation strategies to protect interconnected aquatic systems.

Impacts of aquaculture activities on microbial diversity in the Euphrates River: An eDNA-based assessment

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Abstract ID: 116
Keywords: Amplicon Sequencing, Aquaculture, Environmental Monitoring, Euphrates River, Genomics, Metabarcoding, Microbial Diversity, eDNA

The Euphrates River, one of the most significant freshwater systems in the Middle East, supports diverse aquatic biota and provides critical ecosystem services. However, increasing anthropogenic pressures—particularly aquaculture—may influence microbial community structure, with potential consequences for water quality and ecosystem functioning. Given that microbial diversity serves as a sensitive indicator of aquatic ecosystem health, monitoring these communities is essential for guiding sustainable aquaculture practices.

In this pilot study, we employed environmental DNA (eDNA) metabarcoding targeting the 16S rRNA gene to assess microbial diversity across four sampling stations in the Kızılin and Birecik regions of the Euphrates River. Three stations were situated at varying proximities to a trout aquaculture facility in Birecik, while the Kızılin station, located away from any aquaculture activity, served as a reference site. Water samples were collected and processed for amplicon sequencing, followed by taxonomic classification using established bioinformatic pipelines.

The analysis revealed dominant bacterial taxa across all stations, including Angustibacter aerolatus, Nostocoides australiense, Limnohabitans planktonicus, Fluviicola taffensis, Sanguibacter gelidistatuariae, and Candidatus Pelagibacter. Notably, increased relative abundances of Angustibacter aerolatus, Nostocoides australiense, Micropruina glycogenica, and Candidatus Pelagibacter were observed at the station closest to the aquaculture site, suggesting a localized impact of fish farming on microbial composition.

These initial findings highlight the utility of eDNA-based approaches in freshwater

biomonitoring and underscore the need for longitudinal studies to assess temporal dynamics and potential cumulative effects. Understanding how aquaculture influences microbial biodiversity will be vital for developing environmentally responsible management strategies in riverine systems.

Endosymbiont-associated divergence: *Wolbachia* prevalence and mitochondrial patterns in Sand Flies of Türkiye

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Abstract ID: 56
Keywords: , Endosymbionts, MLST, Phlebotomine, sand fly, selective sweep

Sand flies are key vectors responsible for transmitting various pathogens, notably *Leishmania* spp., the causative agents of leishmaniasis. Endosymbiotic bacteria such as *Wolbachia* have recently gained attention due to their ability to influence arthropod vector biology, reproduction, and pathogen transmission. Despite growing interest, the prevalence, diversity, and ecological roles of *Wolbachia* in sand flies remain insufficiently characterized. We investigated the natural infection status of sand fly taxa across Türkiye and its potential role in mitochondrial genetic divergence observed in certain taxa. A total of 852 sand flies representing 18 taxa from diverse ecological regions of Türkiye were screened for *Wolbachia* sp.using PCR amplification of ~340 bp fragment of *wsp* (*Wolbachia* surface protein) gene. Multilocus sequence typing (MLST), targeting five conserved housekeeping genes (*gatB*, *coxA*, *hcpA*, *ftsZ*, and *fbpA*), was performed on positives to characterize strain diversity and phylogenetic relationships. The overall prevalence was 16.78%, with *Wolbachia* sp. detected exclusively in *Phlebotomus papatasi* (20.59%), *Phlebotomus major* sensu lato (62.74%), *Phlebotomus tobbi*(0.83%), *Phlebotomus economidesi* (100%), and *Sergentomyia minuta* (3.03%). MLST analyses revealed distinct*Wolbachia* strains, all clustering within Supergroup A, infecting both conspecific and heterospecific taxa. Mitochondrial sequence data showed reduced genetic diversity among *Wolbachia*-infected lineages of *Phlebotomus major* complex compared to uninfected ones. This suggests *Wolbachia* may contribute significantly to mitochondrial divergence and lineage differentiation, potentially via genetic hitchhiking. These findings improve our understanding of sand fly vector biology and have important implications for vector control and disease epidemiology. The CLIMOS consortium is co-funded by the European Commission grant 101057690 and UKRI grants 10038150 and 10039289. The six Horizon Europe projects, BlueAdapt, CATALYSE, CLIMOS, HIGH Horizons, IDAlert, and TRIGGER, form the Climate Change and Health Cluster.

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Non-invasive monitoring of predator–prey relationships and microbial diversity via owl pellet metabarcoding

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Abstract ID: 117
Keywords: dietary analysis, eDNA metabarcoding, owl pellet, predator-prey interactions, wildlife

Owl pellets serve as valuable biological archives for reconstructing dietary habits, predator-prey relationships, and associated microbiota through non-invasive molecular methods. In this study, we applied a multi-marker environmental DNA (eDNA) metabarcoding approach to analyze four composite owl pellet samples collected from a minimally disturbed cave ecosystem near the Göksu River in Adıyaman Province, Türkiye. The exact location is withheld due to the presence of a protected species. Although the owl was not observed at the time of sampling, metabarcoding identified the host species as *Tyto alba*.

We performed 16 individual eDNA extractions from the pellet material. Amplicons were generated using MiFish (12S), MiBird (12S), and 12SV5 markers for vertebrate diet analysis, alongside 16S rRNA V3–V4 primers for bacterial community profiling. Illumina NovaSeq6000 sequencing yielded approximately 500,000 paired-end reads per sample. Diet composition based on the 12S datasets revealed a strong preference for arvicoline rodents, including *Microtus guentheri*, *Microtus arvalis*, and *Myodes glareolus*. Additional vertebrate DNA indicated the presence of amphibians (*Pelophylax* sp.), birds (*Ardea cinerea*, *Columba palumbus*), and fish species such as *Alburnus mossulensis*—potentially a novel record for the region—and *Sparus aurata*. Environmental DNA from domestic species (*Gallus gallus*, *Capra hircus*) likely reflects airborne contamination. The unexpected detection of *Hyaena hyaena* DNA suggests shared cave use, supporting the cohabitation hypothesis.

Microbial profiling revealed diverse taxa, including gut-associated bacteria (*Escherichia coli*, *Klebsiella pneumoniae*,*Enterococcus faecalis*), environmental genera (*Bacillus*, *Sporosarcina*,*Carnobacterium*), and potentially pathogenic species such as *Clostridium perfringens* and *Salmonella enterica*.

This study demonstrates the power of eDNA metabarcoding to recover ecological and microbiological insights from owl pellets in natural habitats. The findings provide a comprehensive snapshot of trophic interactions, microbial diversity, and interspecies associations in a low-impact environment, supporting the value of non-invasive molecular monitoring in biospeleological research.

Investigation of selection pressure on cohesin and condensin genes in *Nannospalax xanthodon*

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Abstract ID: 25
Keywords: Chromosomal evolution, Selection pressure, cohesin, condensin

Proper chromosome segregation during cell division is critical for genomic stability, and cohesin-condensin protein complexes play essential roles in this process. These Structural Maintenance of Chromosomes (SMC) complexes are evolutionarily conserved and participate in mitosis, meiosis, gene regulation,and DNA repair. Mutations affecting their function can influence fitness and are implicated in cancer and chromosomal instability. However, the evolutionary dynamics of these complexes remain poorly understood in non-model organisms. This project investigates selection pressures acting on cohesin and condensin genes in Nannospalax xanthodon, a subterranean rodent known for extensive chromosomal diversity. These animals exhibit unique evolutionary and physiological traits, including tolerating hypoxic conditions and resisting tumor formation. Much of their karyotypic variation is attributed to Robertsonian translocations, which play a key role in their genomic evolution and potentially speciation. The study combines comparative genomics and gene expression analyses across different cytotypes and populations. Samples will be collected from four localities in Turkey: two with 2n=60 cytotypes, one with 2n=52 cytotypes, and one with 2n=38 cytotypes. These localities represent major chromosomal forms of Nannospalax and were selected because they share similar ecological and geological characteristics, allowing chromosomal differences to be examined as the main variable. Additionally, Microtus species from the same localities, with stable karyotypes, will serve as evolutionary controls. Target enrichment sequencing will be performed for 19 cohesin and condensin genes, and Western blot will assess protein expression differences. Genes previously identified under positive selection in Israeli mole rats will also be included to validate selection signals. Sequence variation will be analyzed using dN/dS ratios and McDonald–Kreitman tests. This study, supported by the TÜBİTAK 1001 programme under project number 124Z079, is the first to explore cohesin/condensin evolution with cytotypic divergence in *Nannospalax*, providing insights into chromosomal evolution, genome plasticity, and natural selection.

Variability in seed mass, germination, and dormancy in steppe plant communities along a productivity gradient in Central Anatolia

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Abstract ID: 100
Keywords: functional traits, germination, productivity gradient, seeds, steppe

Productivity is an important environmental factor that influences seed traits in plant communities. In this study, we examined how seed traits respond to a productivity gradient across 25 steppe sites in central Anatolia, Türkiye. The sites span a 100-km range from dry lowlands to wetter mountainous areas. Fruits of dominant species at each site were collected from the field, and then prepared for measurements and experiments in the laboratory. We measured key seed traits from over 70 species, including seed mass, dormancy level, germination capacity, and viability. Data were analyzed using linear and non-linear regressions, generalized linear models, and multivariate analysis techniques. Our results indicated a considerable variation in seed traits across species and sites. Germination percentage and dormancy level followed a humped-back pattern along the productivity gradient, with lower germination and higher dormancy values at the both ends of the gradient. Plants in moderately productive areas adjusted their germination and dormancy traits to balance growth success and environmental risk, which is supporting resource-based trade-off theories. Overall, our findings highlight the strong influence of environmental conditions on seed traits in temperate grasslands and provide new insights into the seed ecology of plant communities in the central Anatolian steppe.

Genome meets grave: Molecular identification of tuberculosis in a Byzantine burial

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Abstract ID: 49
Keywords: 16S rRNA sequencing, Mycobacterium tuberculosis, ancient DNA (aDNA), paleopathology, shotgun metagenomics

This study investigates the pathological features of a human skeleton unearthed from the ancient city of Side (Antalya, Türkiye), dated to the Byzantine period, using ancient DNA (aDNA) analysis. The individual exhibited porotic lesions on the vertebrae and was buried outside the necropolis area, suggesting a possible infectious origin. DNA extraction was carried out using the QIAamp DNA Investigator Kit. The presence of amplifiable human DNA was confirmed via gradient PCR and real-time PCR (qPCR) using short human-specific primers. Shotgun sequencing libraries were prepared following the Meyer & Kircher protocol and sequenced on the Illumina NovaSeq 6000 platform. Additionally, 16S rRNA amplicon sequencing was performed to identify potential pathogen DNA, with taxonomic assignments based on the SILVA database. Both shotgun and 16S metagenomic analyses revealed sequences corresponding to the *Mycobacterium tuberculosis* complex. Damage profiller analysis further confirmed the ancient origin of these sequences. These findings provide molecular evidence supporting a diagnosis of tuberculosis in the individual, which had previously been hypothesized based on archaeological and anthropological context. This study demonstrates the complementary use of shotgun and 16S sequencing in ancient pathogen detection and contributes to our understanding of the molecular pathogenesis of historical infectious diseases.

The shifting mosaic: Climate change impacts on endemic vertebrates in the Mediterranean biodiversity hotspot

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Abstract ID: 84
Keywords: Mediterranean Basin, biodiversity informatics, climate change, ecological niche modeling, endemic terrestrial vertebrates

The Mediterranean Basin, a globally recognized biodiversity hotspot, faces profound ecological shifts due to climate change. This presentation will explore the historical distributions and future distributional impacts of climate change on the region's endemic terrestrial vertebrates, specifically amphibians, reptiles, birds, and mammals.

Employing Ecological Niche Modeling (ENM), this research investigates species' responses to significant past climatic periods like the Last Glacial Maximum, the Middle Holocene, and the Last Interglacial by reconstructing their historical suitable habitats. It further projects potential future distributions under various climate scenarios for 2050 and 2070.

Key findings from these distributional analyses reveal distinct vulnerabilities and resilience patterns across taxa. For 36 amphibian species, precipitation emerged as a critical factor shaping their suitable habitats, with projections indicating some current biodiversity hotspots could transition to coldspots. Analysis of 45 bird species showed that historical climate fluctuations drove significant changes in distributions, with future high-emission scenarios likely causing northward shifts in suitable areas. Studies on 31 mammal species underscored the vital role of glacial refugia in maintaining species richness through stable habitat availability, though significant future habitat contractions are anticipated, particularly in southern regions. For 50 reptile species, certain regions have served as long- term biological refugia, providing continuous suitable conditions, but now face severe losses under high-emission scenarios.

Collectively, these results demonstrate the substantial and varied effects of climate change on the distributions of endemic terrestrial vertebrates across the Mediterranean Basin. This underscores the urgent need for dynamic, comprehensive conservation strategies that integrate climatic factors to safeguard this unique regional biodiversity in an era of rapid environmental change.

Taxonomic and functional diversity of macroinvertebrate communities in relation to environmental variables in rural ponds of Ankara, Turkey

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Abstract ID: 110
Keywords: Ecosystem resilience, Freshwater ponds, Functional diversity, Macroinvertebrates, Rural, Taxonomic diversity

Freshwater ponds are essential ecosystems that support biodiversity and provide key ecological functions through various macroinvertebrate species. Understanding how environmental conditions affect macroinvertebrates' taxonomic and functional diversity is critical for effective ecosystem management and conservation efforts. This study focuses on macroinvertebrate communities in rural ponds in Ankara, Turkey, specifically Kahramankazan and Kızılcahamam. Field sampling was carried out in 30 ponds between 2022 and 2023, with 12 ponds resampled in the second year. Macroinvertebrate specimens were collected and identified, and functional features such as habitat preferences, feeding tactics, life-history strategies, body size, and dispersal abilities were assembled using available literature. Environmental characteristics, including pond area, depth, macrophyte coverage (Plant Volume Inhabited - PVI), and nutrient concentrations (total phosphorus, chlorophyll-a) were measured. The core objectives of this study are to assess the taxonomic and functional diversity patterns of macroinvertebrate communities and to investigate their potential links with key environmental variables. Preliminary studies reveal that macroinvertebrate composition varies significantly between ponds, most likely due to changes in environmental circumstances. The study of functional and response diversity will bring light on how macroinvertebrate communities may respond to environmental changes, with implications for understanding ecosystem resilience. The findings of this study are expected to add useful knowledge to freshwater ecosystem conservation methods to preserve biodiversity and improve ecosystem resilience.

We all love success stories, but why is the return of a population not relieving? Concerns over the recovery of the Mediterranean sea turtle population

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Abstract ID: 75
Keywords: Conservation, Mediterranean Sea Turtles, Population recovery, Population status

For species that are widely distributed and long-lived, determining conservation and research priorities at ecologically relevant population levels presents significant challenges. These complexities are reflected in the diverse frameworks applied across national, regional, and global scales to assess conservation status and set priorities. Sea turtles provide a good example of these difficulties due to the extensive global coordination their conservation requires. Thanks to long-term conservation efforts, several sea turtle species have shown signs of recovery worldwide. In the Mediterranean, two subpopulations—the loggerhead (Caretta caretta) and green sea turtle (*Chelonia mydas*)—have been identified. According to International Union for Conservation of Nature (IUCN) Red List criteria, their statuses have improved from "Endangered" to "Least Concern" and "Near Threatened," respectively. Türkiye and Greece host the most important nesting beaches for these species. While Greece began systematic monitoring in the 1980s, Türkiye followed in the early 1990s. Given their age at maturity of 20–30 years, conservation outcomes have become more observable in the last decade. Indeed, significant population increases have occurred. Since the 1980s, the loggerhead turtle nest counts have increased by 225% and the green sea turtle nest counts have increased by 270%. However, this recovery has coincided with intensified threats: degradation of nesting habitats, increased fishing pressure, rising maritime traffic, pollution, and continued poaching—especially in North Africa. In this context, this study aims to evaluate the concerns that attribute the observed population increase to conservation efforts focused on only a few key nesting beaches, despite the increase in factors that have a significant negative impact on the survival rates of Mediterranean sea turtles, through the themes of climate change and fisheries. Additionally, it discusses potential future scenarios in the Mediterranean by comparing changes in different populations around the world.

Novel Protein Language Models for Viral Escape Prediction

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Abstract ID: 16
Keywords: Protein Language Model, machine learning, molecular evolution, viral evolution

Elucidating mechanisms behind viral evolution is crucial for developing effective vaccines and neutralizing antibody (NAb) therapies, yet predicting immune-evading mutations remains challenging. Recent advances in protein language models have led to novel approaches for *in silico* analysis of viral escape.

In this work, we propose CoV-RoBERTa, a light-weight protein language model for efficient prediction of viral escape using only sequence data. CoV-RoBERTa is pre-trained on a high-quality, chronological SARS-CoV-2 Spike protein dataset that we carefully curated. The strength of CoV-RoBERTa lies in its custom tokenizer, designed to produce compact representations. The model maps antigenic variation to semantic change and viral fitness to grammaticality, employing Constrained Semantic Change Search (CSCS) rank-based acquisition function to detect viral escape. To further enhance the effectiveness of CSCS, we introduce inverse perplexity as a novel grammaticality metric. Subsequently, we develop Siamese (CoV-SNN), Triplet (CoV-TNN), and Classifier (CoV-CLS) neural network models, which classify variants by capturing the similarities and differences between their protein sequences through CoV-RoBERTa embeddings. We evaluate our models on novel variant sequences with both real and artificially generated escape mutations. Finally, we evaluate our protein language model's findings within a traditional molecular evolution framework.

Computational methods transforming paleontology

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Abstract ID: 126
Keywords: Machine Learning, Paleoecology, Paleontology

Recent advances in artificial intelligence (AI) have introduced powerful methods for addressing long-standing challenges in paleontological research, particularly in biodiversity quantification, ecological reconstruction, and deep-time data integration. This contribution focuses on the emerging AI-driven methodologies that are redefining fossil data acquisition, organization, and analysis.

Natural language processing (NLP) techniques, including named entity recognition and transformer-based models, are increasingly used to extract structured data from unstructured sources such as legacy publications, museum records, and field notes. These tools enable large-scale, automated compilation of fossil occurrence and trait data.

For spatial and temporal modeling supervised machine learning algorithms such as random forests, gradient boosting, and increasingly deep neural networks are applied to identify predictors of biodiversity dynamics, extinction selectivity, and dispersal patterns. These models are now complemented by generative approaches for simulating paleoecological scenarios and filling data gaps.

Phylogenetic comparative methods are scaled up through AI-supported tree-building algorithms and deep learning tools that operate on tree-structured data. This allows for rapid, high-resolution testing of evolutionary hypotheses across hundreds or thousands of taxa. Integration with trait data enables novel insights into adaptive radiations, evolutionary constraints, and trait-environment correlations.

Graph-based learning methods and knowledge graph construction are emerging as tools for representing complex relationships across fossil datasets, linking taxonomy, geography, stratigraphy, and environmental variables in a unified framework.

This presentation highlights these methodological innovations and discusses their transformative impact on deep-time biodiversity research. By leveraging these AI tools paleontology is evolving into a highly integrative, quantitative, and predictive science capable of addressing large-scale ecological and evolutionary questions.

How pond characteristics affect macrophyte diversity and coverage in rural ponds of Ankara, Türkiye

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Abstract ID: 69
Keywords: PVI, aquatic plants, environmental factors, freshwater ecosystem, macrophytes, pond, shallow lakes

Freshwater ponds, despite their small size, support remarkably diverse aquatic plant communities and play a vital role in maintaining regional biodiversity. These ecosystems often serve as refuges for rare or specialized macrophyte species, offering a range of microhabitats shaped by varying environmental conditions. Their dynamic and heterogeneous nature allows them to host a wide array of ecological interactions, making them important components of the landscape despite being frequently overlooked in conservation planning. As part of the PONDERFUL project, this study investigates macrophyte diversity and coverage in 40 ponds located in rural areas of Ankara, Türkiye. Data were collected during 2022 and 2023, including species identification and coverage assessments using the Plant Volume Inhabited (%PVI) method. The aim of the study is to explore how variation in macrophyte diversity and coverage relates to environmental conditions, focusing on physical and chemical parameters. Preliminary results indicate substantial differences in macrophyte communities across ponds, with certain abiotic variables showing potential influence on diversity and coverage patterns. Identifying which environmental conditions are associated with these patterns can help clarify the role of environmental filtering in shaping macrophyte assemblages. This understanding may support future ecological assessments and conservation strategies for small freshwater ecosystems.

Ancient sedimentary DNA reveals human, animal and microbial activity in El Portalón cave

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Abstract ID: 94
Keywords: Ancient DNA, El Portalone, Sediment DNA, aDNA, domestic cattle, domestic sheep, sedaDNA

El Portalón cave is located in the Sierra de Atapuerca, Spain, and contains a well-preserved and contextualized stratigraphic sequence spanning from the Pleistocene to Medieval period including Neolithic, Chalcolithic, Bronze, Iron, Roman and Medieval Ages. Research indicates that human activity began during the Late Pleistocene, marking the Pleistocene Holocene contact. Favorable preservation conditions have enabled the recovery of human remains as well as domestic and wild fauna. For example, skeletal material from Ovicaprines (sheep and goats), cattle, horse, pig and dog have been recovered from layers that were radiocarbon dated. Given the exceptional preservation of the site, we think that sedimentary DNA methods could provide valuable insights into past anthropogenic activities. To explore this we collected 25 different samples from the early Pleistocene to the Medieval period. Our analysis followed two main approaches: first we classified and authenticated eukaryotic DNA reads to identify domesticated animals and plants; second we used metagenome assemblies to investigate the shifts in bacterial composition across stratigraphic layers. Our results showed presence of domestic sheep, domestic cattle, barley and wheat DNA reads starting from Neolithic layers. Those reads exhibit ancient DNA specific patterns such as deamination signals and fragmented DNA distribution that is consistent with long-term degradation. Metagenome-assembled genomes indicated a shift in microbial communities following the Pleistocene-Holocene contact, suggesting human activity in the cave. Moreover, we observed ancient methanogenic microbial reads that are associated with gut microbiomes, starting from the Bell Beaker layer. These microbes generally thrive in organic-rich anaerobic environments suggesting continuous use of the site by humans and domesticated animals. In summary, our eukaryotic and microbial findings highlight the potential of sedimentary DNA analysis to explore anthropogenic activity, offering valuable insights even in the absence of skeletal remains.

Preliminary assessment of meiofaunal diversity and environmental factors in the intertidal zone of the Filyos and Sefercik Coasts (Black Sea, Zonguldak, Türkiye)

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Abstract ID: 35
Keywords: Anthropogenic impact, coastal biodiversity., habitat protection

Meiofauna play crucial roles in nutrient cycling, organic matter decomposition, and form an essential food source for higher trophic levels. Due to their sensitivity to environmental changes, they are considered effective bioindicators for assessing coastal ecosystem health and anthropogenic pressure.

This study presents preliminary findings from an ongoing investigation of meiofaunal diversity and spatiotemporal patterns along the intertidal zones of Filyos and Sefercik coasts in the western Black Sea region of Türkiye. Monthly sampling was conducted between December 2023 and November 2024 at 15 stations using an el corer to collect the top 20 cm of sediment. Stations were selected to represent varying degrees of anthropogenic influence, including freshwater inflow, sewage discharge, port activity, seasonal tourism, and relatively undisturbed areas.

Harpacticoid copepods and nematodes were the dominant taxa throughout the year. Other groups included Acarii, isopods, oligochaetes, polychaetes, amphipods, calanoid and cyclopoid copepods, chironomids, ostracods, and cladocerans. The highest diversity was recorded in April 2024 and the lowest in January 2024. Stations 4 and 5, with minimal human impact, exhibited the greatest species richness, while Station 13, affected by sewage and intense anthropogenic stress, had the lowest.

Environmental parameters such as dissolved oxygen, total dissolved solids, pH, conductivity, and salinity were measured monthly. Initial results reveal a clear correlation between meiofaunal diversity and anthropogenic pressure.

Given that only one harpacticoid copepod species has been previously reported from this region, the study provides essential baseline data for future ecological and taxonomic research. These findings offer a reference point for monitoring the effects of ongoing industrialization, including the newly constructed Filyos Port, and support the conservation of sandy coastal habitats. This study is a part of MSc thesis of Eylem Gülay.

Understanding the factors affecting the diversity of zooplankton communities in a pond metacommunity

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Abstract ID: 87
Keywords: Community Assembly, Environmental Filtering, Functional Trait Diversity, Pond Metacommunities, Zooplankton

Ponds, though small, are vital freshwater ecosystems that serve as biodiversity hotspots. They support diverse communities of aquatic plants, invertebrates, vertebrates, and microorganisms. These habitats also enhance ecological connectivity by promoting gene flow and species dispersal, making them crucial for the persistence of endemic and specialized species.

Despite their ecological importance, ponds are often understudied compared to larger water bodies. However, their small size, environmental heterogeneity, and spatial isolation make them ideal systems for studying metacommunity dynamics. Functional trait-based approaches go beyond traditional taxonomy by linking species traits to ecological processes and responses to environmental stressors.

This study explores zooplankton functional trait diversity in 40 ponds across rural Ankara, Türkiye. It aims to evaluate how similar these ponds are based on abiotic factors such as physicochemical conditions, morphology, and spatial proximity. The central goal is to assess how environmental filtering shapes zooplankton communities in these ecosystems.

Using multivariate statistical and trait-based analyses, the study investigates the influence of abiotic filters on community assembly and functional composition. Results are expected to reveal patterns of pond similarity and associations between environmental variables and zooplankton traits. Identifying key environmental drivers will help determine which ponds are more vulnerable to change.

Understanding how abiotic conditions influence zooplankton communities enhances our knowledge of freshwater ecosystem functioning. In the face of climate change and increasing anthropogenic pressures, such insights are essential for developing conservation and restoration strategies. This research contributes valuable evidence to support the protection and management of small waterbodies, which, despite their size, play an outsized role in maintaining ecological integrity.

A modeled bioavailable Strontium isoscape (87Sr/86Sr) of Türkiye: A research tool for archaeological mobility reconstruction

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Abstract ID: 76
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Keywords: 87Sr/86Sr, ancient human mobility, bioavailable strontium isotopes, isoscapes, kriging, random forest regression (RFR)

Strontium isotope ratio (^{87}Sr/^{86}Sr) analysis is a well-established methodology in ancient mobility studies. Lifetime mobility of archaeological humans/animals can be determined by comparing analyzed dental remains to bioavailable ^{87}Sr/^{86}Sr derived from geo-referenced proxy samples. ^{87}Sr/^{86}Sr analysis in Anatolian archaeology has grown steadily since the early 2010s; however, a coherent map of the isotopic variability of bioavailable strontium (Sr *isoscape*) does not exist for the region. The paucity of baseline data significantly constrains the interpretation of archaeological data and diminishes the heuristic power of this methodology in Anatolian archaeology. Baseline and 'local range' determination in previous studies have relied on geology maps or various sample types from very limited areas in site- centered studies, and the use of predictive modeling for isoscape reconstruction at regional scales has just begun in Türkiye.

To address this problem, we developed a bioavailable ^{87}Sr/^{86}Sr isoscape of Türkiye to serve as a reference map and a research tool for archaeological mobility studies. We combined all published baseline data from Türkiye with our unpublished data from proxy samples (plants & snail shells) from central Anatolia, and by incorporating this data (n=688) into a recently developed, open-access global database (where data from Türkiye is currently lacking), we created a modeled ^{87}Sr/^{86}Sr isoscape of Türkiye utilizing the open-source R-script and we calculated the predicted standard error for this isoscape. In a recent publication (doi:10.3389/fearc.2025.1520345), we presented a review of extant ^{87}Sr/^{86}Sr analyses and baseline studies in Anatolian archaeology, discussed current methodologies in Sr isoscape reconstruction, and identified beneficial avenues for mobility studies in Anatolian archaeology. This study demonstrates how additional empirical data improves the Türkiye section of the global model using kriging and random forest regression techniques and it discusses how the uneven distribution of data impacts the resultant isoscape.

Afforestation alters epigeic beetle community in Central Anatolian Steppes

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Abstract ID: 58
Keywords: Central Anatolian steppe, afforestation, antifreeze, community ecology, epigeic beetles, pitfall traps, vinegar.

Epigeic beetles, which inhabit the soil surface, play a crucial role in terrestrial ecosystems as they contribute particularly to soil dynamics and nutrient cycling. In our study, we investigated the effect of afforestation on the patterns of diversity and community composition of epigeic beetles (Coleoptera: Carabidae, Scarabaeidae, Tenebrionidae, Staphylinidae) in a steppe habitat in Central Anatolia, Türkiye. We also tested whether different pitfall solutions affect sampling success of epigeic beetles. Three sites were selected for afforested and steppe habitats, and 16 pitfall traps were placed at each site; half included 50% vinegar solution and other half contained antifreeze as trapping fluids. Samples were collected weekly between September and October 2024, and then insects were identified and counted. To compare the epigeic beetle community structure across habitats and methods, we used generalized linear models assuming Poisson distribution for abundance and species richness, ANOVA for Shannon diversity index and non-metric multidimensional scaling for community composition. In total, we sampled 1770 individuals belonging to 17 species, with the highest abundance of Carabidae, specifically *Calathus cinctus*. Afforestation sites had higher species richness and diversity than steppe, but no significant difference was observed between methods. For abundance, we found differences between habitats and between methods. Afforested sites and traps containing vinegar had higher abundance of epigeic beetles than steppe sites and traps with antifreeze. Genera and family diversity and the number of unique taxa had higher values in steppe sites compared to afforested sites. Species composition of epigeic beetle community was significantly different between habitats. Our findings suggest that afforestation in central Anatolian steppes significantly alter epigeic beetle community, and vinegar can be an alternative option for antifreeze to use in pitfall traps, especially for research requiring higher abundance of epigeic insect sample.

The evolving mind subterranean: Mapping neuroanatomical adaptations in subterran rodents

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Abstract ID: 135

Subterranean rodents spend their entire lives within complex underground tunnel networks. As a result of this strictly fossorial lifestyle, they have developed a suite of morphological and physiological traits suited to life below ground. Visual capabilities are greatly diminished, while sensory systems responsible for touch, smell, and hearing are markedly enhanced. These sensory specializations are also mirrored in the neural architecture, particularly in the brain regions that process non-visual sensory input. Generating detailed brain atlases in these species is crucial for identifying how specific brain structures are modified in response to ecological pressures, and provides a foundational framework for future comparative, developmental, and functional studies in evolutionary neuroscience. Interestingly, some Turkish subterranean rodents also exhibit remarkable longevity, similar to the well-studied naked mole-rat, raising the possibility that certain neural specializations may contribute to extended lifespan in these species as well. Studies have shown that fossorial rodents such as Spalacidae exhibit substantial reorganization in their sensory brain regions, with enlarged somatosensory and auditory areas and regressed visual centers, reflecting a profound adaptation to subterranean life.

Studying these traits in non-model organisms is especially valuable, as it broadens our understanding of brain evolution beyond the limited set of commonly used laboratory species. Turkey hosts a rich diversity of subterranean rodents, offering a unique and largely untapped resource for investigating how ecological and evolutionary pressures shape neural systems in extreme environments. This poster aims to investigate brain adaptations in Turkish subterranean rodents, highlight the value of non-model species in sensory and neural evolution, and emphasize the importance of creating brain atlases for future comparative studies, and has been prepared to introduce a model study based on this approach.

Acorn thieves: Uncovering the agents behind oak regeneration

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Abstract ID: 72
Keywords: Acorn caching, Animal-plant interactions, Field vole, Forest regeneration, Microhabitat variation, Quercus, Rodent behavior, Seed dispersal, Wood mice

Oaks (*Quercus spp.*) play a vital ecological role, offering food and habitat for numerous species while contributing to soil health and air quality. They depend on animal-mediated seed dispersal for regeneration, with species such as wood mice (*Apodemus spp*) and Eurasian jay (*Garrulus glandarius*) playing key roles. This study aims to investigate dispersal mechanisms through a combination of field and experimental approaches. Acorns were placed in selected habitats and monitored using live traps and camera traps to identify animal dispersers. Preliminary observations at METU indicate rapid removal of placed acorns, typically within three days. Moreover, it is found that disperser species vary by location: field voles dominate in the wooded area behind the Biological Sciences Building, whereas wood mice are the primary dispersers in the oak-dominated forest behind the School of Foreign Languages. Planned methods include the use of PIT-tagged acorns to track dispersal and caching behavior, germination trials to assess dispersal effectiveness, and cafeteria-style experiments to compare species-specific preferences and strategies. The study also explores whether dispersal behavior in wood mice varies with oak density, suggesting a potential cultural component.

Decoding microplastic-associated microbial communities: eDNA-based insights into diversity and environmental risk

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Abstract ID: 41
Keywords: Melen River, Metabarcoding, Plastisphere, eDNA

Microplastics (MPs) are widespread contaminants in aquatic ecosystems, acting as vectors for microbial colonization and biofilm formation. These biofilms can influence ecological processes and pose potential public health risks. This study investigates the seasonal dynamics of MP- associated microbial communities in the Melen River catchment using an environmental DNA (eDNA) metabarcoding approach. The V3–V4 region of the 16S rRNA gene was amplified and sequenced on the Illumina MiSeq platform (2×300 bp paired-end reads). Our analysis identified approximately 80,000 microbial genera associated with MPs, with polyethylene (PE) and polypropylene (PP) as the most prevalent polymer types. These polymers supported the colonization of bacterial genera such as *Acinetobacter*, *Pseudomonas*, *Flavobacterium*, *Paludibacter*, and *Undibacterium*, many of which are linked to pathogenicity and environmental stress responses. Functional prediction indicated active microbial pathways related to fermentation, vitamin biosynthesis, nucleoside/nucleotide degradation, and secondary metabolite processing. These findings highlight the ecological and health implications of MP pollution in freshwater systems, highlighting the need for continued monitoring of plastic-associated microbial communities to better understand their long-term environmental and public health impacts.

Comparative analysis of $\delta^{13}C$ and $\delta^{15}N$ ratios and trophic positions in two omnivorous fish species along a disturbed urban river gradient

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Abstract ID: 12
Keywords: , Antalya, fish, stable isotope analysis, trophic ecology, urban river

The spatial variation in the trophic base of populations, in relation to geomorphology and human land use, is a key topic in stream ecology. The Aksu River, where this study was conducted, originates in the mountainous areas of Isparta and Burdur and flows into the Mediterranean through Antalya. The upper basin remains relatively natural, while the middle and lower basin face intense land use pressure (urbanization, agriculture, tourism, industry) and contain two reservoirs. This land use pressures water quality and alters trophic structures of organisms.Thus, the Aksu River serves as an important model for evaluating human impact on freshwater ecosystems. Therefore, in this study, we investigated the variations in the stable carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) isotope compositions and trophic positions of two omnivorous fish species (*Capoeta antalyensis* and *Squalius fellowesii*) distributed across the river basin. Fish and environmental parameters were sampled from different locations (middle, and lower basin) along the Aksu River between 2019 and 2020. There was no significant difference between the $\delta^{13}C$ values of *S. fellowesii* and *C. antalyensis*, while the $\delta^{15}N$ value was higher in *S. fellowesii*. *C. antalyensis* reached the highest $\delta^{13}C$ values in the reservoir, whereas *S. fellowesii* peaked in both the reservoir and the tributary. The $\delta^{15}N$ values of both species showed an increasing trend from the middle to the lower basin. The trophic position (TP) of *S. fellowesii* is significantly higher than that of *C. antalyensis*. The TP of *C. antalyensis* did not show significant variation across the basin, while that of *S. fellowesii* was the highest in the reservoir and lowest at the tributary. The TP of the species varied depending on the area, indicating that local environmental conditions play a significant role in shaping trophic ecology of fishes.

Integrating citizen science and non-invasive molecular techniques to reveal the diet of plant-mimicking Mantises (Mantodea: Empusidae)

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Abstract ID: 30
Keywords: diet, empusidae, mantodea, metabarcoding, non-invasive metodology

Praying mantises are ambush predators that primarily consume invertebrates, though they occasionally prey on small vertebrates such as birds, reptiles and small mammals in both the wild and captivity. According to the literature, the prey groups of mantises can vary among species. Previous studies have shown that *Empusa pennata*, *Gongylus gongylodes*, and *E. fasciata* in the Empusidae are more selective in their prey choices compared to other species in the Mantidae. To date, mantis dietary analysis has relied solely on metabarcoding dissected stomach contents. While fecal metabarcoding is widely used in vertebrates, but remains limited in invertebrates, with prior studies focusing on Odonata and Orthoptera. In this study, molecular results were obtained using INS and INS16S primers from fecal samples of five different female *E. fasciata* individuals collected from the field and one control individual kept in captivity and fed only with *Apis mellifera* revealed OTUs from orders such as Diptera, Orthoptera, and Hemiptera. Depending on the primers used, we observed taxonomic differences among the samples. We also found that the two 16S primers matched different taxa. Besides molecular results, we also recorded 15 field feeding observations of *E. fasciata* and 93 additional feeding records of Empusidae members from iNaturalist and various websites. Our results from the feeding observations show that Empusidae members feed on the various species of Lepidoptera (52.8%), Hymenoptera (22.2%), Diptera (16.7%), Arachnida (2.8%), Coleoptera (1.9%), Orthoptera (0.9%), Ephemeroptera (0.9%), Hemiptera (0.9%), Neuroptera (0.9%) orders. All results from online platforms, field studies, and molecular fecal analyses reveal invertebrate ecological niches non-invasively, guiding researchers to non-invasive methods.

Infected but investing: Interactive effects of parasitemia and food availability on reproduction in Great Tits

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Abstract ID: 86
Keywords: Great Tit, Terminal Investment Hypothesis, avian blood parasites, breeding ecology

Studying how parasitic infections and environmental conditions interact to shape reproductive strategies is crucial to understand avian life-history evolution. Here, we investigate the combined effects of avian haemosporidian parasites and food availability on nest success, parental effort, and nestling development in a long-term monitored Great Tit (*Parus major*) population in METU, Turkey. We specifically aim to test the Terminal Investment Hypothesis predictions, such that individuals in poor condition are able to increase reproductive investment to optimize fitness.

We have three research questions. First, we examine the effects of co-infection and parasitemia on the body condition of both adult individuals and their nestlings. Second, we investigate the potential for terminal investment in highly infected adult females and the extent to which elevated parental parasitemia may lead to improved nestling outcomes. Third, we assess the role of habitat quality and food limitation in shaping reproductive success, as well as nestling growth and condition.

Methods included capturing and ringing adult females and nestlings and collecting blood samples to assess parasitemia following Çiloğlu et al. (2019). Nestling growth was assessed through repeated measurements of weight and tarsus length on days 7 and 15. Food availability was quantified using beating sheets, pitfall traps, and biomass estimation of collected arthropods at 7–10 day intervals. We video recorded selected nests to determine provisioning rates per hour. All sampling was conducted across three distinct study sites within METU, comprising 59 artificial nest boxes, which were monitored every five days during the breeding season since 2013.

This research hopes to clarify how parasitic stress and habitat quality influence reproductive decisions, testing whether Great Tits compensate for poor prospects through increased current reproductive effort. Our findings may contribute to broader ecological and evolutionary theories concerning host–parasite dynamics, life-history trade-offs, and the role of environmental resources in shaping reproductive strategies.

Kinship analysis toolkit: A new pipeline consisting of in-house scripts to determine the relationship degree and the type of first-degree relations using low-coverage data

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Abstract ID: 53
Keywords: ancientDNA, bioinformatics, kinship, kinship analysis

There are relatively few methods that can be used to differentiate between different types of first-degree relationships, especially for low coverage, pseudohaploid data, which is common in ancient DNA (aDNA) studies. To address this question, we have developed a new, straightforward, rule-based method that makes use of the different patterns of allele sharing between sibling pairs and parent-offspring pairs along the genome. Our method is well-suited for most ancient DNA datasets, as it can be used on low coverage, pseudohaploid data, and is able to robustly determine the first-degree relationship type of two samples that share as low as 20,000 SNPs (TPR=94%, FPR=4%, for parent-offspring couples and TPR=96%, FPR=6% for siblings). We have tested our method using both simulated data for different numbers of overlapping SNPs between the simulated individuals of known relatedness, and published, real aDNA data. Using our new approach, we were able to determine the relationship type of three first-degree pairs from Aşıklı, which had not been settled before.

The population genetic history of the Hittite capital Hattusa

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Abstract ID: 71
Keywords: ancient DNA, computational biology, demography, population genetics

Boğazköy (Hattuşa), the capital of the Hittite Empire (ca. 1650–1200 BCE), was inhabited for millennia, with layers spanning from the Chalcolithic to the Ottoman period. Located in northeastern central Anatolia, it represents a key intersection of local and interregional dynamics.

Among the populations that inhabited the site, the Hittites stand out for their political and linguistic significance as the earliest attested Indo-European speakers. Ancient DNA (aDNA) from Boğazköy offers a valuable opportunity to explore hypotheses about the spread of Indo-European languages. The site's long occupation also raises questions about whether post- Hittite socio-cultural changes involved population shifts or genetic continuity.

We analyzed genome-wide data from 21 individuals, including 17 newly sequenced genomes, dating from the Early Bronze Age (3200–1900 BCE) to the 2nd millennium AD. Using principal component analysis (PCA), *f4*-statistics, qpAdm, and ADMIXTURE, we assessed genetic continuity and population structure in Boğazköy, as well as its genetic relationships with neighboring populations.

Our results indicate genetic homogeneity across time, suggesting long-term population stability despite historical change. However, we observed a gradual increase in Caucasus- related ancestry, pointing to low-level mobility and admixture into the local gene pool. A Roman-period individual supports this trend, appearing as a genetic outlier in PCA and showing elevated West Asian and Central/South Asian components in ADMIXTURE. These findings suggest occasional gene flow from distant regions, likely through individual mobility, contributed to subtle shifts in the gene pool.

Phylogenetic relationships among weevil subfamilies (Coleoptera: Curculionidae) based on mitochondrial COI sequences

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Abstract ID: 134
Keywords: , COI, Curculionidae, Phylogeny

Weevils (Coleoptera: Curculionidae) are one of the most diverse lineages of beetles, comprising numerous subfamilies with complex evolutionary relationships. Although modern systematic studies generally recognize distinct subfamilies within Curculionidae, the internal phylogenetic relationships among these subfamilies remain partially unresolved. In this study, we investigated the phylogenetic relationships among major subfamilies of the Curculionidae family using mitochondrial cytochrome oxidase I (COI) gene sequences randomly obtained from the NCBI GenBank database. A total of 40 COI sequences representing the main subfamilies of Curculionidae were selected, along with two Brentidae species as outgroups. Sequences were aligned using the MUSCLE algorithm, and phylogenetic trees were constructed using both the Neighbor-Joining (NJ) and Maximum Likelihood (ML) methods in the MEGA-X software. In both phylogenetic trees, the subfamilies Scolytinae, Entiminae, and Platypodinae appeared as well-supported monophyletic clades. In contrast, Curculioninae and Molytinae were intermixed, forming a complex and partially unresolved clade. Dryophthorinae was positioned as a basal lineage in both trees, indicating an early divergence within the family. Other subfamilies exhibited non-monophyletic or unstable placements, showing slight differences between the NJ and ML methods. Our findings contribute to the growing molecular evidence on weevil phylogeny and emphasize the importance of multilocus data and broader taxon sampling in resolving the complex relationships among Curculionidae subfamilies.

Pyrgomorphidae (Orthoptera, Caelifera) mitogenome: characterization and phylogenetic position

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Abstract ID: 70
Keywords: Caelifera, Mitogenome, Phylogeny, Pyrgomorphidae

Mitogenomes frequently used as data sources in evolutionary studies. With development of next generation sequencing, total mitogenom quantity in databases increasing rapidly. In this study, it is aimed to define total mitogenome characteristics of *Pyrgomorpha guentheri* (Orthoptera, Pyrgomorphidae, Pyrgomorphinae) which is gathered by next generation sequencing reads and resolve family-level phylogenetic relationship. Total mitogenome length is 15,628 bp and similiar to other Orthoptera species, it is composed of 13 protein coding region (PCG), 22 tRNA gene, 2 rRNA gene and a AT rich region. The gene order is same with ancestral Pancrustaceae. Total length of PCG is 11,164 bp, total length of 22 tRNA is 1,476 bp, total length of 2 rRNA gene is 2,090 bp. Phylogenetically *Pyrgomorpha guentheri* and *Tanita* sp. forms a sister clade (Pyrgomorphinii) and both together forms monophyletic clade with other Pyrgomorphidae. Two subfamilies of Pyrgomorphidae (Pyrgomorphinae and Orthacridinae) does not form monophyletic clade.

Modeling wildfire occurrence in Türkiye: The role of climate, productivity, and human influence

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Abstract ID: 122
Keywords: Human-caused fires, Lightning, Lightning-induced fires, Wildfire, Wildfire drivers

Wildfires are natural processes that have shaped terrestrial ecosystems for millions of years. Initially ignited by natural sources such as lightning, volcanic activity, and meteor impacts, wildfire regimes have increasingly been influenced by anthropogenic factors due to human development. Today, both natural and anthropogenic drivers play significant roles in wildfire occurrence.

In this study, we analyzed the relationship between wildfire occurrence and environmental variables in Türkiye from 2013 to 2022 using the MaxEnt modeling framework. Predictor variables include natural variables such as climate and topography, and anthropogenic variables such as nighttime lights and road density. In addition to a main model encompassing all of Türkiye, we constructed regional models for fire-prone ecoregions. Fires were modeled separately by ignition type: all fires, lightning-induced, and human- caused.

Our results indicate that both spatial scale and fire ignition cause are critical in determining model performance and variable importance. Variable importance rankings differed based on fire causes, with natural factors generally showing dominant influences. Natural factors were especially determinant in lightning-induced fires. The study revealed that natural factors still significantly influence Türkiye's fire regimes, particularly strongly so in lightning-induced fires. Net primary productivity, precipitation of the wettest month, temperature seasonality, and monthly minimum vapor pressure deficit were identified as key predictors of fire occurrence. Response curves showed distinct patterns based on fire origin.

Importantly, the positive relationship between net primary productivity and lightning- induced fires supports the intermediate fire–productivity hypothesis, suggesting that such fires in Türkiye are associated with fuel-limited regimes. These findings highlight the ongoing relevance of natural drivers in shaping lightning fire patterns, despite increasing human impacts on fire regimes.

Ancient human genomes from medieval Nicaea (İznik)

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Abstract ID: 77
Keywords: ancient DNA, demography, mobility, population genetics

The city of Nicaea in Northwest Anatolia was a major urban centre in Anatolia over the last two millennia. It hosted the Christian Ecumenical Councils of the 4th and 8th centuries; it was the Byzantine capital during the Fourth Crusade in the 13th century and later the Ottoman capital in the 14th century. Here we present preliminary results from a genetic study of skeletal material from 73 individuals buried in three different spaces in Byzantine Nicaea. We used petrous bone, tooth and dental calculus samples, employed Dabney and Meyer-Kirscher protocols for extraction and library preparation, and shotgun sequenced them on Illumina platforms. Of the sequenced libraries, including both petrous bones and teeth, 76% had human endogenous DNA proportions above 10%, indicating high organic preservation. Seventy-two of the individuals could be genetically sexed, and, consistent with anthropological evaluation, we found 90% of burials were male in the "Cavea" (enclosure) area, thought to be soldiers/mercenaries, while samples from the other two spaces had more even sex distributions. The set of individuals also showed clear differences in their population genetic affinities, as predicted based on archaeological evidence. The "Cavea" sample was genetically overlapping with South/Southeast European present-day populations, raising the possibility that they could be related to the Crusades of the late 11th and 12th centuries. Meanwhile, burials in other spaces had diverse ancestries, including similarities to other published genomes from Byzantine Anatolia, more eastern (possibly more Central Asian) genomes, as well as European genomes. Nine skeletons were carbon-14 dated, and all except one dated to roughly the 11th century. The data provide a first insight into high levels of mobility, possibly driven by distinct mechanisms in urban settings in the Byzantine period.

Stochastic DNA damage and repair dynamics as a driver of cellular fitness under radiation

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Abstract ID: 83
Keywords: DNA DSBs, DNA repair, Stochasticity, cell fitness, radiation

Phenotypic variation among genetically identical cells plays a fundamental role in shaping fitness under environmental stress, yet its mechanistic origins and evolutionary implications remain poorly understood. Ionizing radiation is a particular example of environmental stress that induces DNA damage in the form of double-strand breaks (DSBs). This can lead to cell cycle arrest, activate repair pathways, and alter survival and mutation rates. While classical models in radiation biology often treat damage and repair as deterministic and population- averaged, increasing evidence shows that single-cell responses are highly heterogeneous even under controlled conditions, pointing to a role for intrinsic stochasticity.

Here, we develop and analyze stochastic models of DSB accumulation and repair to investigate how randomness in damage and repair processes shapes survival under radiation exposure. Using published experimental data from human cell lines, including gamma H2AX foci measurements across different radiation doses, types, and incubation times, we estimate key model parameters and assess how noise and rate dynamics contribute to observed variability. Our results suggest that stochastic fluctuations can buffer damage accumulation in a subset of cells and generate subpopulations with extended survival beyond the population mean. We further explore how repair rate decay, cell cycle phase, and post-radiation recovery influence radiosensitivity and radioresistance. Lastly, we discuss the growth trajectories of homogeneous and heterogeneous clonal populations with varying repair capacities, illustrating how stochastic repair may impact long-term population and evolutionary dynamics.

Altogether, our findings highlight the evolutionary relevance of non-genetic heterogeneity in cellular stress responses and provide a quantitative framework linking molecular damage dynamics to population-level consequences under radiation stress.

Dual approach to assess gastrointestinal helminth diversity in captive and free-ranging mountain gazelles (*Gazella gazella*) in Hatay, Türkiye

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Abstract ID: 60
Keywords: DNA metabarcoding, One Health, conservation biology, conventional methods, seasonality

Understanding parasite diversity in endangered wildlife is crucial for health monitoring and conservation. In *Gazella gazella*, Türkiye's isolated mountain gazelle population in Hatay provides a unique opportunity to investigate helminth diversity across two population settings, captive and free ranging, using both conventional and molecular methodologic approaches.

This study combines results from two independent methodology conducted on the same populations. The conventional methods, Fulleborn flotation, Benedek sedimentation, Bearman–Wetzel, and McMaster, were used to analyze 105 fresh faecal samples (45 individual and 60 pooled samples). Then DNA metabarcoding was performed on 188 faecal samples to reveal helminth diversity.

The conventional methods revealed 12 helminth taxa, including gastrointestinal nematodes, lungworms, trematodes, and one protozoan, with greater diversity observed in free-ranging gazelles. Trichostrongyloidea family parasites showed variable egg development stages, potentially influenced by environmental factors.

DNA metabarcoding identified eight helminth taxa, six intestinal and two respiratory system nematodes, with four species previously unreported in Türkiye. This approach also revealed seasonal shifts in parasite composition and abundance, closely linked to climatic parameters.

Together, these studies emphasize the value of integrating conventional and molecular diagnostics into wildlife parasitology. They provide complementary insights: conventional

methods assess infection intensity and life stages, while metabarcoding enables high- resolution taxonomic identification. The findings have significant implications for targeted conservation strategies, wildlife health monitoring, and zoonotic risk assessment under a One Health framework

Tracing the relationship between morphological and chromosomal evolution in *Nannospalax sp.* using three-dimensional geometric morphometrics

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Abstract ID: 39
Keywords: 3d geometric morphometrics, Blind mole rats, evolution, taxonomi

Blind mole rats (BMRs) are solitary subterranean rodents that have developed unique physiological and morphological adaptations to adapt to life underground. While these adaptations are fascinating, they have also made their true phylogenetic relationships unclear. However, despite decades of research, their taxonomic and evolutionary relationships remain poorly understood due to convergent evolution and extreme chromosomal diversity. Within the genus Nannospalax, 74 chromosomal forms (CFs) have been described, and most of these are believed to represent reproductively isolated, genetically distinct cryptic species. Despite decades of research, only three nominal superspecies (N. leucodon, N. xanthodon, and N. ehrenbergi) are officially recognized, reflecting a significant gap in taxonomic resolution. The study of such highly specialized, non-model organisms is crucial for expanding our understanding of morphological evolution under extreme ecological pressures. By creating one of the largest digital 3D datasets of subterranean rodent skulls to date, this project will establish a long-term resource for comparative, developmental, and functional studies.

To address this issue, a comprehensive and integrative approach combining molecular, cytogenetic, and geometric morphometric data is required. This project aims to conduct the first large-scale, phylogenetically informed 3D geometric morphometric (GM) analysis of mandibles and skulls from Nannospalax CFs. Patterns of shape variation and covariation, such as allometry, morphological integration, and modularity, will be quantified to test phylogenetic signals and assess the consistency between morphological, chromosomal, and genetic divergence. To this end, xxx specimens from xxx cytotypes will be collected from Turkey and Serbia, and 3D geometric morphometric analyses will be conducted. This will also result in the creation of a species atlas. Ultimately, this study is expected to clarify hidden diversity, improve taxonomic resolution, and support more effective conservation strategies for these evolutionarily intriguing mammals. Supported by MOESTD Serbia (Project No. 123N987–International 2559).

Geometric morphometric analysis of male hind wings and genital structures in Meloidae (Coleoptera): Patterns of morphological differentiation and their phylogenetic implications

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Abstract ID: 131
Keywords: Geometric morphometrics, Hind wing morphology, Male genitalia morphology, Meloidae, Shape variation

Studies on the family Meloidae have predominantly been focused on qualitative morphological characteristics or molecular phylogenetics. In the present study, geometric morphometric analyses were performed on male hind wings and genital structures to investigate patterns of morphological similarity and differentiation among species, genera, and tribes within Meloidae. This represents the first comprehensive geometric morphometric assessment conducted on these structures within the family. The aim was to evaluate the congruence between the morphological patterns obtained and the phylogenetic relationships previously reported in the literature.The specimens were collected during field surveys carried out in the Inner Western Anatolia region of Türkiye in 2019, 2021, and 2022. Landmark and semilandmark data were obtained from three anatomical structures and four datasets: hind wings, aedeagus, tegmen (ventral), and tegmen (lateral). Shape variation was assessed through Procrustes ANOVA, Principal Component Analysis (PCA), Canonical Variate Analysis (CVA), and distance metrics. Statistically significant morphological differentiation was detected among species. The shape variation of male hind wings was found to be largely consistent with phylogenetic relationships at the tribe and genus levels. In contrast, although male genital structures are known to be taxonomically informative at the species level, their shape variation patterns were found to be incongruent with phylogenetic relationships at broader taxonomic scales. However, within certain lower taxonomic groups, such as the tribe Lyttini and the genus *Mylabris*, the shape patterns were shown to partially reflect phylogenetic relationships.These results indicate that male hind wings and genital structures follow distinct evolutionary trajectories, providing evidence for mosaic evolution within the group. Additionally, the strong influence of homoplasy and convergent evolution on male genital morphology was shown to obscure broad-scale phylogenetic signals, whereas reliable phylogenetic information was retained at lower taxonomic levels.

Environmental requirements of Meloidae (Coleoptera) species: A case study from Inner Western Anatolia

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Abstract ID: 132
Keywords: Ecological requirements, HMSC, Meloidae, Species richness, Species-environment relationships

The family Meloidae is recognized as a moderately species-rich group within Coleoptera (Insecta), yet ecological studies investigating their environmental requirements remain considerably limited worldwide. In this study, one of the most comprehensive ecological assessments to date for this family was conducted, aiming to enhance the existing knowledge on their environmental requirements. The specimens analyzed in this study were collected during field surveys carried out in the Inner Western Anatolia region of Türkiye in 2019, 2021, and 2022. To assess ecological differentiation among species, their relationships with a set of environmental variables were examined. These included variables obtained directly from the field, such as air temperature at the time of sampling, sampling month, and altitude, as well as bioclimatic, topographic, and land cover variables retrieved from global databases. Species-environment relationships and the environmental determinants of species richness were analyzed using Hierarchical Modeling of Species Communities (HMSC), a flexible Bayesian framework that allows for the simultaneous modeling of species' responses to environmental gradients, species traits, phylogenetic relationships, and spatio-temporal structures. The results revealed significant ecological differentiation among species. Furthermore, ecological requirements were found to be partially clustered at the genus and tribe levels, providing support for the niche conservatism hypothesis. Temperature seasonality, topographic heterogeneity (roughness), percentage of cropland, normalized difference vegetation index (NDVI), and monthly precipitation were identified as the most influential environmental variables shaping species richness. These findings provide essential baseline information for understanding the ecology of Meloidae and offer a valuable ecological reference for this family.

Types of skin markings in Delphinidae of the Zonguldak region, southwestern Black Sea

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Abstract ID: 15
Keywords: bottlenose dolphin, common dolphin, photo-ID

Photo-identification is a valuable and widely used tool method to investigate scales of residence patterns, social structure, and population size of bottlenose dolphins (*Tursiops truncatus*) and common dolphins (*Delphinus delphis*) worldwide. The photographic data used in this study were collected in Zonguldak, Türkiye, from 2019 to 2023. We evaluated prevalence and sourse of injuries on the dorsal fins and bodies in 30 randomly selected individuals of each cetacean species. Externally visible features and anomalies were detected and categorised into five groups according to their origin. The results revealed a high degree of markings among Delphinidae individuals, with an average of 17 distinct marks per dolphin. Bottlenose dolphins exhibited 1.5 times more distinct marks on their bodies and fins compared to common dolphins. The highest prevalence was noted for distinct notches, scrapes, and tooth-rakes in bottlenose dolphins. The most prevalent mark types for common dolphins were distinct notches and tooth-rakes. A unique mark type for common dolphin was the presence of a white spot on the dorsal fin, which varied in shape and size, and was completely absent in 10 out of 30 individuals. Out of 17 recorded injury incidences, at least 5 (30%) were consistent with anthropogenic injuries, including probable amputations caused by propeller strikes and entanglements. More severe markings of this type were observed in bottlenose dolphins. Considering the increasing human activities in the Black Sea, we suggest that skin marking patterns could serve as indicators of ecosystem health and anthropogenic pressure on dolphin populations. Future field surveys should prioritize obtaining the highest quality photographic material to facilitate mark-recapture studies.

Magnetoreception in birds and mammals: A comparative perspective from quantum biology

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Abstract ID: 23
Keywords: Cryptochrome, Magnetic orientation, Magnetoreception, Quantum biology, Radical pair mechanism

Magnetoreception is a sensory modality that allows organisms to detect the Earth's geomagnetic field and perform behaviors such as orientation, navigation, and migration. This phenomenon involves distinct biophysical mechanisms that vary across animal groups. This study comparatively examines magnetic field perception in birds and mammals from a quantum biology perspective, providing a theoretical framework.

In birds, magnetic sensing is proposed to be mediated by cryptochrome, a flavoprotein in the retina sensitive to blue light. Radical pair reactions within cryptochrome are believed to be influenced by quantum phenomena like entanglement, enabling sensitivity to the Earth's weak magnetic field. This quantum-based compass operates in a light-dependent manner and integrates with visual pathways, allowing birds to extract directional information from geomagnetic cues during migration.

In mammals, especially species adapted to low-light subterranean environments, magnetic sensing was initially thought to occur via non-visual pathways. However, experiments have shown that removal of ocular structures disrupts magnetic orientation in some rodents, suggesting a light-dependent, possibly cryptochrome-based mechanism. Additionally, the trigeminal nerve system may complement this by transmitting magnetic information detected by magnetite-based receptors in specific tissues.

These findings highlight the potential role of quantum processes such as entanglement, tunneling, and superposition in shaping complex behaviors. They challenge traditional biological views and encourage reevaluation of sensory mechanisms. Integrating empirical data with theoretical models can improve understanding of sensory evolution across taxa. Furthermore, exploring these mechanisms may advance neuroscience, bioengineering, and quantum-inspired technologies, including biologically integrated sensors and navigation systems. In this context, a model research outline for the study in question is presented in this paper.

Effects Of wet and dry periods on long term phosphorus and nitrogen budgets and their relationships with lake nutrient and chlorophyll-A concentrations

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Abstract ID: 129
Keywords: Hydraulic retention time, Hydrology, Semi-arid climate, Shallow lakes, Water level fluctuations

The functioning of shallow lakes, which are extremely susceptible to variations in precipitation, evaporation, and water inflows and outflows due to their shallow form, depends heavily on hydrology. Water level changes in shallow lakes have large impacts on the physical and biological features of these ecosystems and water chemistry, nutrient processing, and nutrient retention. Here, we investigated the relationships between lake nutrient and chlorophyll-a (Chl-a) concentrations in Eastern Mediterranean Lakes Mogan and Eymir in the semi-arid climate overall and in dry, mid and wet periods of long-term monitoring. We hypothesized that (i) high alteration in water levels between dry and wet periods will be observed due to the semi-arid climate in the region, (ii) external loadings will play an important role on the in-lake nutrient concentrations, (iii) hydraulic retention time (HRT) will be affected on in-lake concentrations because the longer the HRT higher the water column-sediment interactions and the increase in the internal phosphorus loading, and (iv) increasing temperatures will increase the Chl-a concentrations, especially in dry periods, due to the more profound effects of stratification, which triggers internal phosphorus loading. Mass balance analysis of two shallow semi-arid lakes revealed that climatic variability strongly influences their ecological state. During dry periods, reduced precipitation and increased evaporation raise the risk of lake desiccation. Despite low external nutrient inputs, evaporation-driven water loss led to nutrient accumulation, especially in Lake Mogan. In Lake Eymir, chlorophyll-a levels were mainly driven by temperature, with cyanobacterial blooms likely linked to more frequent thermal stratification and internal loading. These findings highlight how hydrological changes shape nutrient dynamics and algal responses in shallow Mediterranean lakes.

Comparative analysis of leaf flammability traits in forest and shrubland plants of Western Türkiye

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Abstract ID: 109
Keywords: burning experiment, leaf flammability, time to ignition, trait-based ecology

Determining the flammability characteristics of plant species is important for predicting fire risk and effective land management. In this study, the flammability parameters of leaves from different plant species in western Türkiye were experimentally evaluated under laboratory conditions. Five leaf samples were collected from individual plants of each species, dried under appropriate conditions, and subjected to combustion tests in a muffle furnace. The main flammability parameters used in the experiments were time to ignition, smoke duration, burning duration, mass loss rate, and fuel consumption. During the burning experiments, leaves were burned with the furnace door open in a suitable container that prevented surface contact; the process from ignition to complete combustion was recorded on video. The videos were analyzed using digital software, and measurements for each parameter were recorded. The obtained results were used to establish flammability classes at the species level, and the studied species were compared in terms of ignitability, sustainability, combustibility, and consumability components. This study reveals interspecific differences in flammability through leaf-level burning experiments and provides valuable data for fire ecology in the study region.

Morphometric investigation of *Triticum araraticum* Jakubz, *Triticum baeoticum* Boiss., *Triticum dicoccoides* (Körn. ex Asch. & Graebn.) Schweinf. and *Triticum urartu* Thumanjan ex Gandilyan species found in the gene pool of cultivated wheat

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Abstract ID: 95
Keywords: Morphometric Analysis, Plant Taxonomy, Triticum, Wild Wheat

Triticum L. is a genus in the Poaceae family that includes several important cereal crops. It is believed to have first been cultivated in the Fertile Crescent region, which includes southeastern Anatolia in Turkey. Due to the morphological similarity of some natural *Triticum* species found in Turkey, species identification can be problematic. This study aims to reveal morphological differences within and between populations and contribute to taxonomy through population analysis based on the obtained data. The study also aims to determine species boundaries using new character measurements and observations, revise species descriptions to encompass intraspecific morphological variation, and create a species identification key that considers new morphological variation ranges and can distinguish between species. *Triticum araraticum, Triticum dicoccoides, Triticum baeoticum* and *Triticum urartu* are morphologically very similar and are considered to be the ancestral gene origin of cultivated wheat. Given the economic importance of the *Triticum* genus, this confusion complicates planned breeding studies and flora research. This study used detailed morphometric analysis to examine these four ancestral wild species. A total of ten individuals from 106 populations obtained from the Turkish Seed Gene Bank were examined and analysed using 46 morphological characters, 23 of which were qualitative and 23 quantitative. R Programming Language 4.5.0 was used for the cluster analyses with the UPGMA algorithm. The result of the analysis was a dendrogram. According to the dendrogram, the accessions belong to *T. baeoticum* and *T. urartu*, while those belonging to *T. araraticum* and *T. dicoccoides* clustered together as predicted.

Different balancing selection modes leave highly similar temporal genomic signatures

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Abstract ID: 105
Keywords: ancient DNA, balancing selection, the Holocene

Balancing selection is an important evolutionary force maintaining genetic diversity in natural populations. Emerging evidence suggests that there may be a larger number of loci than previously hypothesised under long-term balancing selection in human populations. Evolutionary mechanisms leading to balancing selection include heterozygote advantage, negative frequency-dependent selection, spatially and temporarily fluctuating selection and antagonistic selection. However, it is often not possible to pinpoint specific evolutionary mechanisms behind balancing selection signatures by using present-day genomic data. Genomic time-series data offer a promising alternative, as the signatures of different balancing selection mechanisms left in genomes may differ when looking through time. In this respect, ancient DNA data enables direct observation of allele frequency changes over time, allowing evaluation of theoretical models of balancing selection. To test whether ancient DNA data provides additional sources of information, we conducted forward-time genetic simulations using SLiM under the models of heterozygote advantage and negative frequency-dependent selection, as well as neutral evolution. These simulations incorporated population genetic parameters estimated for modern human populations as well as temporal sampling at 1,000-year intervals for a total of 12,000 years coinciding with the Holocene period. We then computed 33 population genetics summary statistics, including autocorrelations of these statistics through time, on simulated data and used various machine learning tools to differentiate between balancing selection modes. Results indicate that both mechanisms of balancing selection can be distinguished from neutral evolution with high accuracy even with only present-day data. Meanwhile, it was challenging to discriminate between balancing selection modes when using present-day data as well as when utilizing time-series data. This finding indicates that these two modes of balancing selection leave highly similar genetic signatures through time and further investigations are required to develop methods to being able to distinguish between them.

Microbial signatures of species divergence in Alpine butterflies

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Abstract ID: 111
Keywords: 16S, Amplicon sequencing, Erebia, Metabarcoding, Microbiota

The relationships between living organism and their gut microbiota are one of the most common and complex situations. Although the gut microbiota is an important feature of animal life, symbiotic relationships were little known. On the other hand, *Erebia* is a genus of cold-adapted butterflies that diversified in separate glacial refuges during the ice ages. After the glaciers retreated, some distantly related species expanded their ranges and now live together by using different microhabitats. However, closely related species or lineages are often ecologically similar, which can lead to one excluding the other or to the formation of very narrow zones where they meet. The exact factors that allow these species to live together—or keep them from exchanging genes—are still not well understood. The aim of this study was to reveal how the intestinal microbiota differs in the adult stage of *Erebia tyndarus* and *Erebia cassioides* contact zone in Grindelwald, Switzerland with a metabarcoding approach. For this purpose, the gut microbiota of a total of 75 individuals from both species was evaluated by 16S amplicon sequencing. Although the dominant taxa in the samples were determined as *Staphylococcus, Cutibacterium, Corynebacterium, Commensalibacter* the intestinal microbiota showed significant differences between species and even individuals. These findings highlighted the complex interactions between host biology and environmental factors in shaping the gut microbiota of these butterflies. This research provided valuable insights into the microbial diversity associated with *Erebia tyndarus* and *Erebia cassioides* and underscores the importance of considering both host and environmental influences in microbial ecology studies. Furthermore, the observed microbial variations suggested potential adaptive mechanisms and evolutionary processes at play, which could have implications for conservation strategies and understanding the ecological dynamics of butterfly populations in the Alps.

Wisdom from ashes: Exploring traditional fire knowledge and use in Anatolia

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Abstract ID: 51
Keywords: Anatolia, Anthropogenic fires, Cultural burning practices, Fire, Fire management, Traditional fire knowledge

Traditional fire knowledge, considered a type of traditional ecological knowledge, denotes the intentional use of fire by ancient local or indigenous communities to shape their environment and vegetation, or to meet various needs, along with the intergenerational transmission of this fire-related knowledge. However, the adoption and implementation of modern fire management policies, mainly based on fire suppression, have led to the banning of these cultural practices through various state measures. These prohibitions have not only disrupted the ecological knowledge, cultural heritage, and economic activities of these communities, but also have ecological consequences. Globally, research on traditional fire use has been increasing, particularly in regions such as North America and Australia, where policy changes have begun to support the preservation and continuation of indigenous cultural practices. In Anatolia, often referred to as the cradle of civilizations, traces of fire- related traditions and practices can still be observed. Traditional fire practices in Anatolia include several culturally embedded types of burning, including stubble burning to clear agricultural fields after harvest; shepherd fires used for warmth and protection during seasonal grazing; reedbed burning for managing wetlands and renewing reed growth; and shrubland or forest burning carried out to maintain pasturelands or prevent larger wildfires. These types of fire use reflect a deep understanding of local ecosystems and serve diverse purposes, from agricultural management to pastoral needs and ecological regeneration. Nonetheless, academic research on traditional fire use in Anatolia remains very limited, and there have been no notable policy changes addressing it. Studies on traditional fire knowledge, to which we also aim to contribute through this study, would offer an important opportunity to develop alternative solutions that are more adaptive to nature, unlike current fire suppression policies, which have been increasingly challenged by the climate crisis.

Plural values and perceptions for an invasive alien species: The case of Rose-Ringed Parakeets (*Psittacula krameri*) in Türkiye

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Abstract ID: 50
Keywords: IAS, Psittacula krameri, Rose-ringed parakeets, environmental policy, environmental values, invasive alien species

Rose-ringed parakeets (RRPs, *Psittacula krameri*), one of the most invasive bird species globally, have established large non-native populations of at least 85,000 individuals in urban environments across Europe (including the UK) since the 1960s, and pose significant negative impacts on nesting opportunities of native species and on agricultural production in Europe. In Türkiye, RRPs are spread over 30 cities - with an estimated population size of at least 5000 members in Istanbul alone - and no studies exist on the impacts of these populations on native species in the country.

In 2022, the preliminary attempts to regulate RRP populations in Türkiye were met with a strong public resistance, underlining the need to examine public perceptions and potential attitudes towards policies pertaining to this invasive species.

To explore the perceptions and attitudes towards RRPs, and the environmental values (intrinsic, instrumental, relational and ecological) associated with these attitudes, we carried out face-to-face surveys with 160 visitors of urban greenspaces in Istanbul and Ankara. The findings suggest that park visitors in Istanbul and Ankara have strongly positive perceptions and attitudes towards RRPs and are mostly against any interventions to control their populations. We found that relational values, that highlight emotional, cultural, and inter-generational components in human-nature relations, played a dominant role in shaping these positive perceptions and attitudes. We recommend that awareness raising campaigns and policy proposals for the control and management of this charismatic invasive species' populations should be informed by the strong presence of relational values among the urban residents in Turkey in order to be implemented with greater public support.

Ecological insights into microbial persistence in ultrapure water systems: A molecular approach

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Abstract ID: 65

Keywords: 16S rRNA, amplicon sequencing, filtration system, microbial contamination, ultrapure water

Ultrapure water systems are integral to contamination-sensitive laboratory procedures, yet their sterility is often assumed rather than verified. This study aimed to investigate microbial traces within the structural components of a laboratory-grade water purification system using molecular techniques. Seventeen samples were collected from different locations within the water purification system, including sediment layers in carbon and polishing filters, as well as from the upper and lower water outlets. DNA was successfully extracted from all samples. Although conventional PCR targeting the 16S rRNA V3–V4 region produced visible bands in only six samples, all tested positive for bacterial DNA, indicating that microbial traces were present even in low abundance. The six PCR-positive samples from the carbon filter inlet, sediment, and polishing filter outlets were selected for 16S amplicon sequencing to identify their taxonomic composition.

Early-stage samples displayed a broad range of bacterial phyla, including *Pseudomonadota*, *Thermoproteota*, *Acidobacteriota*, *Actinomycetota*, and *Bacillota*. In contrast, microbial diversity decreased noticeably in downstream samples, where *Pseudomonadota* remained the only consistently dominant group. Notably, this phylum includes taxa affiliated with the *Escherichia coli* group, suggesting that potential environmental pathogens may persist throughout the system, even after multiple filtration steps.

Beyond compositional trends, our findings underscore the ability of bacteria to adhere to various internal surfaces such as membranes, sediment particles, and structural materials. These interfaces may act as persistent substrates, enabling spatially structured microbial colonization. From an ecological standpoint, such systems may unintentionally serve as microbial habitats, offering refuge and niche opportunities even under nutrient-poor, artificial conditions.

Biogeographic patterns and population structure of social voles: Evidence of ongoing gene flow in two cryptic species in Anatolia

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Abstract ID: 82
Keywords: Arvicolinae, Sumeriomys, hybridization, microsatellites, mitochondrial DNA, nuclear DNA

Anatolia served as a glacial refugia between Europe and the Middle East during Quaternary climatic oscillations. Identification of biogeographic patterns is important for promoting conservation plans and understanding the evolutionary history of refugial endemic species. Social voles (genus *Microtus*) consists of widespread species from the Balkans to the Middle East, but the range of endemic species that were identified in Anatolia is limited. Phylogenetic studies on Social voles display high level cryptic species diversity. However, the knowledge about the geographic range and population structure of their species within Anatolia is still unclear. In this study, we sequenced the mitochondrial CYTB gene of 264 individuals from 157 localities and utilised them together with GenBank sequences. Additionally, two nuclear exon regions and seven polymorphic microsatellite markers were added to mtDNA dataset. We show that the analysis of mtDNA data reveal two well- supported phylogeographic groups consistent with refugial areas in Anatolia. We observe that the nuclear haplotypes are shared among closely related species. We find that Social voles are relatively young evolutionary lineages that diverged from a most common ancestor during the Middle Pleistocene. Furthermore, microsatellite loci uncover the presence of sympatric admixed populations between two distinct mtDNA clades at Taurus Mountains. These results show that, even though social voles are recognised as distinct species based on mitochondrial data, nuclear regions

are probable to be influenced by introgression, incomplete lineage sorting and recent gene flow. Our data demonstrate that a larger sample size significantly influences the distribution range of mtDNA clades, providing better visualization of the biogeographic patterns. This study highlights that diversity patterns in vole populations support occurrence of refugial areas within Anatolia. Our study will provide an important insight into the evolutionary history and conservation of social voles and clarify taxonomic relations.

Integrating gene expression data into metabolic models: an application of context specific modeling tools to empirical data

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Abstract ID: 90
Keywords: Bioinformatics, Metabolic Flux Analysis, Metabolic Modeling, Transcriptomics

Researchers engineer model organisms to enhance the production of valuable metabolites and this process requires a comprehensive understanding of cellular metabolism. Genome-scale metabolic modeling is a proven way to predict the outcomes of genetic modifications via abstracting the whole metabolism in a mathematical description called the stoichiometry matrix. These models generally calculate flux distributions based on this stoichiometry matrix to illustrate the active metabolic pathways and rates of those reactions in model organisms. However, to accurately predict the expected metabolic phenotypes, it is essential to create context-specific models to simulate realistic cellular behavior by integrating empirical data such as RNA sequencing.

Here, we aim to create context specific genome scale metabolic models to investigate the flux distributions in a genetically engineered organism for increased shikimic acid (SA) production in *Pseudomonas putida* KT2440 model organism. SA is a valuable compound in the pharmaceutical industry and an intermediate molecule produced in the phenylalanine-tyrosine-tryptophan biosynthesis pathway with precursors from primary metabolism.

Our model system includes several gene knockouts and over-expression of some genes in primary metabolism to increase the production and direct necessary precursor metabolites into shikimic acid production pathways.

To capture the impact of gene modifications, we will use the most recently published *P. putida* KT2440 model (iJN1463) and apply different context-specific model construction methods such as GIMME and E-flux, and a modified E-flux method that estimates the connection between gene expression and protein activity. By systematically comparing these methods on our empirical dataset, we aim to identify the most reliable strategy for accommodating both knockout and over-expression. This work will provide insights on creating context specific models using limited data and potential metabolic deviations from the expected metabolic pathways.

Swarm genomics: A unified pipeline for individual-based whole-genome analyses

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Abstract ID: 34
Keywords: Heterozygosity, Mitogenome, NUMT, PSMC, Repeat annotation, Runs of homozygosity, Teaching tool, Unmapped reads

With the rapid advances in sequencing technologies, genomic data has become readily available, enhancing research capabilities in various biological disciplines. A single whole- genome sequence can answer numerous questions, such as understanding population dynamics, identifying genetic variations linked to diseases, and revealing evolutionary relationships. However, the complexity and computational demands of whole-genome sequencing data analysis present significant obstacles, often requiring multiple specialized tools. Here, we present SwarmGenomics, a user-friendly command-line pipeline which addresses these challenges and streamlines whole-genome data assembly and genetic analyses. The pipeline starts with genome assembly and continues with seven modules that perform heterozygosity analysis, runs of homozygosity detection, PSMC analysis, unmapped reads analysis, repeat analysis, mitochondrial genome assembly, and nuclear mitochondrial DNA segment analysis. By combining these analyses into a single, user-friendly pipeline, SwarmGenomics simplifies the process of obtaining comprehensive genetic information, making advanced genomic analyses accessible to researchers with varying levels of expertise. Looking ahead, we aim to enhance the pipeline further by developing additional modules and expanding its capabilities to accommodate different sequencing technologies.

Identification of threatened cave-dwelling bat species and establishment of a national conservation network

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Abstract ID: 119
Keywords: Biodiversity conservation, Cave ecosystems, Population monitoring

Türkiye has one of the richest bat faunas in the Mediterranean Basin, with around 40 recorded bat species. For many of these species, caves serve as critical sites for roosting, hibernation, and reproduction. However, human activities such as mining, tourism, and construction threaten these habitats. Additionally, the lack of data on the distribution and populations of species complicates the development of effective conservation strategies. To address this, supported by the Conservation Leadership Programme (CLP), the project focused on three key objectives: identifying important bat sites, tracking population changes in known sites, and creating a national network for monitoring and protecting bats among caving communities. Within the scope of the study, 80 potential caves were identified by contacting public institutions and local/university caving groups. In 10 field surveys conducted from May to October 2023 and August to October 2024, 52 caves were visited, and 37 of these were identified as active bat shelters. A total of 25,986 individuals were recorded during the surveys, with over 100 individuals observed in 22 caves. Seven previously identified bat roosts were re-evaluated. One was inaccessible due to flooding, four showed population increases, and two showed decreases. In addition to field surveys, awareness-raising activities were conducted to support conservation efforts. Training sessions were organized to inform cavers about the ecological importance of cave ecosystems and the role of bats. A conservation action report will be prepared based on the findings of the study and submitted to authorities to support legal protection measures for important bat roosts. This study aims to form the basis of long-term protection and monitoring studies for cave-dwelling bats in Türkiye.

Integrating ecological and genomic diversity for climate resilient marine spatial planning

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Abstract ID: 133
Keywords: , biodiversity, genomic vulnerability, intraspecific diversity, spatial planning

Rising temperatures, ocean acidification, deoxygenation, and changing sea levels severely stress marine environments. Anthropogenic activities such as pollution, habitat destruction, and overfishing further threaten biodiversity and ecosystem health on both temporal and spatial scales. While conservation of biodiversity and habitat restoration are highlighted by management authorities, determining which areas and species to prioritize presents a significant challenge. Enhancing management strategies requires an evaluation of the current and potential impacts of climate change. To evaluate those impacts, our understanding of climate change vulnerability must grow not only on species but also on the community and ecosystem levels.

We focus on various biodiversity metrics using sugar kelp in Danish waters. We tackle the question of how biodiversity can be preserved in a changing climate through spatial planning and habitat restoration. We use an ecosystem engineering species, sugar kelp (*Saccharina latissima*), both as target species, and as ecosystem indicator. We will investigate its intra- ,and interspecific diversity. We will evaluate sugar kelp associated species diversity and its potential for biomonitoring by using eDNA data from a range of locations. We will explore the possibility to link eDNA with genomic data via collating eDNA samples and associated biological data and performing molecular analyses of eDNA. We will make predictions of species and population vulnerability to future climate change through genome scans, genotype-environment associations and connectivity assessments.

Investigating developmental robustness in genetically uniform and variable *Drosophila* populations

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Abstract ID: 31
Keywords: Drosophila melanogaster, Isogenic lines, Phenotypic variation, Temperature perturbation

Phenotypic variation is often linked to genetic differences, but even genetically identical individuals can show variation in developmental traits. This raises important questions about the origins of variation when genetic factors are held constant. In this study, we explore how non-genetic influences—such as environmental conditions and stochastic developmental processes—contribute to early embryonic variation in Drosophila melanogaster, using temperature as a controlled perturbation to expose variation that emerges despite genetic uniformity.
We examined early embryonic development in wild-type isogenic lines at 22°C, 25°C, and 29°C. We also analyzed weak Bcd mutant lines at 22°C and 25°C. Positional patterning shifts were assessed through analysis of key expression domains during early development. Additionally, we evaluated larval cuticle phenotypes and survival rates under each temperature condition. This design allowed us to evaluate developmental responses at both molecular and morphological levels across isogenic lines.

Our findings show that developmental patterning remained consistent at 22°C and 25°C, but changes became apparent only at 29°C. In contrast, weak Bcd mutant lines exhibited patterning shifts and increased frequencies of mutant cuticle phenotypes at 25°C, indicating reduced robustness and heightened sensitivity to even mild environmental perturbation.

These results highlight the role of non-genetic factors—such as random developmental noise—in shaping early development. In parallel, by analyzing wild-caught mass populations (retaining genetic variability through random mating) alongside isogenic lines derived from them, we are investigating the role of genetic variability in developmental robustness under temperature perturbation. This approach provides a way to study how developmental patterning varies in the absence and presence of genetic variation.

Temporal evolution of the gut microbiome in aging African Turquoise Killifish

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Abstract ID: 17
Keywords: Gut microbiome, aging, evolution, killifish

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. 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 the temporal patterns and mechanisms driving age- related alterations in gut microbial communities, as well as their potential impacts on host health across different life stages. Leveraging the naturally short lifespan of the African turquoise killifish (*Nothobranchius furzeri*) as a model organism, which possesses a diverse gut microbiota, we aim to characterise the compositional and functional shifts in gut microbiome throughout the ageing process. Our research will explore the interplay between host ageing and microbial dynamics. Ultimately, this work seeks to provide novel insights into the ecological and evolutionary dynamics of host–microbe interactions during ageing, with potential implications for microbiome-based strategies to promote healthy ageing.

Population and genetic structure of the Southern Caucasus from the Neolithic to the Early Middle Ages

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Abstract ID: 85
Keywords: Ancient DNA, Human mobility, Population Genetics, Southern Caucasus

Archaeological evidence suggests that the Neolithization of the Caucasus began 3-4 thousand years after that of the Fertile Crescent, the region most critical to the demographic and cultural development of the South Caucasus. Material culture data indicate that Neolithic lifeways spread into the South Caucasus from southern Anatolia and/or Mesopotamia, rather than emerging locally through the adoption of farming by Caucasus Mesolithic hunter-gatherers. Archaeological findings also point to sustained two- way interactions between the South Caucasus and Anatolia from the Neolithic to the Middle Ages.

Although previous archaeogenomic studies, based on limited samples, support this view, the population dynamics within the Caucasus and its interaction with the surrounding regions remain poorly understood. Here, we present genome-wide data from 57 ancient individuals (0.01X–0.52X coverage) from 11 sites in Azerbaijan, supplemented by previously published data from the Neolithic to Early Feudal periods.

Our analyses using the principal component analysis (PCA), *f4*-statistics, and Admixture confirm that South Caucasus Neolithic populations are genetically closer to Southwest Asian Neolithic groups than to local Mesolithic hunter-gatherers, supporting the southern Anatolian/Mesopotamian origin of Caucasus Neolithic farmers. We also observe a clear genetic distinction between Neolithic and Bronze Age populations in the region, reflecting high mobility and changing population structure over time.

Additionally, we detect the influx of Eastern Hunter-Gatherer (EHG) ancestry to the South Caucasus during the Bronze Age, likely via the North Caucasus, adding to the region's demographic complexity. The Iron Age is marked by increasing human mobility and admixture, followed by a phase of genetic continuity from the post-Iron Age onward, suggesting stabilization of the gene pool.

Ethnobotanical properties of Gülağaç (Aksaray), Güzelyurt (Aksaray), Çiftlik (Niğde) and Altunhisar (Niğde) Districts

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Abstract ID: 74
Keywords: Biology, Biology Program, Graduate School of Science and Engineering, Hacettepe University

This research aims to present a detailed ethnobotanical inventory of the Gülağaç and Güzelyurt districts in the Aksaray province and the Çiftlik and Altunhisar districts in the Niğde province.

Fieldwork for this study included visits to 14 neighbourhoods/villages in the Niğde province and 18 neighbourhoods/villages in the Aksaray province in 2024 vegetation period. During these visits, interviews were conducted with local people, and information was collected on the local names, usage patterns, purposes, preparation methods and applications of the plants. Based on this information, plant samples were collected in the field, dried according to herbarium techniques and scientific names were determined. As a result of this study, 88 taxa were recorded as being used by local people. According to the research results, 74 taxa were used for medical purposes, 43 for food, 3 for dyes, and 36 for animal feed. Additionally, two taxa were used to treat animal diseases, and 29 plants were used for other purposes. The local names of all mentioned plants were recorded.

Our research reveals that, although plants are still used extensively in the Niğde and Aksaray provinces, the transmission of cultural and local knowledge is decreasing due to the gradual decline in the number of young people living in the region. This study has documented the ethnobotanical uses of plants in the region and ensured that this knowledge is passed on to future generations.

Uncovering subterranean life: A pilot eDNA-based biodiversity study across contrasting cave habitats

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Abstract ID: 114
Keywords: Biospeleology, Cave Biodiversity, Environmental DNA, Metabarcoding, Subterranean Ecosystem

Cave ecosystems represent isolated and understudied habitats with distinct physicochemical conditions that shape both microbial and macro-organismal communities. In this pilot study, we explored the biodiversity of two structurally and ecologically contrasting caves in Turkey: one a dry, fossil cave and the other an active, oligotrophic system with continuous water flow. Our aim was to evaluate the effectiveness of environmental DNA (eDNA) metabarcoding in capturing the taxonomic composition across different cave microhabitats.

From both caves, we collected soil, water, and surface swab samples. To survey broad taxonomic diversity, we employed multiple primer sets: 16S rRNA for bacteria, 12S rRNA for vertebrates, 18S rRNA for invertebrates and protists, and ITS for fungi. The 16S dataset revealed *Vicinamibacter silvestris* and *Solirubrobacter ginsenosidimutans* as dominant bacterial taxa. 12S primarily detected the bat species *Miniopterus schreibersii*. The 18S marker, while largely dominated by fungi such as Absidia glauca and members of Cryptomycota, also identified invertebrates like *Baruscapillaria appendiculata* and *Gregarina species*. ITS sequencing highlighted fungal taxa including *Tricholoma terreum*, *Russula* spp., and *Absidia urquhartii*.

Our multi-marker approach enabled non-invasive, multi-kingdom biodiversity profiling and revealed clear differences in community structure between the two caves. These differences appear to be shaped by environmental variables such as hydrological activity, nutrient input, and light availability. The study also suggests that sample type plays a critical role in biodiversity detection, with different matrices yielding complementary taxonomic signals. These preliminary findings underscore the potential of eDNA-based monitoring for biospeleological research and call for the development of standardized protocols tailored to subterranean environments.

Genome-related feature studies

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Abstract ID: 5
Keywords: Eukaryote, count, exon, genome, intron, length, lncRNAs

Genome related features inherently has an evolutionary aspect. We inspected relevant information of eukaryotes through data from the reports of the NCBI Eukaryotic genome Annotation Pipeline, which was obtained on 18.08.2018. Eukaryotes included primates, rodents, birds, fishes, insects, and plants. We presented features related to introns and exons (doi: 10.1101/2023.09.20.558659) earlier, at the 9th International Congress of the Molecular Biology Association of Turkey. That study revealed that the genes' mean lengths were positively correlated with the collective data of the counts of exons in coding transcripts, as well as the mean lengths and counts of introns in coding transcripts. Mean lengths of introns in non-coding transcripts were also positively correlated, and that with the counts' data was absent for the plants' and fishes' data. These were also valid for the median lengths. Introns *vs* exons revealed separation of the inspected eukaryotes. Further, we observed pareto fronts in the cumulative data. In the current study, here we present counts of genes *vs* lncRNAs in eukaryotes, revealing linear correlations, with varying slopes in the data. Slopes of the data of primates (1.29) and rodents (1.24) were closer, and the highest, while that of birds (1.19) was similar, but lower. Their goodness of fit (R2) values were high. Namely, 0.84, for that of primates; 0.88, for that of rodents; and 0.90, for that of birds. Goodness of fit values were lower for plants' (0.58) and fishes' (0.55) data, and the lowest for the insects' data (0.40). Slopes of the respective data were 0.23, 0.19, and 0.20, correspondingly. In conclusion, results in conjunction with lncRNAs is an interesting feature that deserves further attention since, e.g., lncRNAs have relevance with certain human disease pathologies. Considering our earlier studies, and current results, genome-related feature studies are promising.

Analysing the effects of nutrition on reproductive performance of male Fruit Flies

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Abstract ID: 45
Keywords: Drosophila melanogaster, behavioral response, food intake, genotype, nutrition, physiological adaptation, protein:carbohydrate ratio, reproductive fitness

Understanding how nutrition and genetic background interact to shape male reproductive performance is essential to dissect the evolutionary and physiological mechanisms of dietary adaptation. In this study, we examined the effects of varying protein-to-carbohydrate (P:C) dietary ratios on food consumption behavior and fitness outcomes in male *Drosophila melanogaster* across three genotypes. Males were exposed to four diets (P:C = 1:1, 1:2, 1:4, and 1:8), and both food intake and body energy—used as a proxy for reproductive fitness—were measured. While genotype alone did not significantly influence overall consumption or fitness, significant genotype-by-diet interactions emerged. Specifically, food intake differed between genotypes at P:C ratios of 1:1 and 1:8, and diet-specific fitness differences were observed at the 1:2 ratio. Across genotypes, flies consumed the most on the carbohydrate-rich 1:8 diet, but achieved highest fitness on the balanced 1:1 diet, indicating a potential mismatch between intake preference and optimal physiological performance. Variance decomposition analysis revealed that diet type accounted for the largest proportion of fitness variation (20.6%), followed by behavioral intake response (6.8%), while genotype contributed minimally (1.1%). These findings suggest that behavioral plasticity in food intake may be a stronger determinant of male fitness than intrinsic genetic differences under controlled conditions. However, the presence of genotype-specific responses to certain diets points to the need for further molecular investigations. Together, these results underscore the nuanced relationship between nutrition, genotype, and reproductive success, and provide new insight into the nutritional ecology of male fruit flies.

The impact of locomotor mode and phylogenetic clades on skeletal measurements in frogs

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Abstract ID: 46

Keywords: Frog locomotion, anuran evolution, biomechanics, hindlimb anatomy, phylogeny, principal component analysis, skeletal morphology

Frogs exhibit a remarkable diversity of locomotor strategies—ranging from jumping and swimming to walking and burrowing—each supported by distinct skeletal adaptations. However, the extent to which locomotor mode and phylogenetic clade independently shape skeletal morphology remains poorly resolved. In this study, we investigated the influence of locomotor mode and evolutionary lineage on hindlimb and pelvic traits across 164 frog species, encompassing five locomotor types and four major clades. We quantified six skeletal parameters, including snout-vent length (SVL), expansion of sacral diapophyses (ESD), and the lengths of the femur, tibiofibula, calcaneus, and foot. After size standardization and outlier exclusion, we applied linear regression, ANOVA, and principal component analysis (PCA) to assess morphological variation and its association with ecological and phylogenetic factors. Our results reveal that locomotor mode significantly predicts skeletal variation, particularly in the femur, tibiofibula, and calcaneus. Walkers and burrowers tend to exhibit shorter hindlimb bones, whereas jumpers possess longer ones, supporting biomechanical specialization for different types of terrestrial movement. Aquatic species display intermediate traits but high internal variability. Notably, ESD also varies with locomotor strategy, being lowest in jumpers and highest in walkers. PCA identified tibiofibular length as the strongest driver of morphological divergence (PC1), explaining over 60% of total variance. Conversely, phylogenetic clade was not a consistent predictor of skeletal traits, suggesting evolutionary conservation or convergent adaptation across clades. Taken together, our findings emphasize locomotor ecology as the primary determinant of skeletal form in frogs, with phylogenetic identity playing a secondary role. These insights contribute to understanding the evolutionary biomechanics of vertebrate locomotion and provide a framework for future research integrating genetics, function, and form.

Unveiling the population genetic structure of European Hornbeams in the Hainault Forest: Determining the extent of clonality, genetic diversity and spatiality

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Abstract ID: 47
Keywords: Carpinus betulus, European hornbeam, Hainault Forest, LISA, Moran's I, SNP markers, clonality, conservation genetics, forest conservation, genetic diversity, genetic homogeneity, k-means clustering, multilocus genotype, non-clonal population, observed heterozygosity, population genetics, principal component analysis, spatial autocorrelation, spatial genetic structure

Understanding the genetic structure of plant populations is essential for informing conservation strategies, particularly under the increasing pressure of climate change and anthropogenic influence. This study investigates the population genetics of European hornbeams (*Carpinus betulus*) in the Hainault Forest, with a focus on clonality, nuclear genetic diversity, and spatial genetic structure. A total of 77 hornbeam samples were genotyped using SNP markers, and multilocus genotype (MLG) analysis revealed no evidence of clonality, with each sample representing a distinct genotype. Analysis of observed heterozygosity (HO) across eight nuclear chromosomes revealed consistently low values (mean HO = 0.0483), indicating low genetic diversity within the population. Principal component analysis (PCA) and k-means clustering confirmed the absence of genetically distinct sub-populations. Furthermore, regression analyses and spatial autocorrelation tests (Moran's I and LISA) showed no significant association between genetic variation and geographic coordinates, suggesting a random spatial distribution of genetic diversity. These findings imply that the hornbeam population in Hainault Forest is genetically homogenous and non-clonal, with minimal spatial genetic structure. This contrasts with expectations for long-lived woody species and highlights the importance of considering increasing heterozygosity in local conservation efforts. Future studies should increase sample size, include organellar genomes, and develop a hornbeam reference genome to better characterize evolutionary and ecological dynamics across broader landscapes.

Integrating FlowCam imaging and AI-assisted classification to assess phytoplankton responses to experimental salinization

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Abstract ID: 66
Keywords: Artificial Intelligence, FlowCam, Imaging Flow Cytometry, Machine Learning, Microscopy, Phytoplankton, Salinity Gradient

Phytoplankton are essential primary producers in aquatic habitats. Traditional identification using microscopy is laborious and s substantial taxonomic proficiency. High- throughput, image-based flow cytometry techniques, as demonstrated by the FlowCam (YOKOGAWA), offer an efficient solution for the rapid study of live plankton. This capability is particularly significant for identifying delicate species and structures, such as naked ciliates and colonies, which are often compromised during fixation and are essential for ecological analysis.

Considering the benefits of automated imaging systems, the substantial amount of generated image data necessitates extensive post-processing. Despite employing software like VisualSpreadsheet, analysis remains a labor-intensive task. To address this limitation, our research integrates artificial intelligence (AI) with FlowCam images to enhance the speed, precision, and reliability of phytoplankton categorization. A comparative assessment of phytoplankton samples was conducted during a mesocosm experiment at METU Mesocosm System II, Türkiye, as part of the EU H2020-INFRAIA AQUACOSM-plus (No. 871081) and TÜBİTAK 232 programs. The experiment examined 16 salinity levels to analyze the structural and functional responses of lake ecosystems. Phytoplankton were analyzed using FlowCam and traditional microscopy to evaluate taxonomic composition and morphological characteristics. Annotated FlowCam records from the experiment were utilized to develop a machine learning model for automated taxonomic classification. The results were corroborated by microscopy-based identifications. Our findings indicate that FlowCam, enhanced by AI classification, provides reliable phytoplankton identification comparable to traditional methods. This study highlights the potential of combining image flow cytometry with machine learning to enable accessible, high-throughput monitoring of phytoplankton populations, offering a scalable and open-source option for ecological research and long-term monitoring initiatives.

Genome size: Did flight loss relax genome size constraints in birds?

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Abstract ID: 6

Keywords: birds, evolution, flightless, genome

Genome size and its role in genome evolution has long been debated in evolutionary biology, with different trends emerging across taxonomic groups. Birds—compared to mammals and reptiles—are known to have a more conservative range of genome sizes, often attributed to the energetic demands of flight and the associated need for reduced cell size. In this study, we investigate whether flight loss in birds has released the genome size constraint observed in their volant relatives. To address this question, we constructed a dataset comprising short-read sequencing data of 30 bird species (13 taxonomic families) obtained from the NCBI database, including 15 flightless and 15 flighted species, representing 25% of extant flightless birds. Genome size estimations were performed using GenomeScope, revealing that ratites and penguins possess significantly larger genome sizes than “other” flightless birds (7 species) and their flying relatives. The “other” flightless birds did not deviate in genome size compared to their flying relatives. Regressions further indicate that body mass, together with flight ability, explain 48% of the variance in genome size. Based on our preliminary results, we plan to broaden our analyses by incorporating extreme body mass comparisons and applying models that account for phylogenetic relationships. We aim to extend this analysis across the broader avian phylogeny, with a focus on species that evolved flightlessness more recently, to better understand the evolutionary relationship between genome size and flight capability.