PhDay

18th & 19th
December
2025

Evolutionary Biology and Ecology

PhD Day Organising Committee

Valeria Santini
Alessandro Russo
Marcella Sozzoni
Duccio Cavalieri
Alessio Papini

Keynote Speakers

Andrea Quagliariello
Paola Bonfante
Elena Pilli
Teresa Rinaldi
Fiorenza Micheli

Cover illustration

Leonardo Girlanda

PhDay brief program

Thursday, 18 December
DAY 1

8:30 - 9:00	Registration
9:00 - 9:30	Opening Remarks and Institutional Greetings - Duccio Cavalieri and Stefano Cannicci
9:30 - 11:00	Andrea Quagliariello University of Florence Assistant Professor
11:00 - 11:20	Giorgia Ciappi
11:20 - 11:50	Coffee break
11:50 - 12:10	Marta Montagnini
12:10 - 12:30	Francesco Savarino
12:30 - 12:50	Beatrice Sammarco
12:50 - 13:10	Alessia Ardenghi
13:10 - 14:30	Lunch
14:30 - 16:00	Paola Bonfante Turin University Emeritus Professor Member of the Accademia dei Lincei
16:00 - 16:20	Veronica Butelli
16:20 - 16:50	Coffee break
16:50 - 17:10	Alexander Cannaerts (online)
17:10 - 17:30	Gaia Regini
17:30 - 17:50	Giulia Giovanna Salerno (online)
17:50 - 17:55	Matilda Bellini
17:55 - 18:00	Viola Ceccherini
18:00 - 18:05	Francesca Coscione
18:05 - 18:10	Beatrice Chiavacci
18:10 - 18:15	Antonio Verolino
18:15 - 18:20	Federica Castagnoli (online)
18:20 - 18:25	Jesús Lenin Lara Galván
18:25 - 18:30	Andrea Passini
18:30 - 18:35	Elena Buccarelli

Friday, 19 December
DAY 2

9:00 - 10:30	Elena Pilli University of Florence Associate Professor FIS3 winner
10:30 - 10:50	Tommaso Marinoni
10:50 - 11:10	Giorgia Staffoni (online)
11:10 - 11:40	Coffee break
11:40 - 12:00	Marta Nerini
12:00 - 12:20	Matilde Marconi
12:20 - 13: 20	Teresa Rinaldi Sapienza University of Rome Associate Professor
13:20 - 14:20	Lunch
14:20 - 14:40	Alice Rispoli
14:40 - 15:00	Flavia di Cesare
15:00 - 15:20	Lara Gazzoldi
15:20 - 15:40	Giulia Bertoletti
15:40 - 16:00	Break
16:00 - 16:20	Eugenia Siccardi (online)
16:20 - 16:40	Linda Pratesi (online)
16:40 - 18:10	Fiorenza Micheli Stanford University David and Lucile Packard Professor of Marine Science Chair, Oceans Department Co-Director of Stanford Center for Ocean Solutions Senior Fellow at Woods Institute for the Environment Hopkins Marine Station
18:10 - 18:30	Final Greetings - David Caramelli

Lecture
Genetica ed Evoluzione
Biologia e Biotecnologie vegetali
Ecologia ed Etologia
First-year students

Important notes to oral presenters

The meeting supports PowerPoint or PDF presentations
16:9 landscape mode is optimal
Please be present at least 10 minutes before your scheduled presentation time, although you are encouraged to attend the meeting in full
Your presentation is strictly timed. Most contributed talks are given 10 minutes. After the talk, there will be a maximum of 10 minutes for questions. Please respect these timings and remember that the question time belongs to the audience, not to the speaker.
If you have been given permission to present remotely, we will send you separate link to join the meeting. Please be ready 10 minutes before your schedule presentation time.

Please email your presentation to dottoratobee@unifi.it by 16 December.

Complete Program

Thursday, 18 December

8:30 - 9:00 Registration

9:00 - 9:30 Opening Remarks and Institutional Greetings

9:30 - 11:00 Opening Lecture

QUAGLIARIELLO A. - Integrating parrotfish microbiome ecology into the coral reef bioerosion paradigm

11:00 - 14:30 **Genetic and Evolution - PhD Students' Talks**

CIAPPI G. - Skeletal growth patterns and evidence of selective burial practices among late upper paleolithic hunter-gatherers

11:20 - 11:50 *Coffee Break*

MONTAGNINI M. - Diachronic paleogenomic study of central italy: analysis of the remains from the palazzone necropolis and the hypogeum of the volumni (5th century bc – 1st century ad)

SAVARINO F. - Paleogenomic analysis on human individuals found in pompeii

SAMMARCO B. - Tracing the origins of non-native *Littorina saxatilis* populations: genomic insights into colonization outcome

ARDENGHI A. - Conservation genetics of mediterranean populations of the *Salmo* genus (*Salmo marmoratus, Salmo cettii,* and *Salmo ghigii*)

13:10 - 14:30 *Lunch Break*

14:30 - 16:00 Invited Lecture

BONFANTE P. - Mycorrhizae: a complex biological system for studying plant-microbe interactions

16:00 - 17:50 **Plant Biology and Biotechnology - PhD Students' Talks**

BUTELLI V. - Testing the potential of polymer-complexed magnetites as nanofertilizers on the model plant *Tillandsia usneoides*

16:20 - 16:50 *Coffee Break*

CANNAERTS A. - Linking the Effects of global change on mycorrhizal communities and plant functioning in grasslands

REGINI G. - Physiological, biochemical and molecular analysis of thallium hyperaccumulation and hypertolerance of *Silene latifolia*

SALERNO G.G. - Formation of the vascular system: an auxin-dependent physiological process involved in plant organogenesis

17:50 - 18:35 **First-year students' Short Talks**

PASSINI A. - Sustainable management of feral horse populations for the conservation of mountain grasslands

CECCHERINI V. - Cyanobacterial blooms in alpine lakes: genomic and functional characterization

COSCIONE F. - Decoding the bacterial epigenome in host–microbe interaction

CHIAVACCI B. - Shedding lights into transgenerational memory to abiotic and biotic stresses in legumes

VEROLINO A. - The role of ants in deadwood colonization and saproxylic community assembly

CASTAGNOLI F. - Artificial intelligence applications for biodiversity monitoring and protection

LARA GALVAN J. L. - Biodiversity of the endemic malagasy chameleons of the genus *Calumma*: distribution patterns and ethnobiological knowledge

BELLINI M. - Eco-evolutionary dynamics analysis of yeast-insects interactions: role of *saccharomyces cerevisiae*-derived vocs in modulating attractiveness

BUCCARELLI E. - The biography reconstruction of Enrica Calabresi: passionate zoologist, scientist and teacher in the first half of the twentieth century

Friday, 19 December

9:00 - 10:30 Opening Lecture

PILLI E. - Artificial Intelligence and Forensic Genomics for Human Biodiversity

10:30 - 12:20 **Ecology and Ethology - PhD Students' Talks (I)**

MARINONI T. - Impact of *Nypa fruticans* and Thalassinidae on mangrove crab community and assessment of non-invasive monitoring techniques

STAFFONI G. - From temperate streams to tropical mangroves: the future of biodiversity monitoring and conservation using environmental dna

11:10 - 11:40 *Coffee Break*

NERINI M. - Investigating microbial interactions in agricultural soils from bovine tuberculosis-affected and tuberculosis-free farms

MARCONI M. - The impact of anthropogenic and natural disturbance on interactions between mammals and forests, and on ecosystem services: preliminary results from two case studies.

12: 20 - 13:20 Invited speaker

RINALDI T. - European Dual Use Regulation: Definition and Implications for Scientific Research

13:20 - 14:20 *Lunch break*

14:20 - 16:40 **Ecology and Ethology - PhD Students' Talks (II)**

RISPOLI A. - Effects of the introduction of *apis mellifera* on the trophic and behavioral dynamics of native pollinators on giannutri island

DI CESARE F. - Biopesticides and pollinators: lethal and sub-lethal effects on *apis mellifera* and *bombus terrestris*

GAZZOLDI L - Effects of hydraulic connectivity and nutrients availability on benthic metabolism and nitrogen cycling in perifluvial wetlands

BERTOLETTI G. - Invasion of *Mnemiopsis leidyi* and risk of regime shift in european marine ecosystems

15:40 - 16:00 *Break*

SICCARDI E. - Context-dependent effects of land abandonment: evidence from semi-natural pastures and artificial chestnut groves

PRATESI L. - The origin of social inequalities in northern Italy: clues from ancient genomes

16:40 - 18:10 Closing Lecture

MICHELI F. - Ocean Solutions for Nature and People

18:10 Final Greetings

9:30 - 11:00 LECTURE

Integrating parrotfish microbiome ecology into the coral reef bioerosion paradigm

SPEAKER
Andrea Quagliariello

11:00- 11:20

Skeletal growth patterns and evidence of selective burial practices among late upper paleolithic hunter-gatherers

Giorgia Ciappi

With the end of the Pleistocene, European hunter-gatherers faced extreme environmental conditions and climatic fluctuations. The human groups of this period show selective funerary practices, often reserved for "exceptional individuals/events," associated with illness or violent death. In this context, two sites from the Final Upper Palaeolithic were analysed: the Caverna delle Arene Candide (Liguria), dated to the Youger Dryas (12,900–11,600 BP), and the Grotta di Maritza (Abruzzo), which yielded the remains of a subadult and an adult who lived after this climatic event. Since environmental stress can cause delays in growth and maturation, the degree of developmental completion was calculated for Epigravettian subadults and compared with a modern reference sample (Denver Growth Study, DGS). The children from Arene Candide show developmental delays relative to the DGS, whereas the subadult Maritza1 and two children from Grotte des Enfants, who lived before the final glacial event, do not show such delays. These data suggest a possible correlation between the climatic deterioration of the Younger Dryas and the ontogenetic development of the Epigravettian individuals from Arene Candide. Conversely, the adult Maritza2 shows abnormal bone remodeling in the craniofacial region, compatible with pathological conditions such as acromegaly. Advanced analyses were conducted on the cranium and long bones using virtual anthropology, cross-sectional-geometry and geometric morphometrics, comparing the results with Epigravettian, Mesolithic and Neolithic adults, documented cases of pituitary gigantism, and modern individuals. Although Maritza2 exhibits skeletal dimensions at the upper limit of the variability observed in contemporaneous individuals—suggesting a larger-than-average adult—the cranial morphology does not show strong similarity to individuals affected by pituitary gigantism. At the current state of research, therefore, no definitive evidence of acromegaly emerges. Overall, these individuals raise questions regarding the selectivity of burials, levels of inbreeding, and possible forms of social care within these communities.

11:50 - 12:10

Diachronic paleogenomic study of central italy: analysis of the remains from the palazzone necropolis and the hypogeum of the volumni (5th century bc – 1st century ad)

Marta Montagnini

This PhD project aims to reconstruct the genetic history of central Italian populations through the analysis of human remains from Etrusco-Umbrian archaeological contexts: the Palazzone necropolis and the Volumni Hypogeum, as well as the Deruta necropolis. The two funerary complexes, located on opposite banks of the Tiber, provide an ideal case study to investigate genetic differences between geographically close but culturally distinct communities. Throughout the year, sampling, DNA extraction, and library preparation were carried out. The samples were analyzed through shallow shotgun sequencing to obtain a preliminary assessment of endogenous DNA content. Mitochondrial DNA target enrichement approach was also adopted to increase the possibility to analyze more deteriorated samples and to evaluate modern contamination levels.

Additionally, a significant part of the work focused on developing a specific protocol to optimize DNA recovery from incinerated remains. Raw reads were processed using the EAGER pipeline, showing proper endogenous DNA preservation in 7 out of 29 samples, highlighting the need for further optimization of protocols for cremated remains. The genotyping of samples allowed investigations into genetic variability through PCA, which showed that the analyzed individuals cluster into two distinct groups, both falling within the genetic variability of Central Italy. Tools such as READ and KIN provided information on kinship and consanguinity, identifying two first-degree relationships among individuals from Deruta necropolis.

12:10 - 12:30

Paleogenomic analysis on human individuals found in pompeii

Francesco Savarino

Paleogenomics makes it possible to reconstruct the genetic variability, demographic dynamics and evolutionary processes of ancient populations by integrating genomic, archaeological and cultural data. In this study, the genome of Marcus Venerius Secundio, the only known mummified individual from Pompeii who lived immediately before the eruption of 79 CE, was analysed. The genome, sequenced at a mean coverage of 5×, was interpreted through a Genotype Likelihood–based approach, including Principal Component Analysis, estimation of ancestry components, analysis of uniparental markers, probabilistic phenotypic prediction, and spatio-temporal modelling of genetic similarity through Gaussian processes (Gaussian Process Regression), based on the interpolation of genetic distances with respect to georeferenced ancient samples. The analyses indicate predominant genetic affinities with populations from the Caucasus, consistent with the atypical nature of the burial and with the historical-archaeological evidence relating to the individual. Furthermore, 12 Pompeian samples characterized by a high percentage of endogenous DNA were selected and subjected to deep-shotgun sequencing to maximise informational yield. The ongoing analyses involve the processing of Genotype Likelihoods using the same approaches applied to the data from Marcus Venerius Secundio, with the aim of integrating these individuals into a coherent comparative framework and contributing to the reconstruction of the genetic variability associated with the Pompeian population. A secondary project concerns the analysis of individuals from the Etruscan necropolis of Santa Maria Capua Vetere (8th–5th centuries BCE), with the aim of investigating the genetic dynamics of pre-Roman communities in the Campanian region.

12:30 - 12:50

Tracing the origins of non-native *Littorina saxatilis* populations: genomic insights into colonization outcomes

Beatrice Sammarco

Biological invasions represent an ideal model to investigate the evolutionary processes underlying local adaptation and geographic expansion. Littorina saxatilis, a small marine gastropod native to the North Atlantic coasts, is an excellent model system to explore the genetic and genomic factors that may determine the success or failure of colonization processes. This species has undergone multiple range expansion events with contrasting outcomes, offering a unique opportunity to compare expansion and extinction dynamics within the same species. The Venetian population of L. saxatilis represents the oldest documented case of alien introduction in the Mediterranean Sea and is an emblematic example of a failed colonization. Understanding its origin can provide crucial insights into whether specific genetic or genomic components underlie this failure. Within the framework of the PRIN 2022 PNRR FIASCO project, our goal is to compare two recent colonization events with opposite outcomes: Venice (unsuccessful) and San Francisco (successful). By expanding the available whole-genome sequencing dataset and incorporating new high-coverage data, we aim to investigate the role of structural variants and genetic load in shaping the fate of introduced populations. Finally, demographic analyses based on the site frequency spectrum (SFS) will allow us to reconstruct the evolutionary history of the species and to better understand how genetic and ecological processes interact in determining the outcome of biological invasions.

12:50 - 13:10

Conservation genetics of mediterranean populations of the *Salmo* genus (*Salmo marmoratus, Salmo cettii,* and *Salmo ghigii*)

Alessia Ardenghi

The conservation of Mediterranean Salmo populations represents a critical priority due to the high number of endemic lineages threatened by anthropogenic pressures. The recent suspension of the derogation established by the Italian Ministerial Decree of 2 April 2020 prohibits the release of non-native salmonid stocks into natural ecosystems, thereby emphasizing the need for robust genomic tools to safeguard native evolutionary lineages.

The PhD project initiated first-level genetic analyses using mitochondrial (d-loop) and nuclear (LDH) markers on Italian Salmo populations. These preliminary results enabled the selection of samples included in a proposal submitted to the Human Technopole call, based on a WGS genomic approach targeting individuals belonging to the Mediterranean ESUs *(S. trutta, S. marmoratus, S. ghigii, S.cetti, S. fibreni*), as well as fertile hybrids.

A specific focus was dedicated to Salmo marmoratus, with a study on the genetic characterization of males from the Adige, Brenta, and Piave river basins intended for breeding programs. The best breeders were selected based on genetic results (D-loop, LDH-C1, microsatellites) and functional sperm parameters, supporting the creation of a cryopreserved germplasm bank. In parallel, a machine- and deep-learning classification system (EfficientNet, CNN) was developed using labeled images of *S. marmoratus, S. trutta*, and hybrids to identify discriminant morphometric features. Such a visual classification tool would provide an innovative and non-invasive resource for institutions responsible for population management. Complementary research based on an eDNA analysis protocol further integrated these activities, with the aim of offering an advanced operational framework for the future conservation-oriented management of Mediterranean Salmo populations.

14:30 - 16:00 LECTURE

Mycorrhizae: a complex biological system for studying plant-microbe interactions

SPEAKER
Paola Bonfante

16:00 - 16:20

Testing the potential of polymer-complexed magnetites as nanofertilizers on the model plant *Tillandsia usneoides*

Veronica Butelli

Biofortification represents a process capable of improving the nutritional value of crops during plant growth. In this context, nanofertilizers are particularly promising, thanks to their efficient and controlled micronutrient release compared to traditional approaches. In this work, magnetite nanoparticles coated with citrate (FeCi) were complexed with polymers extracted either from the succulent plant *Aloe vera* (APS) or from the cyanobacteria *Cyanospira capsulata* (EPS). The obtained nanosystems were tested on the epiphyte model plant *Tillandsia usneoides,* allowing a direct observation of micronutrient plant uptake by its leaves. The physico-chemical properties of the nanoparticles were studied by DLS and ZP measurements. Both coated and complexed nanosystems provided to be time and thermally stable, characterized by an average size below 300nm and an increase in the surface charge in presence of the polymers. During this experiment, *T.*usneoides strands were hung on a net and the treatments were administered by foliar spray. The treatment lasted for 31 days, during which plant growth and photosynthetic activitiy were monitored. At the end of the experiment, the strands were dried and pulverized to quantify the micronutrient amount by XRF technique. A significant increase in length and iron absorption were found in plants treated with APS-complexed magnetites, which was higher than plants treated with EPS-complexed nanoparticles. An improvement of photosynthetic activity was observed in FeCi+APS. These results suggest that the nanocomplexes produced may be employed as nanofertilizers, opening to administration on plants with agronomic interest.

16:50 - 17:10

Linking the Effects of global change on mycorrhizal communities and plant functioning in grasslands

Alexander Cannaerts

Recent studies show that fertilisation alters the drought-sensitivity of grassland vegetation. However, the direction and strength of these changes vary between species, functional groups and sites. While several mechanisms have been proposed to explain these variations, no conclusive framework has been found.Few studies have considered the role of mycorrhizal fungi in fertilisation-induced altered drought-sensitivity. Mycorrhizal fungi form symbiotic associations with plant roots in which fungal derived nutrients are exchanged for plant photosynthesised sugars. Mycorrhizal fungi provide additional benefits for plants, such as enhancing plant drought-tolerance. Concurrently, excessive fertilisation is known to decrease the diversity and abundance of mycorrhizal fungi. Thus, it is reasonable to suggest that negative effects of fertilisation on mycorrhizal fungi could contribute to altered drought-sensitivity of fertilised grasslands. How mycorrhizal fungi respond to fertilisation and drought simultaneously, and how these responses influence plant drought-sensitivity, is currently unknown. My PhD project aims to answer this question, using different experiments and approaches. In one of these studies, we carried out a mesocosm experiment with monoliths exposed to 3 fertilisation levels combined with 2 precipitation levels. In 2025, we carried out the pilot study off this mesocosm, from which we will present the preliminary results. In 2026 we will repeat the study, refining where necessary. Alongside the mesocosm results, we will briefly present my other projects, which focus on mycorrhizal diversity under fertilisation, drought and warming at a global scale. Sample processing for this research is underway, and data analysis will be finalised in 2027.

17:10 - 17:30

Physiological, biochemical and molecular analysis of thallium hyperaccumulation and hypertolerance of *Silene latifolia*

Gaia Regini

Thallium (Tl) pollution has recently become an environmental concern worldwide. The increasing release of this metal in the environment is primarily driven by mining activities in which Tl forms an impurity. The metallicolous populations of the facultative Tl hyperaccumulator *Silene latifolia* are extraordinarily tolerant and capable of accumulating up to 80,000 µg Tl g^{-1} in nature. A growth stimulatory effect of Tl was observed, and this study set out to determine possible mechanisms. Plants from non-metallicolous and metallicolous populations were subjected to hydroponics dosing experiments at 2.5 and 10 µM Tl. Metal impact on stomatal and non-stomatal photosynthetic constraints, light energy conversion processes, and plant anatomy/ultrastructure was assessed over time.Photosynthetic rates improved in 10 µM Tl-treated metallicolous plants by 20% compared to controls, partly due to increased stomatal conductance. The latter was mainly driven by Tl-induced anatomical changes, such as increased central cylinder area and stomatal density, likely to enhance water uptake/translocation and, consequently, leaf metal accumulation. The apparently Tl-favoured CO_2 trafficking resulted in ameliorated maximal photosynthetic capacity. The first signs of photosynthetic declines appeared only at very high Tl leaf concentrations (15,000 µg Tl g^{-1}), with limitations involving stomatal and biochemical factors, whereas the photochemical reactions remained functional. The observed Tl-induced stimulatory response in growth and net photosynthetic rate in metallicolous plants shows that Tl improves physiological performance in Silene latifolia, mainly through improved stomatal conductance.

17:30 - 17:50

Formation of the vascular system: an auxin-dependent physiological process involved in plant organogenesis

Giulia Giovanna Salerno

The formation of the vascular system in plants, which is essential for the transport of water, nutrients, and signaling molecules, is regulated by the hormone auxin and is probably mediated by its binding to the receptor Auxin Binding Protein 1 (ABP1). During the first year of the PhD, morphological observations were carried out to analyze the effect that two synthetic ureide derivatives, N,N’-bis-(2,3-methylenedioxyphenyl)urea (2,3-MDPU) and

1,3-di(benzo[d]oxazol-5-yl)urea (5-BDPU), exert on the formation of the transport system in the cotyledon model of *Arabidopsis thaliana*. Since these molecules amplify the auxin effect in certain physiological processes, such as adventitious root formation, morphological analyses were continued during the second year by comparing the effects of synthetic urea derivative with those of natural molecules, in order to evaluate whether similar or divergent physiological responses could be observed. The effects of the exogenous application of two natural cytokinins, 2-isopentenyladenine (2iP) and 6-benzylaminopurine (BAP), were therefore studied in order to understand the influence of the auxin/cytokinin ratio on the process under investigation. Since urea derivatives inhibit the enzyme cytokinin oxidase (CKX), an analysis was conducted with mass spectrometry to quantify endogenous cytokinins in plants treated with 2,3-MDPU and 5-BDPU either individually or in combination with 1-naphthaleneacetic acid (NAA). This analysis has highlighted the effect of "pure CKX inhibitors", which, although lacking cytokinin activity, modulate plant development, increasing the endogenous cytokinin content. Furthermore, *in vitro* enzymatic assay allowed the evaluation of the affinity of three different susbtrates: trans-zeatina, 2iP and BAP with CKX1 by identifying the cytokinin with the highest binding affinity. Lastly, using the same experimental system, the effect of serotonin, a natural molecule that appears to enhance auxin activity, was also examined.

17:50 - 17:55

Sustainable management of feral horse populations for the conservation of mountain grasslands

Andrea Passini

The abandonment of agricultural practices in recent decades has favored forest regrowth at the expense of biodiversity-rich secondary grasslands located on the top of mountains. In recent years, rewilding has become an important option for the conservation of these habitats. There is growing scientific evidence that the reintroduction of large, non-domestic grazing herbivores, particularly horses (*Equus ferus caballus*), may have positive effects on the maintenance of plant biodiversity. My research project will focus on the dynamics of a feral horse population inhabiting the Calvana mountains (a Site of Community Importance: IT5150001) near Firenze. This population originated from the release of an unknown number of horses that occurred more than 40 years ago, and today is composed of more than 100 individuals, fully adapted to life in the wild. This population is therefore an interesting case-study to analyze the long-term effects of rewilding practices for the conservation of mountain grasslands. The study aims to answer four key questions: what is the effect of horse grazing on the soil and vegetation of mountain-top grasslands? Has the population delayed the advance of shrubs? What is the maximum carrying capacity of the ecosystem? Is there any inbreeding effect, given the origin of this population from a small group of founders? The methods include characterization of plant communities and analysis of historical dynamics of pastures (with exclusion areas and analysis of aerial pictures), quantification of the effect of grazing (direct observations, drones, camera trapping), genetic analysis of fecal samples to quantify the degree of inbreeding, and, finally, awareness-raising and community engagement initiatives. These data will be used to model population growth and to provide an estimate of the long-term impact of horse grazing, to be used for the development of management guidelines for this population.

17:55 - 18:00

Cyanobacterial blooms in alpine lakes: genomic and functional characterization

Viola Ceccherini

Cyanobacteria are photosynthetic prokaryotic microorganisms widely distributed in global aquatic ecosystems. However, under favorable environmental conditions, these organisms can proliferate uncontrollably, leading to massive blooms with potential negative ecological, sanitary and economic impact. The development of cyanobacterial blooms is primarily driven by two factors: eutrophication and global warming, which cause an increase in surface temperature and greater thermal stability of the water column. This project is set in this context, aiming to investigate in depth the dynamics of cyanobacterial blooms in Lake Serraia (TN), an alpine lake ecosystem of high naturalistic and recreational value, which has been subject to frequent blooms in the past few years, with direct implications for public health and tourist-recreational activities. This project proposes to integrate genomic, metagenomic and metabolomic approaches for a comprehensive characterization of the cyanobacterial populations and the entire microbial community of the lake. The goal is to understand the ecological, genetic and functional mechanisms underlying toxic blooms and to support future monitoring and management strategies.

18:00 - 18:05

Decoding the bacterial epigenome in host–microbe interaction

Francesca Coscione

Epigenetic modifications, such as DNA methylation and chromatin compaction, represent in prokaryotes a still underexplored regulatory layer, whose role in adaptation and environmental response processes remains is not yet fully defined. This PhD project aims to clarify how the bacterial epigenome responds to environmental changes and to what extent such variations affect gene expression and bacterial fitness. The study model is *Sinorhizobium meliloti*, a bacterium capable of thriving in diverse environmental conditions and of establishing facultative mutualistic symbioses with leguminous plants, within which it differentiates into specialized forms devoted to nitrogen fixation. This plasticity, together with the multipartite structure of its genome (comprising a chromosome and megaplasmids subject to horizontal gene transfer) makes it an ideal system to investigate the contribution of epigenetic modifications to gene regulation, adaptation, and genome evolution. To achieve these goals, the project will combine observational and inferential approaches, employing methylomic, genomic, and transcriptomic analyses alongside gene knock-out and experimental evolution assays. Methylation and gene expression profiles will be characterized under different conditions, both in free-living cultures and in symbiosis. Mutants lacking orphan DNA methyltransferases and Nucleoid-Associated Proteins will allow assessment of the causal effects of epigenetic modifications on transcriptional regulation and cellular differentiation during symbiosis. Finally, evolution experiments under stress conditions and fitness assays will be used to estimate the stability, heritability, and phenotypic consequences of epigenetic variation, providing an integrated view of the role of the bacterial epigenome in adaptive and evolutionary processes.

18:05 - 18:10

Shedding lights into transgenerational memory to abiotic and biotic stresses in legumes

Beatrice Chiavacci

Modern agriculture faces the crucial challenge of managing environmental stresses to sustain crop productivity in the context of accelerating climate change. Understanding the transgenerational effects of abiotic and biotic stresses on crop performance is therefore crucial for developing climate-smart varieties with enhanced resilience. This project will investigate the transgenerational response to abiotic (such as drought and salinity) and pathogenic stress using chickpea (*Cicer arietinum* (L.), as a model species for all grain legumes. Chickpea is one of the most important legume crops worldwide, serving as a key source of plant-derived proteins for human consumption. Previous studies in our laboratory revealed that chickpea plants exposed to drought stress exhibit adaptive traits transmitted to the next generation, including reduced plant height, smaller leaf area, and modifications in root architecture, typical indicators of physiological stress memory under water deficit conditions. Based on these findings, *A. thaliana* mutants will be used to validate the role of candidate genes involved in transgenerational memory of drought stress.

In this doctoral project, we want to examine another abiotic stress, salinity, and a biotic stress (caused by *Ascochyta rabiei*) across three generations F_0, F_1, and F_2. To gain deeper insights into these mechanisms, we will integrate omics approaches (methylome, transcriptome, and metabolome) with physiological and biochemical analyses, including measurements of photosynthetic efficiency, chlorophyll content, and stress biomarkers. Understanding stress memory in plants is a key step toward developing new genotypes with enhanced resilience to climate change through both biotechnological and conventional breeding approaches.

18:10 - 18:15

The role of ants in deadwood colonization and saproxylic community assembly

Antonio Verolino

The project aims to analyze the role of ants as saproxylic organisms and the various interactions they may have with other biotic components (plants, animals, and microorganisms) involved in the processes of deadwood transformation. During the project, ant communities associated with deadwood will be characterized in detail for the first time across different forest biomes and in relation to various climatic zones along the Italian peninsula. Field experiments will allow the identification of colonization patterns in relation to different forest species and the physical-chemical characteristics of the wood. The results will make it possible to define the saproxylic habitus role of different ant species through the development of a “potential colonization index,” similar to those already used for several other insect species. The aim is to assess the effects of ants on the decomposition processes of deadwood and on carbon storage. This would provide a solid basis for developing monitoring protocols applicable in forest ecosystems. The analysis of fungal and microbial communities associated with different ant species may also reveal new species-specific associations or mechanisms in wood colonization. The results will contribute to filling significant knowledge gaps concerning aspects of forest ecology related to deadwood and will offer useful insights for the management and conservation of forest biodiversity.

18:15 - 18:20

Artificial intelligence applications for biodiversity monitoring and protection

Federica Castagnoli

Artificial Intelligence is an effective tool for ecological monitoring and conservation, that allows the management of large amounts of data and is often more efficient than traditional methods, such as multivariate statistics. Applications range from niche modeling, to predict how climate and environmental changes will affect the distribution of organisms, to the automated recognition of individuals from images and sounds recordings. Footage from camera traps, drones, and satellites can be analyzed by Deep Neural Networks, which can identify the presence of animals and the distribution of plants with up to 99% accuracy. The higher the image resolution, the greater the ability to recognize and distinguish different taxa. Passive acoustic monitoring (PAM) allows for the detection of alien and elusive species, thanks to the automated identification of species using machine learning algorithms. Different individuals from population of social species can be tell apart through the recognition of individual voiceprints or specific morphological characteristics.

18:20 - 18:25

Biodiversity of the endemic malagasy chameleons of the genus *Calumma*: distribution patterns and ethnobiological knowledge

Jesús Lenin Lara Galván

Chameleons of the genus *Calumma* are an iconic and highly representative reptiles of Madagascar. Despite an increase in their study over the last decade, there are multiple knowledge gaps on their distribution, ecology, and natural history. This research seeks to fill this gap by inferring the distribution patterns of these reptiles, as well as to determine the environmental, biological, and social variables that favor their presence in different habitats. We will determine areas of high species diversity, and will deploy environmental education strategies in the field to assess the likelihood of their population persistence. To do this, surveys in the field will be coupled with interviews with local communities to inquire on the perception and ethnobiological knowledge that the locals have about these reptiles, which will be used to design new conservation strategies.

18:25 - 18:30

Eco-evolutionary dynamics analysis of yeast-insects interactions: role of *saccharomyces cerevisiae*-derived vocs in modulating attractiveness

Matilda Bellini

Saccharomyces cerevisiae and insect interactions are crucial for yeast's dispersal and evolution. Social insects can acquire *S. cerevisiae* from the environment, facilitating its dissemination across natural substrates. Specifically, the gut of social wasps provides a natural niche where *Saccharomyces cerevisiae* can sporulate, germinate, and undergo both intra- and interspecific sexual reproduction, promoting genetic recombination and contributing to biodiversity. In this context, yeast-derived Volatile Organic Compounds (VOCs) could act as chemical signals that attract insects, potentially influencing selection during the uptake process and promoting the preferential spread of strains adapted to insect-associated environment. The role of VOCs produced by different *S. cerevisiae* strains was investigated by simulating floral nectar, assessing their attractiveness and characterizing the compounds through GC–MS, which revealed strain-specific differences in volatile profiles and differential responses in *Polistes dominula* and *Apis mellifera*. Building on these findings, this project aims to investigate the genetic basis of these interactions, focusing on gene deletions of key genes involved in the production of relevant VOCs. By knocking out these genes, the study seeks to directly link VOC production to specific genetic factors and evaluate the resulting effects on insect behavior.

18:30 - 18:35

The biography reconstruction of Enrica Calabresi: passionate zoologist, scientist and teacher in the first half of the twentieth century

Elena Buccarelli

The project aims to reconstruct the biography of Enrica Calabresi, analyzing her scientific works and reconstructing the historical and social context in which she operated. The aim of this research is to trace the personal and academic experiences she faced, shedding light on aspects of the zoologist's life that remained understudied or even unknown still today. It will explore how the Jewish identity and gender influenced her academic and scientific career. Documents held at the Archives of the University of Florence, the Archives of the University of Pisa (where Enrica taught from 1936 to 1938), and the papers held at the Italian Entomological Society, from which she was expelled in 1939, will be examined. The places where the scholar worked throughout her life will be explored, such as the Royal Galileo Galilei Technical Institute and the Galileo Lyceum, where she had as a student Margherita Hack. Particular attention will be paid to documents held at the "La Specola" Natural History Museum, where Calabresi worked for many years. It will investigate the entomology and herpetology collections, preserved in the florentine museum, that Enrica studied. In order to effectively reconstruct the historical and social context in which the entomologist lived, one of the aims of this study will be to trace a network of Jewish women scientists who lived in the first half of the twentieth century and who, like Enrica, saw their careers interrupted by the fascist regime and the racial laws.

9:00 - 10:30 LECTURE

Artificial Intelligence and Forensic Genomics for Human Biodiversity

SPEAKER
Elena Pilli

10:30 - 10:50

Impact of *Nypa fruticans* and Thalassinidae on mangrove crab community and assessment of non-invasive monitoring techniques

Tommaso Marinoni

Crabs play a key role in mangrove ecosystems, shaping vegetation structure, sediment characteristics and fundamental ecological processes. This study addressed both an ecological and a methodological question. The ecological study, conducted in Setiu Wetland (Malaysia), investigated how nipa palm (*Nypa fruticans*) dominance and the presence of mud mounds produced by the burrowing activity of Thalassinidae affect mangrove crab communities. The reduced leaf-litter production and dense rhizomes of nipa palms may limit crabs' feeding and burrowing activities, while large Thalassinidae mounds alter soil structure and create heterogeneous microhabitats. To quantify these effects, I sampled six 2 × 2m plots across two nipa-dominated and two mixed mangroves areas ($\Sigma = 24$). Within each area, three plots were placed on mud mounds and three on the forest floor. Crab species and their relative abundances were recorded through visual and photographic counts during spring low tides, when crabs' activity peaks.

The methodological component, carried out in Hong Kong mangroves, evaluated non-invasive techniques for estimating the density and species composition of crab communities across different sites and forest types. I compared visual, photographic and video surveys as well as AI assisted identification. Twenty-six randomly distributed 1 × 1m plots were sampled, at spring low tides, across six sites characterized by a wide range of different habitats and substrates.

Together, these studies contribute to our understanding of habitat-driven variation in crab communities and identify the most efficient and practical technique to monitor mangrove crab diversity.

10:50 - 11:10

From temperate streams to tropical mangroves: the future of biodiversity monitoring and conservation using environmental dna

Giorgia Staffoni

The use of genetic approaches for biodiversity monitoring and the development of conservation strategies is rapidly increasing. Among these, environmental DNA (eDNA) is of particular interest for its non-invasive nature, its ability to provide a broad-scale representation of biological communities, and its effectiveness in detecting elusive or rare species. Within this research project, eDNA has been applied in several monitoring programs in Italy in the past year. Two projects focused on amphibian and fish communities across four Natura 2000 sites in Liguria, while a third developed an integrated camera-trap-eDNA system for mammal detection in the Casentino National Park, testing the complementarity of molecular signals and direct observations. The eDNA approach was subsequently extended to tropical ecosystems, with water and sediment sampling in the mangroves of Malaysia and Hong Kong to assess eDNA performance in structurally complex habitats. Building on previous projects, additional samples were collected to generate reference sequences for Malaysian mangrove crabs. This line of research builds on the BGE iBOL Europe initiative, which produced and validated over 12,000 barcodes, and the construction of a reference library of Italian inland water fish species. The latest project is now being expanded with functional trait integration, to enable future fun-eDNA analyses. These studies highlight how molecular approaches provide a powerful tool for guiding rapid and effective conservation actions, enabling reliable ecosystem assessments and targeted management strategies across both temperate and tropical environments.

11:40 - 12:00

Investigating microbial interactions in agricultural soils from bovine tuberculosis-affected and tuberculosis-free farms

Marta Nerini

This study investigates the composition and interactions of microbial communities in agricultural soils from farms affected by bovine tuberculosis (bTB). Six dairy farms—three with a history of bTB and three tuberculosis-free—were selected in collaboration with Consorzi Agrari d'Italia and the Istituto di Sicurezza e Legislazione Alimentare. Sampling sites common to all farms were identified, including soil from hay storage, machinery areas, outdoor shelters, barn interiors, barns exterior and manure storage. Soil and manure samples were collected, and physical-chemical parameters (temperature, redox potential, electrical conductivity, salinity, and pH) were measured *in situ*. Cultivable bacteria were isolated, leading to the isolation of 200 bacterial strains. These isolates were tested in competition assays with *Mycobacterium smegmatis*, the most common non-pathogenic surrogate for pathogenic mycobacteria, to assess antagonistic or synergistic interactions and potential degradation of mycolic acid and arabinogalactan. In parallel, a systematic review to evaluate the use of non-pathogenic mycobacteria as surrogate models for pathogenic species and their relevance in different research contexts was published as part of this project. DNA extraction and Next Generation Sequencing are ongoing to characterize microbial community composition and identify bacterial taxa potentially associated with bTB-positive environments. A collaboration is being established with the Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia-Romagna, the national reference center for bovine tuberculosis, to expand this research. Understanding the ecological dynamics between mycobacteria and soil microbial communities may reveal environmental reservoirs of *Mycobacterium bovis* and contribute to improved strategies for the control and prevention of bovine tuberculosis.

12:00 - 12:20

The impact of anthropogenic and natural disturbance on interactions between mammals and forests, and on ecosystem services: preliminary results from two case studies.

Matilde Marconi

Mammals play key roles in forests, regulating forest dynamics and ecosystem services. Alterations in these fauna–forest interactions can compromise crucial ecological processes. This study investigated how two types of disturbance, one anthropogenic and one natural, affect mammal communities and forest dynamics in tropical and temperate ecosystems. In the first case study, we compared two forests in Tanzania, one of which has undergone defaunation as a consequence of poaching. Through forest surveys, we analysed the composition of the tree layer and forest regeneration in the two areas in terms of species and functional richness. In the impacted forest, we found a significant reduction both in mammal-dispersed species within the regeneration layer and in large trees in the canopy layer, elements that are crucial for carbon storage. In the second case study, we assessed the effects of the storm Vaia in an area of Trentino characterized by different impact levels. We monitored the mammal community through two live-trapping sessions for small mammals and camera trapping sessions for medium- to large-sized species, combined with forest surveys. Overall, site-specific richness and Relative Abundance Indices of camera-trapped species were lower in high-impact sites. Moreover, when comparing a set of environmental covariates, impact level emerged as one of the most relevant predictors both in modelling the number of camera-trap events and the number of individuals captured per transect for most of the sampled mammal species.

12:20 - 13:20 LECTURE

European Dual Use Regulation: Definition and Implications for Scientific Research

SPEAKER
Teresa Rinaldi

14:20 - 14:40

Effects of the introduction of *apis mellifera* on the trophic and behavioral dynamics of native pollinators on giannutri island

Alice Rispoli

In areas with limited resources in terms of quality and quantity, and characterized by low climatic predictability, the dietary preferences of pollinators may change over time, also in response to interactions with other species. The introduction of a high number of honey bees into environments where they are not naturally present can alter the use of trophic resources by native pollinators. On the island of Giannutri, the feeding choices and foraging behaviours of *Bombus terrestris* and *Anthophora dispar* have been analysed in relation to the changes induced by the presence of *Apis mellifera*. The study, still ongoing, began in 2022, the year honey bees were introduced on the island. Between 2021 and 2024, *Bombus terrestris* modified its foraging choices, showing a preference for *Borago officinalis* and consequently reducing its trophic overlap with *Apis mellifera*. The observed shift is not attributable to a decline in resource quality, as no comparable variations were detected in *A. mellifera* or *A. dispar*. Despite this dietary adjustment, *B. terrestris* exhibited a marked numerical decline on the island. Furthermore, alterations in the foraging behaviours of wild apoids were observed as a function of the number of honey bees present: such changes are detectable even with a small number of honey bee individuals. These findings may prove useful for defining, in the future, the number of managed honey bee hives that can be considered sustainable within ecologically valuable areas, enabling management practices that do not negatively affect native wild bee populations.

14:40 - 15:00

Biopesticides and pollinators: lethal and sub-lethal effects on *apis mellifera* and *bombus terrestris*

Flavia Di Cesare

The increasing use of biopesticides as alternatives to synthetic pesticides requires more accurate ecotoxicological assessments, including sublethal effects that are often overlooked in standard risk-assessment protocols. In this study, *Apis mellifera* and *Bombus terrestris* were exposed to the bacterial biopesticide *Bacillus amyloliquefaciens* QST713. Mortality was evaluated under optimal and suboptimal nutritional conditions, and no adverse effects were observed in either species. The investigation then focused on sublethal effects, with particular attention to learning and memory. In *B. terrestris*, significant impairments in long-term memory emerged, suggesting possible implications for foraging efficiency. In light of this evidence, a semi-field experiment was conducted to explore potential impacts on this behaviour.

In a subsequent phase of the research, the focus shifted to another category of biocontrol agents: entomopathogenic nematodes (EPNs). Given the biology of bumblebees, in which queens overwinter and establish nests in the soil, contact with soil-applied EPNs represents an ecologically realistic but understudied exposure scenario. *B. terrestris* was exposed to *Heterorhabditis bacteriophora* and *Steinernema carpocapsae* at field-realistic concentrations typically used in agricultural applications. Mortality was assessed, and carcasses were analysed using White traps to determine nematode presence and reproduction within the host.

Overall, this study contributes to clarifying the potential risks associated with different biocontrol agents and highlights the importance of including behavioural endpoints and pollinator-specific ecological traits into risk-assessment frameworks.

15:00 - 15:20

Effects of hydraulic connectivity and nutrients availability on benthic metabolism and nitrogen cycling in perifluvial wetlands

Lara Gazzoldi

Perifluvial wetlands are areas adjacent to watercourses, and their dynamics are strongly influenced by hydrology. They regulate biogeochemical cycles, particularly by attenuating nitrogen (N) loads through N retention and transformation. However, the role of specific benthic biogeochemical processes under different hydrological conditions remains poorly understood. This thesis investigates how hydrological connectivity influences water and sediment characteristics and benthic nitrogen metabolism. It addresses two main questions: how does hydrological connectivity affect sediment N biogeochemistry and the contributions of microbial processes (denitrification, anammox, and DNRA) and primary producer assimilation to benthic N transformation? How does the relative availability of C, N, and P influence autotrophic and heterotrophic benthic metabolism and the partitioning between N removal and recycling? Seven perifluvial wetlands along the Po River were selected. Two sampling campaigns were conducted under contrasting hydrological conditions, focusing on wet post-reconnection and dry summer phases. Intact sediment cores were collected to assess benthic metabolism, nitrogen fluxes, denitrification and DNRA rates. Manipulative experiments were conducted to measure potential denitrification and ANAMMOX rates. Activities also included physico-chemical characterization of water and sediment. Preliminary results indicate that there is high variability in chemical characteristics among sites, but all of them acted as nitrogen sinks. Denitrification rates were quantified from sediment cores, although data analysis is still ongoing. Further sampling campaigns are planned for next year to expand and complete the study, including more specific analyses to investigate the role of nutrient stoichiometry on benthic nitrogen metabolism.

15:20-15:40 (online)

Invasion of *Mnemiopsis leidyi* and risk of regime shift in european marine ecosystems

Giulia Bertoletti

Invasions by non-indigenous species (NIS) represent one of the main pressures on marine ecosystems, with significant effects on biodiversity and the functioning of food webs. Interactions such as predation and competition with native species can lead to profound changes in community structure, including the reduction or local extinction of native taxa, with potential socio-economic consequences. *Mnemiopsis leidyi*, listed among the 100 most invasive marine species worldwide, has spread across numerous European ecosystems characterized by heterogeneous environmental and trophic conditions, demonstrating high ecological plasticity. This study examines the effects of the expansion of *M. leidyi* on the structure and stability of marine communities in four systems particularly affected by the invasion: the Black Sea, the western Baltic Sea, the Caspian Sea, and the Northern Adriatic Sea. By integrating ecological data, modelling approaches, and comparative analyses, we will assess how varying intensities of predation on zooplankton and fish larvae, combined with additional climatic and anthropogenic stressors, influence energy flows and ecosystem resilience. The aim is to identify coherent mechanisms across different environmental gradients and clarify the contribution of *M. leidyi* to the dynamics of ecological imbalance that can determine regime shifts in marine ecosystems. The results will provide a scientific basis for more effective ecosystem-based management and elucidate the role of *M. leidyi* in driving changes in marine ecosystem functioning, supporting the implementation of the EU Marine Strategy Framework Directive.

16:00-16:20 (online)

Context-dependent effects of land abandonment: evidence from semi-natural pastures and artificial chestnut groves

Eugenia Siccardi

Land abandonment is a significant and complex global process, generating diverse and often contradictory environmental and socio-economic impacts. This abstract presents a non-comparative analysis of two distinct instances of land abandonment: one occurring in semi-natural pastures and the other in artificial chestnut woodlands. The first case study is a core component of the CAROLINA (ClimAte Resilience Over Land use change In semi-Natural grAsslands) project. CAROLINA aims to explore the potential of extensive grassland management for biodiversity conservation and to investigate ecosystem resilience to climate change. The project combines a manipulation experiment with a chronosequence analysis across three sites. Data collection is now complete, and the first preliminary results, in terms of taxonomic and functional richness, are emerging. The second case study forms a national research effort focusing on European chestnut (*Castanea sativa*) groves across Italy, involving ten collaborating research groups. This investigation explored the critical influence of the interaction between geographic location and management (coppice/fruit grove vs. abandoned equivalents) on stand health and understorey biodiversity. Preliminary analysis revealed that observed management differences were highly site-specific and non-uniform across the Italian peninsula. Active fruit grove management generally showed significantly higher Species Richness (SR) and better stand health than the abandoned ex-fruit type. Conversely, at other sites, abandoned coppice exhibited significantly higher SR than the actively managed coppice. The complexity of this situation is challenging, yet clear trends are visible, and the best method must be found to analyse this complexity without losing crucial information.

16:20 -16:40 (online)

The origin of social inequalities in northern Italy: clues from ancient genomes

Linda Pratesi

Understanding the dynamics that promoted the onset and perpetuation of social inequalities in prehistoric societies is a major challenge. The increase in genomic data from ancient remains, the development of kinship estimation methods, and computational approaches for reconstructing. evolutionary dynamics from low-coverage data, now provide a unique opportunity to describe past population structures and shed light on the processes underlying inequalities. Archaeogenetics has revealed that the Neolithic expansion and the Bronze Age migration from the Steppe profoundly impacted the genomic composition of Europeans. However, our genetic knowledge is largely based on pan-European sampling strategies, limiting understanding of how these migrations affected individual societies.

This project proposes a high-resolution multidisciplinary study of approximately 120 individuals from three necropolises in north-eastern Italy: Valdaro Paganella (Neolithic), Corna Nibbia di Bione (Eneolithic), and Arano (Bronze Age). Whole-genome analyses will reconstruct biological relatedness within each necropolis, infer population structure and admixture proportions, and model past demographic dynamics. We already have an almost exhaustive paleogenomic overview of Corna Nibbia, while analyses of Arano are yielding substantial data that enable the drafting of a preliminary pedigree. Genomic analyses of the Neolithic site are still ongoing.

The integration of genomic data with precise chronologies, archaeological evidence, and stable isotope analyses on diet and mobility will allow investigation of potential inequalities among individuals and recognition of mechanisms behind the transmission of status and wealth. This multidisciplinary strategy will help us to clarify the origins of social inequalities in north-eastern Italy and the processes that fostered their development.

12:20 - 13:20 LECTURE

Ocean Solutions for Nature and People

SPEAKER
Fiorenza Micheli

The ocean is Earth’s last frontier. It comprises most of its habitable volume, is home to a unique and extraordinary diversity of plants, animals, and microbes; regulates its climate; and provides food and livelihood for billions of people. Our future is inextricably linked to the ocean, and to maintaining the flow of critical and irreplaceable benefits healthy oceans provide. While much investigation and discussion are focused on risks and impacts, there is a critical need and opportunity to develop solutions. I will present and discuss insights and ocean-based solutions to three interconnected grand challenges, biodiversity loss, climate change and food security.