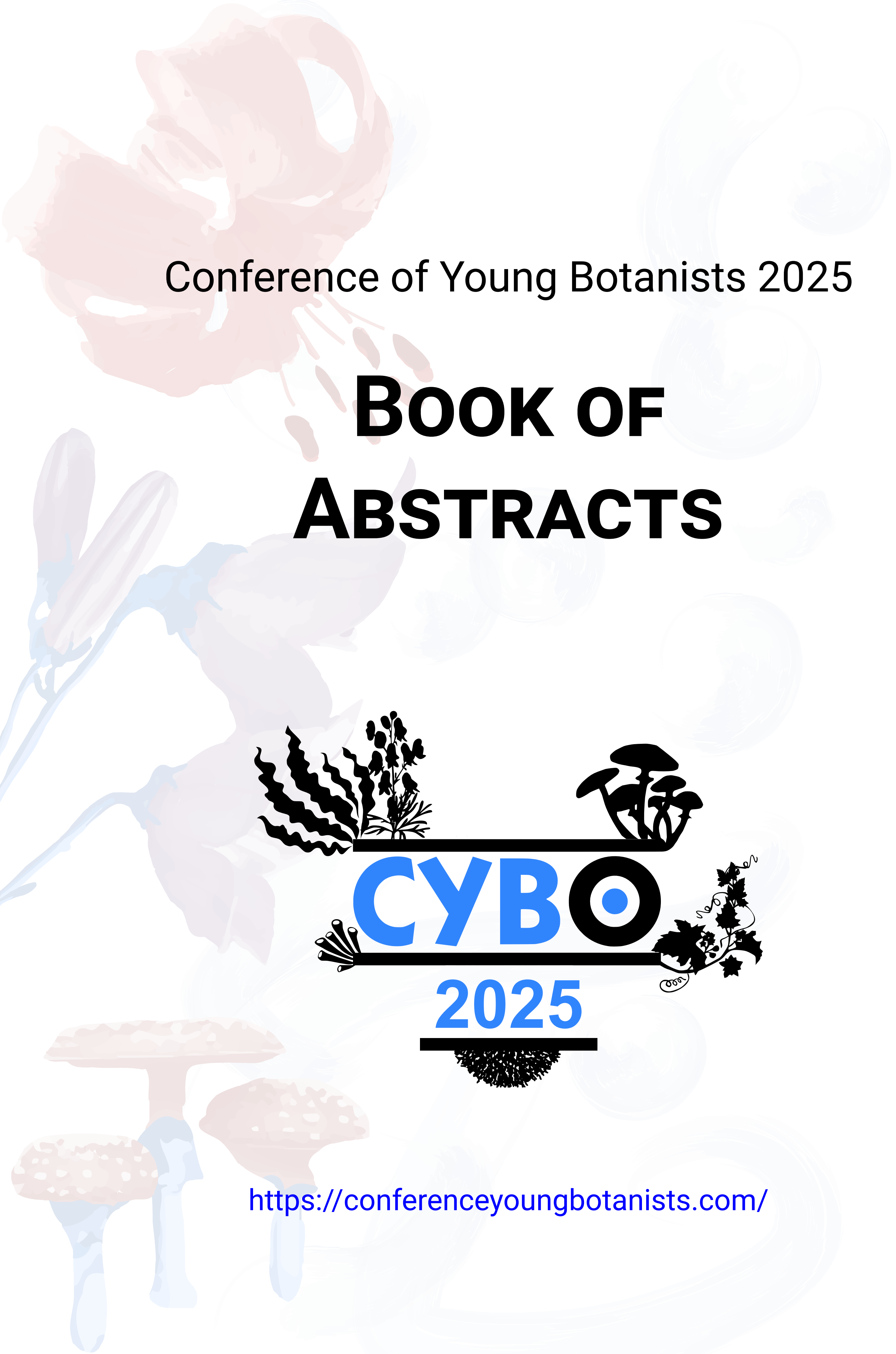

Conference of Young Botanists 2025

BOOK OF ABSTRACTS

CYBO

2025

https://conferenceyoungbotanists.com/

Index

1. Systematics, phylogenetics, biogeography and evolution

2. Ecology

to prolonged dormancy

- Talk *Carlo Maria Cusaro*: Herbicide Resistance and soil microbial composition
- Talk *Chiara Bonifazio*: The pollination network of Campanula sabatia De Not.
- Talk *Chiara Macolino*: Preliminary investigations of the Bryophyte Flora in the Hazel Groves of the Aveto Regional Natural Park (Ligurian Apennines)
- Talk *Dario Comunello*: Trait-based study as a conservation tool for protected species: the case study of Trifolium saxatile in the Gran Paradiso National Park
- Talk *Davide Casalino*: Niche variation in endemic Gentiana ligustica between two biogeographical regions
- Talk *Elena Cini*: Long-term Dynamics of Coastal Dune Landscapes and Floristic Diversity: Insights from a Quarter Century of Resurveys in Castelporziano Presidential Estate
- Poster *Emilia Pafumi*: Monitoring riparian vegetation from space: developing a cloud-based application in Google Earth Engine
- Talk *Eugenia Siccardi*: Revisiting Pianosa (Italy): how the vegetation of a small Mediterranean island has changed in the last 15 years
- Talk *Gilda Perri*: Assessment of heavy metals in soils and their accumulation rates in native plants under anthropogenic and natural pollution in Calabria, Southern Italy
- Talk *Ginevra Nota*: Climate change drives plant compositional changes in alpine snowbed communities: a 10-year study in the Monte Rosa massif
- Poster *Giovanni Spinelli*: Exploring Morphological Structure and VOC Emissions in Olive Fruits: Potential Interactions with Bactrocera oleae Infestation
- Talk *Giulia Canali*: Populations of Lobaria pulmonaria in Contrasting Climates appear Morphologically Similar but Physiologically Different
- Poster *Ian Briozzo*: Differentiation of ecological niches of Campanula sect. Heterophylla in the Southwestern Alps
- Talk *Irene Ventura*: Seed Germination Strategies in Salicornia perennans Willd. subsp. perennans: The Role of Salinity, Seed Morphology, and Ecotype
- Talk *Laura Ferigato*: Mount Spundascia's fen: how a microbotanical record sheds light on the last 3000 years of a subalpine landscape's development
- Talk *Leonardo Malvezzi*: Morpho-functional characterization of bryophytes from high and low elevation
- Talk *Martina Tarascio*: Photic barriers in a warming world: the crucial role of photoperiod in shaping plant responses to climate change
- Talk *Miriam Bazzicalupo*: Floral traits and reproductive ecology of the Mediterranean subendemic orchid Serapias neglecta De Not.
- Poster *Nicola Postiglione*: EXPLORING PATTERNS OF INTRASPECIFIC TRAIT VARIABILITY IN ENDEMIC AND NON-ENDEMIC SPECIES: INSIGHTS FOR CONSERVATION STRATEGIES
- Poster *Nubia Guzmán*: Understanding the role of bacterial communities associated with the roots of Alnus acuminata: a pathway to improve restoration strategies of degraded lands in Ecuador
- Poster *Simone Balestra*: The impact of monoculture tree plantations on biodiversity in the Italian Prealps
- Talk *Thinles Chondol*: Seasonal dynamics and interspecific variability of photochemical performance in plants from cold-arid Himalayas
- Talk *Viola Alessandrini*: Ecological Characterisation and Invasive Potential of Salpichroa origanifolia in a Meso-hygrophilous Forest Ecosystem
- Poster *Waad Bousselmi*: Combined effect of Hedysarum coronarium- Medicago sativa intercropping on the agronomic parameters of Brassica napus, biodiversity and health soil under water stress

3. Biodiversity and global change

- TALK *Agnese Denaro*: Assessing vegetation changes in coastal dunes: historical plot resurveys in a Mediterranean archipelago
- TALK *Alice Dalla Vecchia*: Predicting functional traits of invasive aquatic plants across native and invasive ranges: new advances with DIVE IN MSCA-Global project.
- TALK *Carolina Stringa Basile*: The project ACCLIMATE - Acclimation to Climate Change of Lichens in Mountain Alpine Terricolous Environments
- POSTER *Claudia Zitarelli*: Resurveying alpine grasslands in central and southern Apennines
- POSTER *Cristina Gasperini*: Leaf trait variability in Mediterranean forest endemics and their divergence from widespread species: a study of 45 taxa and 26 congeneric pairs
- POSTER *Daan Curwiel*: The Living Archive: Building a National Seedbank for (threatened) wild plants in the Netherlands based upon scientific principles.
- TALK *Danilo Monari*: Reintroduction perspectives for Limonium intermedium (Guss.) Brullo: the only globally "Extinct in the Wild" species of the Italian Flora
- TALK *Domenico Amantea*: High-resolution species distribution models for two ecologically contrasting, closely related plant species
- TALK *Fiona White*: Can 20 year old stored seeds be used for plant translocation? An investigation in the arctic-alpine specialist Viscaria alpina
- POSTER *Francesco Ponticelli*: REVISITING ELBA ISLAND (ITALY): TAXONOMIC AND FUNCTIONAL VARIATIONS IN THE LAST 20 YEARS
- TALK *Friederike Westrich*: Effects of global warming on the alpine vegetation of four peaks in the Texel Group, South Tyrol, as part of the GLORIA project
- TALK *Giammarco Dadà*: Inventorying the Tuscan forests for the "Rete Nazionale dei Boschi Vetusti"
- TALK *Irene Mazza*: The surprising fungal diversity of biancana badlands
- TALK *Jacopo Calevo*: Past adaptations shape future persistence: climate change responses of orchids in Mediterranean climation regions
- TALK *Jacopo Franzoni*: The vascular flora of Pisa (Tuscany, Italy): towards a citizen science-based monitoring of urban floras
- TALK *Jasmin Lepper*: Forty Years of Change: Assessing Species Dynamics and Conservation Success in Swiss Jura Calcareous Grasslands
- POSTER *Leonardo Salvatori*: MULTI-TAXON MONITORING IN THE STRICT NATURE RESERVE "MONTAGNA DI TORRICCHIO" (ITALY)
- TALK *Lucia Doni*: Distribution shift of semi-natural grasslands priority habitats (92/43/EEC) in the European Alps under future climates.
- TALK *Margherita Tognela*: Seed longevity could predicts alpine plant resilience to climate warming
- TALK *Marta Agostini*: BioConLobaria: Successful translocations for the conservation of the threatened lichen Lobaria pulmonaria (L.) Hoffm
- TALK *Maura Francioni*: Long-term Dynamics of Understory Plant Diversity in Italian Forest Ecosystems: Trends and Drivers
- TALK *Raffaele De Matteis*: The giant hogweed on the Alps: niche dynamics of a burning invasive alien plant across the alpine region
- TALK *Sara Ribotta*: Predicting the Future Distribution of Alpine Lichens under Climate Change Scenarios
- TALK *Silvia Cannucci*: Farmland ponds as unique ecosystems for plant diversity across diverse pondscapes
- TALK *Silvia Giusto*: Fungi in Multi-Taxon Analysis: the experience of PRIN project Multi-ForDiv
- POSTER *Silvia Macis*: The Impacts of Climate Change on Coastal Wetlands in Mediter-

ranean Regions
- Talk *Simone Pedrini*: Native Seeds for ecological restoration: Improving the seed supply chain with technology, training and Community Engagement
- Talk *Thuy Hang Le*: Micro-scale plant diversity in traditional wood pastures
- Poster *Vanessa Manuzi*: Tree Monoculture Plantations Decrease Plant Diversity in the Italian Prealps
- Poster *Virginia Amanda Volanti*: CAROLINA PROJECT: PRELIMINARY RESULTS OF TAXONOMIC AND FUNCTIONAL PLANT DIVERSITY
- Poster *Vivien Lábadi*: Marsh gladiolus flowers prefer to bloom in forests rather than in meadows - Reproductive characteristics of forest and meadow populations in Hungary

4. Structure, physiology, and development

- Poster *Angela Martina*: PHOTOSYNTHETIC PHENOTYPE OF TWO CICHORIUM INTYBUS L. CULTIVARS: THYLAKOID ULTRASTRUCTURE, PHOTOCHEMISTRY AND CARBON ISOTOPIC ANALYSIS
- Talk *Antonio De Agostini*: Living on the edge: How Lunularia cruciata thrives on polluted mining waste
- Talk *Beatrice Chiavacci*: Pathogenic susceptibility in microplastic-exposed crops: the case of Solanum lycopersicum var San Marzano nano
- Talk *Bruno Bighignoli*: Effects of acoustic vibration on Olea europaea cv “Leccino”
- Poster *Charline Gennat*: Challenged (by) parasites: Acclimation kinetics of a plant-plant-pathosystem
- Poster *Chiara Pezzuto*: Analysis of vascular cambium response to drought and heat stress through integrated omics approaches to identify tolerance mechanisms and key factors in forest resilience strategies
- Poster *Christopher Großmann*: Regulation of the Golden2-like 1 (GLK1) transcription factor
- Talk *Claudia Russo*: Investigating below-ground plant-bacteria interaction through the analysis of volatile compounds released by bacteria and roots
- Talk *Cristiana Rizzi*: Optimisation of an Analytical Method for VOC Sampling in the Rhizosphere Using HS-SPME and GC-MS
- Talk *Cristina Danna*: Essential oil from rhizome and leaf of Peucedanum ostruthium W. D. J. Koch: comparative micromorphological and phytochemical analyses
- Talk *Erika Bellini*: Orange Peel Waste-Derived White-Rot Fungus Digestate: A Promising Approach to Enhance Plant Resistance against Botrytis cinerea
- Talk *Fanny Defant*: Sprouting ability of Sonchus arvensis at different growth stages
- Poster *Federica Betuzzi*: Microscopy coupled with DNA barcoding-based analysis as diagnostic tools to identify toxic plants
- Talk *Francesca Alderotti*: Which crown defoliation level may be considered a threshold for severe physiological impairment in Quercus ilex L.? ? Results of a two-year field study in a Mediterranean forest
- Talk *Gaia Regini*: Silene latifolia: a striking thallium facultative hypertolerant and hyperaccumulating species
- Poster *Giorgia Benati*: Optimization of enzymatic digestions on tomato seeds to recover proteins and peptides
- Poster *Giorgia Tonielli*: MicroRNA-induced regulation of wheat (Triticum aestivum L.) root architecture and function
- Poster *Giulia Mozzo*: Impact of Acoustic Vibration on Rhizobium-Legume Symbiosis

- TALK *Giulia Raffaele*: Nitric Oxide role in rice root formation and development exposed to viable and autoclaved mycorrhizal spores
- POSTER *Marcello Bigoni*: Asparagus officinalis L.: a food plant model for monitoring heavy metal contamination in fields bordering roadways in the Ferrara province (Italy)?
- TALK *Marco Dainelli*: Deciphering plant-microplastic interactions in freshwaters through Spirodela polyrhiza: towards phytoremediation applications
- TALK *Mariel Isidra Arellano*: Unrevealing the Role of Epidermal Patterning Factor-Like Peptides in the Root Nodule Symbiosis.
- POSTER *Marta Beccaluva*: Urban stress and plant adaptation: exploring the morphological, genetic and physiological changes in Populus alba"
- POSTER *Nayara Machado*: Evolution of fleshy fruits in Myrtaceae: initial impressions in the subgenera of Syzygium
- TALK *Pablo Carril*: Biostimulants in action: enhancing nickel phytoextraction in Odontarrhena decipiens (Nyár.) grown in serpentine soil
- TALK *Pierluigi Giacò*: Urban wastewater phytoremediation by autochthonous microalgae in winter season: indoor and outdoor trials
- TALK *Saverio Savio*: Enhancing plant resistance to Botrytis cinerea using Cylindrotheca closterium extract
- TALK *Silvia Piccinelli*: Disentangling Intra-annual Tree Growth Responses to Hydro-Climatic Conditions: Insights from Quantitative Wood Anatomy in Peatlands

5. Genetics, genomics, and bioinformatics

- TALK *Anna Pasinato*: Unveiling the biosynthetic potential of lichens: a comparative genomic analysis of secondary metabolite diversity in ascomycetes
- POSTER *Chiara Dassow*: The Mystery of Blue Flowers: Sequencing and Analysis of the Cornflower Genome
- TALK *Chiara Paleni*: First steps towards conservation of endemic Salvia in Italy with population genomics
- TALK *Dario Galanti*: Adaptation to ash dieback disease in natural populations of European ash
- TALK *Giulia Ghirardello*: Exploring rhizobacteria-induced molecular pathways in Solanum lycopersicum
- TALK *Jacopo Vujovic*: Genomic and phylogenomic analyses of Bradyrhizobia associated with Tuber magnatum
- POSTER *Paloma Perez-Bello Gil*: The LIFE Seedforce project: a comprehensive genotyping initiative to assist the conservation of endangered Habitat Directive plant species
- TALK *Simone Graziosi*: FISH technique to detect T. magnatum colonization in plant roots

6. Plants, Fungi and Society

- TALK *Alberto Massimi*: Antifungal activity of components from essential oils against microfungi isolated from industrial resins.
- TALK *Alex Alberto*: Landraces for valorising mountain areas: the case study of 'Articiok di Malegno' (Cynara cardunculus subsp. scolymus L. Hayek)
- TALK *Dario Nicola Tangredi*: Epiphytic lichen biodiversity and species distribution in the area of the University Campus of Salerno (Italy).
- TALK *Fabrizia Milani*: Urban Ethnobotany: selection process of a foreign community inte-

grated in Milan, North of Italy.

- Talk *Federico Puliga*: Conversion of grape pomace into fungal biomass: a study of Pleurotus cultivation for a sustainable agro-residue management
- Poster *Francesca Emili*: Fungal Bioresources for Mycoremediation of Glyphosate- and AMPA-Contaminated Agricultural Soils
- Poster *Guido Silvano*: Mycosium: sporulating knowledge. Why fungi?
- Talk *Letizia Conti*: Study on the cultivation of the white truffle in abandoned fields
- Talk *Mario Pentassuglia*: Floristic inventory of wild edible plants in the Tirli area (Northern Maremma, Italy)
- Talk *Martina Bottoni*: The interdisciplinarity of Urban Ethnobotany: taking the first steps within the Peruvian community living in Milan (North of Italy).
- Talk *Sara Beltrami*: Enhancing plant photosynthetic performances by boosting plant carbonic anhydrase activity
- Poster *Valentina Boscariol*: Unlocking the potential of herbarium collections: a case study from the digitization of Silvia Zenari's specimens
- Talk *Veronica Spinelli*: Fungi's got talent: a study on fungal interactions with Gallium, Germanium, Indium and Yttrium for bio-recovery applications
- Talk *Virág Grónás*: Mapping Hedera crebrescens with citizen science method

POSTER – On the way to elucidating the complex evolutionary history and cryptic diversity of the Balkan-Anatolian Cardamine (Brassicaceae) species complex

Adam Kantor[1], Marek Šlenker[1], Dušan Senko[1], Lenka Mártonfiová[2], Gabriela Šrámková[3], Veronika Cetlová[1], Ali A. Dönmez[4], Sırrı Yüzbaşıoğlu[5], Judita Zozomová-Lihová[1]

[1] Plant Science and Biodiversity Centre, Slovak Academy of Sciences, Bratislava, Slovak Republic; [2] Botanical Garden of P. J. Šafárik University in Košice, Košice, Slovak Republic; [3] Department of Botany, Faculty of Science, Charles University, Prague, Czech Republic; [4] Department of Biology, Faculty of Science, Hacettepe University, Beytepe-Ankara, Türkiye; [5] Department of Botany, Faculty of Science, İstanbul University, Istanbul, Türkiye

Deciphering patterns of diversification at the lower taxonomic levels is crucial for understanding evolution of biodiversity of a specific region in a broader context. For example, we know little about the significance of interplay of specific mechanisms and factors shaping evolution of most individual species. Resolving evolutionary histories may be especially important but challenging in regions such as the Balkan Peninsula, which represents center of species and genetic diversity with a high representation of endemics. Survival and diversification of species in this area was facilitated by several specifics of this area, including its topographical heterogeneity, diversity of habitats and favorable conditions during the Pleistocene climatic oscillations. In the recently published study, we focused on unravelling the diversity of mountain hygrophytes from the species complex Cardamine acris s.l., which in its original understanding included the Balkan species C. acris (with three recognized subspecies) and the species C. anatolica, endemic to northwestern Anatolia. We used a series of phylogenetic and phylogeographic analyses based on data obtained by restriction-site associated DNA sequencing (RADseq) and target enrichment (Hyb-Seq), supplemented by habitat suitability modelling. This combination of methods provided us with surprising results that had not been discovered in multiple previous studies which were based on far less robust sequence data. Instead of four originally recognized entities, we were able to distinguish six within the studied complex, while the Asian clade of C. anatolica turned out to be nested within the other Balkan lineages. The Balkan lineages most likely arose by vicariance, being allopatrically distributed, although we found also direct evidence of gene flow between two of them. Habitat suitability dynamics modelling shown that the ecological confinement of these plants to mountains and humid habitats played a fundamental role in expansion and diversification of the species complex. Another novel finding concerned the cytotype diversity of the complex: all taxa were previously thought to be exclusively diploid, however, we discovered populations of four different ploidy levels in the Balkans, originating both via intra- and inter-lineage polyploidization. Our results underline already known complexity of plant evolution in the Balkans, which has been shaped by interlaced combination of multiple processes. In the current study in progress, we aim to further analyze this recently discovered cryptic diversity and investigate if and how it links to phenotype and DNA content of the members of the species complex. We use multivariate morphometric analyses and genome size measurements acquired by flow cytometry to evaluate differentiation among the six entities. Outcomes of these analyses will be used to provide reevaluated taxonomic concept for the challenging species complex of C. acris s.l. This study is supported by the Slovak Research and Development Agency (Grant no. APVV-021-0044).

https://conferenceyoungbotanists.com/abstracts/adam.kantor

TALK – From seeds to sprouts: the effects of whole-genome multiplication on clonal and sexual reproduction in Pilosella rhodopea

Agnieszka Adamska[1]

[1] Department of Botany, Faculty of Science, Charles University, Benátská 2, 128 01 Prague, Czechia; Plant Science and Biodiversity Centre, Slovak Academy of Sciences, Dúbravská cesta 9, 845 23 Bratislava, Slovakia

Polyploidy occurs when an organism has more than two complete sets in somatic cells. It's one of the most important evolutionary drivers that may lead to the formation of evolutionary novelties. Polyploidy is categorized into two types: allopolyploidy, which means that subgenomes are made from different parent species, and autopolyploidy, when the subgenomes are derived from a single parent species through genome multiplication. Autopolyploids often struggle with reduced fertility because of disturbed meiosis. This means that their sexual reproduction can be limited. However, some plants deal with this problem through enhanced clonal reproduction. It is unknown if the increased clonal growth is directly caused by polyploidization, what are its underlying genetic and physiological factors, and finally what is the ecological impact of such reproduction shift between closely related cytotypes. Understanding the consequences of polyploidy in the model system of Pilosella rhodopea (Asteraceae) can shed light on how autopolyploids establish and persist in nature. Pilosella rhodopea is a diploid–autopolyploid complex, with up to five ploidy levels (2x–6x) that occur in numerous mixed-ploidy populations. Its contact zone, in the Balkans, is believed to be the biggest primary diploid-autopolyploid contact zone ever recorded in angiosperms. Pilosella rhodopea is a perennial species forming accessory rosettes from hypocotyl meristems but additionally can reproduce clonally via root sprouts. It has been documented that with higher ploidy levels the sexual reproduction decreases, while clonal, vegetative reproduction increases. Moreover, root sprouts do not appear in diploids. My PhD project focuses on: - Root sprout formation and growth: investigating the triggers behind the formation, anatomy and phytohormones of root sprouts. - Inheritance of clonal traits: studying how clonal traits are passed onto offspring in controlled experiments. - Impact of clonal reproduction on genetic diversity: exploring how increased clonal growth affects the spatial genetic structure of populations of Pilosella rhodopea in the Balkan Peninsula - Effects on reproductive cell development: examining consequences of whole genome multiplication on a female and male gametogenesis and sporogenesis This study, funded by the Czech Science Foundation (GAČR 24-12318S, 2024-2026), will integrate many approaches - from genes to distributional patterns - to provide a comprehensive understanding of how polyploidy alters reproduction strategies in autopolyploids. This will give insight into factors that drive shifts from sexual to clonal reproduction in plants, which is a key survival strategy in many species.

https://conferenceyoungbotanists.com/abstracts/adamskaag

TALK – Taxonomy, systematics and conservation status of Centaurea veneris (Asteraceae), a cliff dwelling Ligurian endemic species

Antonio Giacò[1], Samuele Maestri[1], Andrea Coppi[2], Lorenzo Peruzzi[1]

[1] University of Pisa, Pisa, Italy; [2] University of Firenze, Firenze, Italy

Centaurea veneris (Sommier) Bég. (Asteraceae) is a cliff dwelling diploid species endemic to the promontory of Portovenere and the islands of Palmaria, Tino, and Tinetto (western Liguria, Italy). Traditionally, it was included in the C. cineraria L. group, but previous population genetic studies showed a close relationship with western Ligurian populations of C. aplolepa Moretti, a diploid species endemic to central and northern Italy. To verify the taxonomic position of C. veneris and the biosystematic relations with C. aplolepa, we conducted an integrative taxonomic investigation involving both morphometric and AFLP population genetic analyses. We sampled two populations of C. veneris, one at the Palmaria island and one at Portovenere. In this latter location, at less than 100 m from the collection site of C. veneris, we sampled also a population of C. aplolepa subsp. levantina Arrigoni. Then, two additional populations of C. aplolepa were sampled in western Liguria at Sestri Levante (C. aplolepa subsp. levantina) and at Bocca di Magra (C. aplolepa subsp. lunensis (Fiori) Dostál). For each population, 10–30 individuals for morphometrics and 10–14 individuals for population genetics were sampled. Both morphometric (PCA, univariate analyses and boxplots) and population genetic analyses (AMOVA, PCoA and structure analysis) confirm the taxonomic status of C. veneris as an evolutionary close but distinct species with respect to C. aplolepa. However, the genetic structure analysis detected slight levels of admixture in some individuals of C. veneris from Portovenere, possibly suggesting introgression with C. aplolepa. This hypothesis seems to be confirmed by some individuals of both species from this latter location showing an intermediate morphology. Thanks to the field observations and the new data produced, it is also possible to confirm the conservation status of C. veneris as a near threatened (NT) species. Indeed, due to the small distribution range and some threats (e.g., climate change and grazing by goats), this species nearly satisfies the criterion B (Geographic range) of IUCN for critically endangered (CR). However, the levels of heterozygosity detected in both populations of C. veneris suggest that this narrow endemic species does not suffer of low genetic variability. Thus, unless new threats would endanger this species in the near future, an imminent decline due to population dynamics is unlikely.

https://conferenceyoungbotanists.com/abstracts/antonio.giaco

POSTER – Morphological and ecological analysis of Rumex scutatus subsp. aetnensis (Polygonaceae)

Claudia Colombo[1], S. Brullo[1], S. Cambria[1], S. Sciandrello[1], G. P. Giusso del Galdo[1]

[1] Department of Biological, Geological and Environmental Sciences University of Catania Via A. Longo, 19, I – 95125 Catania

Rumex scutatus subsp. aetnensis C. Presl (Polygonaceae) is an endemic plant of Sicily, circumscribed to the basaltic substrates on Mt. Etna (NE Sicily). This taxon belongs to the very variable group of Rumex scutatus L., which is widely distributed across the temperate areas of Europe and Asia. It includes several infraspecific taxa chiefly linked to rocky and glareicolous habitats with gravelly or rocky soils. According to Pignatti (2017), three subspecies are currently recognized in Italy: R. scutatus subsp. scutatus, R. scutatus subsp. aetnensis C. Presl and R. scutatus subsp. glaucescens Guss. Main aim of our study is to investigate the taxonomic position of R. scutatus subsp. aetnensis and in its relationships with subsp. scutatus. The analyses is based on data derived from literature as concerns the subsp. scutatus, while the subsp. aetnensis was sampled in several stands of Mt. Etna ranging from 1.800 and 2.900 m a.s.l. during the period May–July and October 2024. The morphological analysis was performed both on living plants and dried specimens. Also, the pollen micro-morphology was studied on fresh material and examined by using a scanning electron microscopy (SEM). Our investigation reveals many relevant morphological differences for some characters, such as leaf blade size, floral structures, fruits and pollen. The first results confirm the taxonomical importance of these traits and support the recognition of subsp. aetnensis as a well distinct taxa from the typical one. Further studies, including molecular and biochemical investigations, will shed light into the phylogenetic relationships and adaptive strategies of this narrow endemic taxa.

https://conferenceyoungbotanists.com/abstracts/claudia.colombo97

Talk – Exploring factors shaping the evolution, diversification, and adaptation of selected Daphne (Thymelaeaceae) members to extreme environments

Eliška Krtilová[1], Zuzana Gajdošová[2], Andrea Melichárková[2], Jaromír Kučera[2], Zuzana Kolaříková[3], Radka Sudová[4], Jana Rýdlová[3], Roswitha Schmickl[5], Miroslav Caboň[2], Marek Slovák[1]

[1] Department of Botany, Charles University, Faculty of Science, Prague, Czech Republic and Plant Science and Biodiversity Centre, Institute of Botany, Slovak Academy of Sciences, Bratislava, Slovakia; [2] Plant Science and Biodiversity Centre, Institute of Botany, Slovak Academy of Sciences, Bratislava, Slovakia; [3] Institute of Botany, Czech Academy of Sciences, Pruhonice, Czechia; [4] Department of Mycorrhizal Symbioses, Czech Academy of Sciences, Pruhonice, Czechia; [5] Department of Botany, Charles University, Faculty of Science, Prague, Czech Republic

Rare and endemic species represent a vital component of global biodiversity. Despite extensive research into their systematic, evolutionary, and diversification dynamics, our understanding of the intrinsic and extrinsic mechanisms underlying their evolution, speciation, and long-term persistence remains incomplete. This study focuses on the woody vascular plant genus Daphne (Thymeleaceae), an ancient relictual lineage predominantly comprising species classified as endemic. These species are often characterized by highly restricted distribution ranges and an ability to thrive in environmentally extreme and inhospitable habitats, particularly on exposed rocky outcrops. Our research addresses two main themes: the evolutionary processes shaping selected rock dwelling Daphne species and the mechanisms driving their adaptation to rocky environment. We will investigate the role of interspecific gene flow as a potential source of genetic variability and its implications for the fitness and long-term persistence of endemic, in selected rock-dwelling species. We will also explores the interactions between selected Daphne species and their associated endobiont mycobiomes, with a focus on the potential role of root-associated fungal communities in maintaining fitness and ensuring the survival of rock-dwelling species. To achieve these objectives, the study employs an integrative approach, combining population genomics, metagenomics, morphological assessments, karyological investigations, and ecological analyses. This multi-approach methodology aims not only to enhance our understanding of the biology and ecology of selected Daphne species but also to contribute to our knowledge of how vascular plants evolve and adapt to challenging rocky environments. This work was supported by the Slovak Research and DevelopmentAgency (grant number APVV-22- 0365) and by the Slovak Academy of Sciences (VEGA no. 2/0098/22).

https://conferenceyoungbotanists.com/abstracts/eliska.krtilova

Talk – Distribution of Mediterranean forests in Italy and climate connections: a large-scale overview

Geordie Biffoni[1], Chiara Bonifazio[1], Ian Briozzo[1], Maria Guerrina[1], Silvia Tripi[1], Lucia Doni[1], Luigi Minuto[1], Gabriele Casazza[1]

[1] DISTAV - Dipartimento di Scienze della Terra, dell'Ambiente e della Vita

The Mediterranean Basin is a well-known biodiversity hotspot, particularly affected by climate change and intense land use, leading to biodiversity loss. The INTEGRADIV project aims to enhance the understanding of Mediterranean forest ecosystems and promote protective and restorative actions for the Mediterranean biome, considering its taxonomic, functional, and phylogenetic biodiversity facets. In this context, this work focuses on analysing tree and shrub species distribution in Italy, investigating their aggregation patterns and identifying the climatic variables that drive their distribution. Occurrence data were collected within 10km x 10km cells across the Italian territory during two fieldwork seasons. Hierarchical cluster analysis and correlation tests will be performed to provide a large-scale overview of Mediterranean forests, offering important tools for the integrated management of biodiversity in Italy. In summary, these analyses will help identify the distribution of Mediterranean forests, assess their preservation status, and determine the climatic factors influencing their spread across the Italian territory. Moreover, these results will contribute to understanding the ecological integrity of the Mediterranean biome in Italy and its vulnerability to climate change and land use, providing valuable tools for achieving the INTEGRADIV objectives.

https://conferenceyoungbotanists.com/abstracts/geordie.biffoni

TALK – Vernonieae (Asteraceae): a palynotaxonomy update to Madagascar and Tropical Africa

Higor Antonio-Domingues[1], Benoit Loeuille[1], Mihajamalala Andotiana Andriamanohera
Isabel Larridon[1], Morgan Gostel[3], Ana Rita G. Simões[1]

[1] Royal Botanic Gardens, Kew, Richmond, Surrey, UK; [2] Botanical Research Institute of Texas, Texas, USA; Royal Botanic Gardens, Kew, Richmond, Surrey, UK; [3] Botanical Research Institute of Texas, Texas, USA

One of the largest tribes in Asteraceae, Vernonieae, has proven intractable for taxonomic revision, with more than 1,000 of the ca. 1,500 species being recognised in the genus Vernonia. This genus has recently been re-circumscribed to include just 21 accepted species in the Americas (Vernonia s.s.), urging the reclassification of ca. 1,000 species out of Vernonia. Much of this work has been completed in the Tropical America, but few studies have been undertaken for the more than 700 species of Vernonieae in the in Madagascar, Tropical Africa and Tropical Asia, including the 564 species in Tropical Africa and Madagascar. At least 226 African species remain in Vernonia, but because of poor generic delimitation in this tribe, it is unclear to which genus they belong. We have performed the most complete palynotaxonomy study of Malagasy and Tropical Africa representatives of the tribe Pollen grains and micromorphological reproductive characters were analysed under light microscopy and SEM. Our results demonstrate the eurypalynous status of tribe Vernonieae tribe based on variations in pollen grain size, aperture and ultrasculpture types. Novelties regarding the number and position of the apertures, presence of the operculum and details of the exine ultrasculpture were documented. Further study that includes more comprehensive molecular sampling of species in Vernonieae is in progress and will be elemental for further understanding the diversity and evolution of pollen within this tribe.

https://conferenceyoungbotanists.com/abstracts/h.antoniodomingues

POSTER – A population genetics study of dwarf-shrub communities with circumboreal and Arctic-Alpine distribution, focusing on Apennine relict sites

Ilaria Mezza[1], Romeo Di Pietro[2], Paola Fortini[3]

[1] PLAN:TA lab. Dept. of Bioscience and Territory, University of Molise, Pesche, Italy; [2] Dept. of Planning, Design and Architecture Technology, Sapienza University of Rome, Italy; [3] PLAN:TA lab. Dept. of Bioscience and Territory, University of Molise, Italy

The dwarf-shrub communities, together with the primary and secondary grasslands, represent typical ecosystems of the subalpine and (sometimes) of the alpine belts of the main Central and Southern European mountain ranges, at altitudes between 1800 and 2800 m asl. These communities are dominated by several genera depending on the environmental characteristics of the sites. Among these genera there are Salix and Vaccinium, which occur with several circumboreal and arctic-alpine chorotype species displaying a nano-phanotherophyte and reptose chamaephyte life form respectively. The central Apennines, due to their role as a refuge for the boreal flora during the Quaternary glaciations, represent for many species the lowermost limit of the distribution range in the Italian peninsula, where their communities (e.g. Armerio-Salicetum herbaceae, Hyperico-Vaccinietum myrtilli etc.) exhibit a fragmented distribution along the highest peaks of the range. Because of their rarity and biogeographical interest, some of these habitats are protected at European level under the Habitats Directive (Dir. 92/43/CEE), as they are included in two distinct formations “4060: Alpine and Boreal heaths” and “4080: Sub-Arctic Salix spp. scrub”. The aim of this project, which is in its early stages, is to investigate the genetic variability and phylogenetic relationships within the Salix and Vaccinium relict populations of the central Apennines, and to compare them with the genetic traits found in other European populations. This study will focus on the following species: Salix hastata L., Salix herbacea L. and Vaccinium uliginosum L. subsp. microphyllum (Lange) Tolm. The study area will cover the entire European distribution range of these communities, from the Arctic zones to the mountain ranges of Central and Southern Europe. The fieldwork phase started in 2022 and is still ongoing. For each sampling site, which was recorded by coordinates and then mapped using GIS software, one or more populations of Salix and/or Vaccinium were identified, and 20 to 30 individuals were collected for each population; for each individual, 10 to 15 leaves were then isolated and prepared for extractions of plastidial and nuclear DNA. In the meantime, the sampled populations have been catalogued in a database and collected in the Herbarium of the University of Molise. The future molecular analysis will be crucial to provide, a first large-scale picture of the genetic variability which characterize the species in issue, highlighting possible hypothesis of genetic depletion of the Apennine populations due to their isolation. The final ambition is to obtain results useful for the definition of conservation lines for these rare and peculiar boreal species and habitats under the current global warming situation.

https://conferenceyoungbotanists.com/abstracts/i.mezza

POSTER – Widespread pollen limitation and the influence of geographical gradients on flowering population size and fecundity in orchids

Karl Duffy[1], Marco G. Balducci[1]

[1] University of Naples Federico II

Biodiversity is unevenly distributed globally. Whether the outcome of mutualistic interactions, such as plant pollination by animals, also varies along geographical gradients is unclear. As animal pollinators vary in their responses to flowering plant aggregation on the population level, the extent to which plant fecundity is pollen limited may be influenced by flowering population size. Orchids have a global distribution and are generally pollen limited, hence geographical variation in flowering population size may result in geographical variation in plant fecundity. We performed literature surveys to; (i) quantify the extent of orchid pollen limitation and natural fruit set from experimental hand-pollination studies on 85 species in a phylogenetic context, according to life-form and geographical region and, (ii) quantify how both orchid flowering population size and fecundity varied according to reward strategy and life-form, in a phylogenetic context for 113 species. As the majority of species were represented by a single population, we tested whether fecundity varied along latitudinal and longitudinal gradients for 25 species represented by at least five populations controlling for reward strategy, pollinator type, habitat, and life-form. Pollen limitation was widespread with no phylogenetic signal, yet was higher in epiphytic orchids, while natural fruit set had strong phylogenetic signal. Fecundity covaried with population size and reward strategy, with fecundity increasing with population size in rewarding orchids and decreasing with population size in sexually deceptive orchids. Flowering population sizes increased at mid and high latitudes and did not vary with longitude. Fecundity varied non-linearly according to latitude while decreased with increasing longitude, indicating that orchid fecundity may vary along geographical gradients. These results indicate that interactions between population size according to reward strategy and orchid fecundity varies along geographical gradients. This supports the hypothesis that the outcome of biotic interactions varies geographically and may play a key role in explaining the limits to orchid distributions.

https://conferenceyoungbotanists.com/abstracts/karljoseph.duffy

Poster – Unraveling the Rarity and Evolution of Blue Flower Colouration through Phylogenetics

Laura Fischer[1], David Wulsdorf[1]

[1] Plant Biotechnology and Bioinformatics, Institute of Plant Biology & BRICS, TU Braunschweig, 38106 Braunschweig, Germany; SynBio2024-Team, Plant Biotechnology and Bioinformatics, Institute of Plant Biology & BRICS, TU Braunschweig, 38106 Braunschweig, Germany

Flavonoids, renowned for their antioxidant properties, are a focal point of contemporary research. While anthocyanins producing red hues have been extensively studied, the exploration of blue flower colouration remains incomplete. This rare and captivating trait is an enigma in the plant kingdom, arising from intricate biochemical pathways and genetic innovations. The SynBio2024-Team of TU Braunschweig is committed to investigating the phylogenetic origins and mechanisms underlying blue flower colouration, employing a systematic framework to elucidate its evolutionary and genetic basis. Our research focuses on assembling a comprehensive phylogenetic tree of blue-flowering species to reveal their evolutionary relationships and explore correlations between lineage-specific traits and colouration mechanisms. The blue cornflower (Centaurea cyanus) serves as a detailed case study for blue colour complexation, providing insights into the genetic and biochemical pathways responsible for this unique hue. The formation of blue pigment complexes will be further validated by heterologous transformation into Arabidopsis thaliana, enabling functional analysis of the identified genes. This phylogenetic approach systematically integrates the study of coloration mechanisms with evolutionary history, shedding light on the rarity of blue pigmentation and its underlying processes. Beyond deepening our understanding of floral diversity, this research explores the potential of blue flower colouration as a biomarker for disease detection or its application in engineering ornamental plants, bridging fundamental science and practical innovation.

https://conferenceyoungbotanists.com/abstracts/lau.fischer

TALK – Taxonomic investigations on Polygonum gussonei Tod., a neglected species of the Italian Flora

Manuela Porrovecchio[1], Salvatore Cambria[1], Giuseppe Diego Puglia[2], Saverio Sciandrello[1]

[1] Dipartimento di Scienze Biologiche, Geologiche e Ambientali, Università di Catania, 95128 Catania, Italia; [2] Consiglio Nazionale di Ricerca d'Italia, Istituto per i Sistemi Agricoli e Forestali nel Mediterraneo, Via Empedocle, 58, 95128, Catania, Italia

In the frame of studies on the taxonomy of the Italian endemic flora, the first results of a study on the real consistency of Polygonum gussonei, a taxon described by Todaro in 1874 for Campania and Sicily, are presented. The species has often been synonymized with Polygonum arenastrum Boreau, in recent Italian Flora checklists (Pignatti 2016-2019, Bartolucci 2024). This treatment follows the study by Raffaelli (1982) on the genus Polygonum in Italy, where the author considered P. gussonei as a simple morphotype of P. arenastrum linked to particularly xeric climatic conditions. Conversely, P. gussonei is reported as a distinct species in Flora Europaea (1993) and POWO database (2024+). The aim of this study is to definitively clarify the status of this species through an integrated approach including in-depth morphological studies of the main diagnostic characters (including SEM study of pollen and seed microstructure), molecular and ecological investigations. As regards the morphological study, numerous characters were taken into consideration, such as basal stem diameter, length of the ocreas and internodes, shape and size of the leaves, of the perigonium and the tepals. These traits were measured on 10 specimens of 2 different populations both for P. gussonei and P. arenastrum. The results obtained show a certain morphological divergence between the two taxa that could support the treatment of P. gussonei as a different taxon from P. arenastrum. One-way ANOVA shows a significant difference for the following features: leaf length, basal ocreas length, basal internode length, apical ocreas length, ratio ocreas/apical internodes, tepal limb and tube size. Furthermore, P. gussonei always shows a perennial habit, with a highly branched root, very short apical internodes, succulent leaves, inflorescences particularly rich in flowers, perigonium always consisting of 5 tepals and the apex of the achene slightly protruding from the perigonium. SEM images revealed that P. gussonei has achenes that are narrower at the base, ovate in shape, and with a fruit surface featuring less pronounced ornamentation compared to P. arenastrum, which has pear-shaped and larger achenes. However, further studies are planned to demonstrate the maintenance of these morphological characteristics under the same cultivation conditions and above all molecular investigations will be able to confirm or deny the data obtained. Finally, further field and herbarium investigations will be able to better clarify the distribution of P. gussonei in Italy.

https://conferenceyoungbotanists.com/abstracts/porrovecchiomanuela

TALK – Genes diversity and population dynamics in the Western Alps: from genes to anthropogenic impact

Martino Adamo[1], Maria Guerrina[2], Florian Boucher[3], Gabriele Casazza[2], Marco Mucciarelli[1]

[1] Dipartimento di Scienze della Vita e Biologia dei Sistemi, Università degli Studi di Torino, Torino, Italy; [2] Dipartimento di Scienze della Terra, dell'Ambiente e della Vita, Università degli Studi di Genova, Genova, Italy; [3] Laboratoire de Écologie Alpine (LECA), Université Grenoble Alpes, Grenoble, France

Alpine grasslands are rich habitats, and their history is closely linked to human use. Local studies, based on environmental DNA extracted from lake sediments, have identified some key periods in the history of mankind marked by a sharp increase of human activities impacting vegetation in the Western Alps: late Bronze Age (~3000BC), the Roman Period and the Middle Ages. Agricultural activities and raising livestock lowered the treeline and favoured the establishing and persistence of semi-natural alpine grasslands. This habitat is one of those with the greatest biodiversity in Europe, particularly in the southwestern Alps. The establishment of secondary grasslands has contributed to change the composition of the natural vegetation with repercussions on the demography of some species. A different fate, on the other hand, would have the vegetation of relatively untouched habitats, such as screes and cliffs. Currently, this habitat is at risk due to the land-use change. In view of these observations, understanding whether the population trends of endemic grassland species have been influenced by human use is important for their conservation. For this purpose, we selected twelve endemic species from habitats affected or not by human use, namely semi-natural alpine grasslands, or siliceous and calcareous screes and cliffs. We included populations from the whole distribution range and then we sampled the information available in the genome by ddRAD sequencing. Our goal is to study the inter-specific trends in population structure and past demography through a coalescence approach. Preliminary analyses showed different genetic structures when comparing grasslands species and those growing on mountain screes and cliffs. By coupling the studied trends with the main events of the past human history on the W-Alps, it should be possible to verify if trends in endemics plants genetics are linked to the history of semi-natural alpine grasslands or they are independent.

https://conferenceyoungbotanists.com/abstracts/martino.adamo

Poster – Population Genomics Analysis of Endangered and endemic Plant Species: A Tool for Conservation and Evolutionary Insights.

Marwen Amari[1], Alberto Biscontin[2], Michele Morgante[2]

[1] UNIPA/NBFC/UNIUD; [2] UNIUD

Population genomics offers an unprecedented opportunity to understand the evolutionary dynamics and genetic diversity of endangered plant species, which are often threatened by habitat loss, climate change, and anthropogenic pressures. By leveraging high-throughput sequencing technologies and advanced computational tools, population genomics provides detailed insights into genetic variability, population structure, adaptive potential, and evolutionary history. This study focuses on applying population genomics to endangered plant species, aiming to uncover genetic patterns that inform conservation strategies and enhance our understanding of their evolutionary trajectories. Using whole-genome sequencing and single nucleotide polymorphism (SNP) genotyping, we analyzed several populations of a critically endangered plant species to assess genetic diversity, population differentiation, and gene flow. Our study underscores the power of population genomics in addressing key questions in conservation biology, such as identifying units for conservation management and understanding the role of adaptive variation in species resilience. By integrating genomic data with ecological and environmental information, we provide a holistic framework for preserving genetic diversity and enhancing the adaptive capacity of endangered plant species. Our findings also highlight areas of genetic vulnerability. Low levels of genetic diversity were detected in some populations, likely due to habitat fragmentation and population bottlenecks. This erosion of genetic variation underscores the urgency for conservation interventions. Regions with high genetic diversity or unique alleles were identified as priority conservation zones, serving as reservoirs of genetic resources. Genome-environment association analyses revealed loci under selection, linked to traits such as flood tolerance, drought resistance, and pest resilience—key adaptations for survival in dynamic riparian habitats. These adaptive traits provide valuable insights for habitat restoration and assisted migration initiatives aimed at mitigating the impacts of climate change. In conclusion, population genomics is a transformative approach for conserving endangered plant species, providing actionable insights into their genetic diversity, evolutionary history, and adaptive potential. This approach not only enhances our understanding of plant biodiversity but also equips us with the tools to address the challenges posed by a rapidly changing environment.

https://conferenceyoungbotanists.com/abstracts/marwen.amari

TALK – A new species of Festuca L. (Poaceae) endemic to the Sila plateau in Italy.

Mattia Pallanza[1], Nicola Maria Giuseppe Ardenghi[2], Liliana Bernardo[3], Petr Šmarda[4], Petra Šarhanová[4], Orsenigo Simone[1], Graziano Rossi[5], Bruno Foggi[6]

[1] Dipartimento di Scienze della Terra e dell'Ambiente, Università degli Studi di Pavia, Via Sant'Epifanio 14, 27100 Pavia; National Biodiversity Future centre, 90133 Palermo.; [2] Orto Botanico, Sistema Museale di Ateneo, Università degli Studi di Pavia, Via Sant'Epifanio 14, 27100 Pavia.; [3] Dipartimento di Biologia, Ecologia e Scienze della Terra, Università della Calabria, Via Pietro Bucci, 87030 Arcavacata di Rende (Cosenza).; [4] Department of Botany and Zoology, Faculty of Science, Masaryk University, Kotlářská 2, 61137 Brno, Czech Republic.; [5] Dipartimento di Scienze della Terra e dell'Ambiente, Università degli Studi di Pavia, Via Sant'Epifanio 14, 27100 Pavia.; [6] Dipartimento di Biologia, Università degli Studi di Firenze, Via G. La Pira 4, 50121 Firenze.

During a sampling campaign aimed at revising the Festuca marginata (Hack.) K.Richt. (= F. circummediterranea Patzke) group in the Mediterranean, a curious taxon belonging to the genus Festuca was found on the Sila plateau. Historically, specimens with similar morphology had been collected in the area by Sarfatti and identified as Festuca ovina L. subsp. laevis Hack. var. gallica (Hack.) St.-Yves subvar. costei St.-Yves (≡ Festuca costei (St.-Yves) Markgr.-Dann.) by Markgraf-Dannenberg. However, the specimens displayed quite an unique morphology resembling other members of the F. marginata group (to which F. costei belongs) but occasionally showed a complete sclerenchymatic ring with irregular thickness, a trait typically associated with the Festuca stricta Host group. Preliminary chromosome counts revealed that this taxon is hexaploid ($2n=6\times=42$), differing from the consistently diploid F. marginata ($2n=2\times=14$) and tetraploid F. costei ($2n=4\times=28$), confirming the inconsistencies that emerged from a preliminar morphological study. This distinctive combination of morphological traits and unusual ploidy level lead to further investigations using an integrated taxonomic approach. To clarify the identity of this taxon, four additional comparative taxa were selected based on shared morphological and karyological characteristics: Festuca stricta Host, Festuca rupicola Heuff., Festuca trachyphylla (Hack.) R.P.Murray, and Festuca marginata (Hack.) K. Richt. A total of 158 individuals from 25 populations across the Alps and Apennines were sampled. Of these, 47 were analyzed via flow cytometry to estimate genome size and infer ploidy levels. Additionally, morphometric analyses included 19 herbarium specimens housed at FI. Flow cytometry results confirmed that the Sila taxon is consistently hexaploid, as are other species within the F. stricta complex, while all F. marginata samples were diploid, as expected in accordance with literature. Morphometric analysis involved 35 diagnostic traits (17 continuous numerical, 15 ordinal categorical, and 3 binary) selected based on prior studies of the genus Festuca. An exploratory Principal Coordinate Analysis (PCoA) revealed three primary morphological groups: one comprising F. stricta, F. rupicola, and F. trachyphylla; another of F. marginata individuals; and a distinct cluster of hexaploid Sila individuals positioned between the other two groups. The groups identified via PCoA were subsequently tested using Linear Discriminant Analysis (LDA) with jackknife resampling. Additionally, ddRADseq analyses were carried out to better clarify the genetic relationships within the different taxa, revealing that despite the mixed morphological characters the new taxon from the Sila is more closely related to the F. marginata group rather than the F. stricta group. Overall, all performed analyses suggest that the hexaploid populations from Sila represent a distinct taxon separate from other similar fescues present in the italian flora. It is likely that it originated through auto- or allopolyploidization events of other F. marginata group members present in the area, as suggested by the preliminary genomic analyses.

https://conferenceyoungbotanists.com/abstracts/mattia.pallanza02

Poster – The role of roadside and concrete surfaces in facilitating the spread of Sedum caespitosum (Cav.) DC. in the Pannonian Ecoregion

Szabolcs Kis[1], Henrietta Bak[1], Réka Fekete[2], Gusztáv Jakab[3], Attila Molnár V.[1]

[1] HUN-REN-UD Conservation Biology Research Group, University of Debrecen, Department of Botany; [2] HUN-REN Centre for Ecological Research, Seed Ecology Research Group; [3] Eötvös Loránd University, Department of Environmental and Landscape Geography

Sedum caespitosum is an annual plant species characteristic of Mediterranean and sub-Mediterranean regions. Within the Mediterranean area, it predominantly inhabits pioneer environments, including open-soil and stony-loamy habitats. Sedum caespitosum is a rare species within the Pannonian Ecoregion. It is classified as a rare species on the Red List of Flora of Romania, recognised as rare in Serbia, and considered potentially endangered in Hungary, where it is protected under national conservation legislation. However, it is also frequently found in anthropogenic habitats, such as along roadsides and within urbanised environments. This study aimed to evaluate the geographical distribution of the species along roads, the population sizes within roadside environments and other anthropogenic habitats (e.g., concrete surfaces near oil wells), and the spatial distribution of individuals in relation to their proximity to roads. For this study, road sections within the Pannonian Ecoregion in Serbia, Romania, and Hungary were surveyed between late March and early May 2023. During sampling, 100-metre segments were examined, documenting the presence or absence of Sedum caespitosum, estimating population sizes, and measuring the distance of individuals from the road where the species was present. A total of 406 sampling points were surveyed within roadside habitats, with Sedum caespitosum detected at 20 of these locations. The average population size was 5,293 individuals, ranging from a minimum of 4 to a maximum of approximately 15,000 individuals. However, within an anthropogenic habitat located further from the road, a population of approximately 60,000 individuals was identified. Overall, the distance of the observed individuals from the road ranged from 1 cm to 370 cm, with a median value of 19 cm. An important conclusion is that for certain roadside populations, the species was found in areas where it does not occur in the surrounding landscape. This suggests that roads may influence the distribution of the species in continental climatic conditions. As ecological corridors, motorways can facilitate the dispersal and expansion of rare plant species.

https://conferenceyoungbotanists.com/abstracts/kis.szabi17

POSTER – Phylogeny and dating of divergences in N. pseudonarcissus L. using plastome sequences

Valeria Fochi[1], Martino Adamo[1], Virgile Noble[2], Giuseppina Barberis[3], Marco Mucciarelli[1]

[1] Dipartimento di Scienze della Vita e Biologia dei Sistemi, Università degli Studi di Torino, Torino, Italy.; [2] Conservatoire Botanique National Méditerranéen, Hyères, France.; [3] Dipartimento di Scienze della Terra, dell'Ambiente e della Vita, Università di Genova, Italy.

Narcissus pseudonarcissus L. (Amaryllidaceae) is a perennial geophyte native to Europe and distributed in different habitats, from grasslands to temperate nemoral forests. It is a species of great horticultural interest, but also an endangered and protected plant in the wild where it is threatened by loss of natural habitats. The species exhibits considerable morphological and genetic variation with numerous subspecies identified to date. For this study, a population of wild N. pseudonarcissus was sampled from a natural habitat in the Ligurian Alps at Monte Carmo di Loano (SV). This region at the boundary between the temperate alpine climate and the mild Mediterranean climate fosters a rich variety of plant species, many of which are endemic to the region. Currently, only two published chloroplast genomes are available for daffodils native to Europe: N. tazetta L. and N. poeticus L., the type species of the genus. Here, we report the complete chloroplast genome sequence of N. pseudonarcissus to address this and to identify new regions of genomic variability. Complete plastid genome was assembled from next-generation sequencing data obtaining a circular genome of 160,008 bp long assembly. It comprises a large single-copy region (108,400 bp), and a small single-copy region (16,434 bp), encoding 131 genes (87 protein coding genes, 37 tRNA genes and seven rRNA genes). Phylogeny run on currently available plastid genomes in Amaryllidaceae showed the monophyly of the genus within the subfamily Amaryllidoideae and the close relationship between N. pseudonarcissus and N. poeticus. Among the various subspecies of N. pseudonarcissus, the subspecies "provincialis" has long been recognized as a geographically isolated taxon native to the Alps of France. Nevertheless, the lack of a clear morphological delimitation has resulted in taxonomic ambiguity and its presence on the mountains of Italy remains undetermined. Given the ease with which Narcissus undergo spontaneous hybridization, even between distantly related species, having access to the plastid genome of N. pseudonarcissus represents an opportunity to further investigate the genetic basis of its variability at the wild state. Moreover, by integrating data from genetic analysis with flower morphometry and niche evolution we were able to demonstrate the genetic distinctiveness of two separate lineages currently found in the wild state in southern Alps and northern Apennines of Italy.

https://conferenceyoungbotanists.com/abstracts/valeria.fochi

POSTER – Influence of aromatic dwarf-shrub canopies on plant community diversity and composition in Sardinian coastal harsh habitats

Alfredo Maccioni[1], Erika BAZZATO[2], Silvia MACIS[2], Michela MARIGNANI[2], Emmanuele FARRIS[3]

[1] 1 Department of Chemical, Physical, Mathematical and Natural Sciences, University of Sassari, Via Piandanna, 4, 07100 Sassari (SS), Sardinia, Italy - 2 e.INS- Ecosystem of Innovation for Next Generation Sardinia; [2] 2 e.INS- Ecosystem of Innovation for Next Generation Sardinia - 3 Department of Life and Environmental Sciences, University of Cagliari, Viale S. Ignazio, 13, 09123 Cagliari (CA), Sardinia, Italy; [3] 1 Department of Chemical, Physical, Mathematical and Natural Sciences, University of Sassari, Via Piandanna, 4, 07100 Sassari (SS), Sardinia, Italy - 2 e.INS- Ecosystem of Innovation for Next Generation Sardinia - 4 National Biodiversity Future Center NBFC, Palermo 90133, Italy

Numerous ecological processes define plant species richness and community composition: plant establishment and survival are particularly sensitive to micro-habitat structure and environmental conditions, especially in Mediterranean harsh environments. To assess whether plant community richness and composition in a mosaic of coastal Mediterranean herb and garrigue habitats was determined by the canopy of aromatic dwarf-shrubs, between April and July 2023 we conducted a study on three model species (Helichrysum italicum subsp. tyrrhenicum, Teucrium capitatum subsp. capitatum, and Salvia rosmarinus) and examined each species at three different sites in North-Western Sardinia (Italy). At each species × site combination, we randomly sampled 10 individuals. We recorded the presence or absence of vascular plants both under the shrub canopies and in adjacent open areas, using point transects. Statistical analyses revealed significant differences in community composition between areas under and those outside the canopies of all the three model species. While the presence of canopies did not influence species richness, it did affect beta dispersion for all three shrub species and the mean community composition of H. italicum subsp. tyrrhenicum and T. capitatum subsp. capitatum. Preliminary data suggest that the presence of these canopies led to significant differences in species composition between areas beneath the dwarf-shrubs and adjacent open areas, indicating that conditions under the canopies may influence plant diversity in comparison to the surrounding open habitat. Moreover, our results highlight significant differences in species richness, mean composition, and beta dispersion beneath the canopies of the model species, suggesting that the dominant species play a key role in shaping plant diversity. We hypothesize that these preliminary outcomes, which provide insight into the dynamics of biocoenosis and plant-plant interactions in Mediterranean harsh environments, may be more strongly influenced by plant specialized metabolites at both in soil litter and aerial parts and roots of aromatic dwarf-shrubs, rather than by the simple shading effects of the canopies themselves.

https://conferenceyoungbotanists.com/abstracts/amaccioni

TALK – Investigation of the priority forest habitats of Val di Mello Natural Reserve

Alice Grandi[1], Marina Borgatti[1], Marco Caccianiga[1], Leonardo Malvezzi[1], Barbara Valle[2]

[1] Department of Biosciences, Università degli Studi di Milano, Milan, Italy; [2] Università degli Studi di Siena; NBFC – National Biodiversity Future Center, Palermo

Val di Mello represents the eastern extension of Val Masino (Sondrio province, Italian Alps), a major lateral valley on the right hydrographic side of Valtellina. Since 2009 Val di Mello is almost entirely included in “Val di Mello Natural Reserve”, becoming the largest protected reserve in Lombardy. The aim of our work consists in monitoring the priority natural habitats of the valley as defined by the Habitat Directive (Council Directive 92/43/EEC) using a phytosociological approach. We performed phytosociological relevés to examine the following habitats: - 91E0* - “Alluvial forests with Alnus glutinosa and Fraxinus excelsior (Alno-Padion, Alnion incanae, Salicion albae)” - 9180* - “Tilio-Acerion forests of slopes, screes and ravines”. Our sampling design was partly defined according to the plots already marked by a group of forestry experts, which was involved in parallel for the forestry assessment of the habitats. Further plots have been determined on the field consulting the map of habitat types, also trying to assess the presence of additional areas which could deserve higher protection. Furthermore, our work was paralleled by a sampling aimed at verifying the occurrence of the two bryophyte species included in the Annex II of the Habitat Directive, namely Orthotrichum rogeri Brid. and Buxbaumia viridis (Lam. & DC.) Moug. & Nestl., confirming most of the earlier reports and discovering a new site for the latter specie. The data collected have been processed with a cluster analysis in order to investigate the phytosociological characterization of the forest vegetation. Surveys from areas earlier reported as 9180* habitat turned out to be differentiated into two clusters: the first one belongs to Arunco-Aceretum Moor 1952 association, thus confirming the habitat 9180* attribution, while it wasn’t possible to define the second cluster’s phytosociology even at the order level, because of the simultaneous occurrence of typical species relevant to Quercetalia roboris Tüxen 1931 and Fagetalia sylvaticae Pawłowski in Pawłowski, Sokołowski et Wallisch 1928. On the other hand, the assignation of habitat 91E0* finds confirmation in the results of our analysis, which lead to the attribution of the Aceri-Alnetum incanae Beger 1922 association. Ultimately, our preliminary results confirm the far from easy categorization of the 9180* habitat, often subject to floristic depletion, and underline some discrepancies with respect to the map of habitat types, expressing the necessity of further investigation.

https://conferenceyoungbotanists.com/abstracts/alice.grandi2

TALK – Syntaxonomy of a species of Community interest across the entire alpine range: the endemic Trifolium saxatile

Andrea Mainetti[1], Ginevra Nota[2], Michele Lonati[2]

[1] Andrea Mainetti, Gran Paradiso National Park; [2] DISAFA, University of Torino (IT)

Trifolium saxatile is an endemic species of the Alps, with a fragmented distribution split into two main areas: one in the Western Alps spanning Italy, France, and southwestern Switzerland, and another in the Eastern Alps between Tyrol and South Tyrol. Likely a relict species (Favarger 1989), it is listed in Annex II of the EU Habitats Directive , necessitating periodic monitoring and conservation commitments at the EU level. However, the habitat selection and phytosociological significance of this species remain debated. Some authors classified it as a characteristic species of alpine riverbed communities (Epilobion fleischeri according to Villaret et al. 2017, Epilobietalia fleischeri according to Grabherr and Mucina 1993). Others have proposed T. saxatile as characteristic of a new phytosociological association ranked in the alpine siliceous scree communities (Androsacion alpinae, Dellinger and Berger 2009). Nevertheless, this latter proposal is poorly defined phytosociologically, contested by some authors (Unterluggauer et al. 2013), and based on phytosociological surveys conducted in a limited portion of the species' range in Austria. These findings raise the question of whether some of these habitats might represent the species' primary and original environments, while others could be secondary. This study aims to reassess the ecological significance of T. saxatile and comprehensively describe the habitats where it grows through a phytosociological study based on surveys encompassing the entire distribution range of the species, integrating published and original data. Thirty-five new phytosociological relevés were conducted in the Italian Western Alps, while publications and databases containing relevés from France (CBNA 2023), Switzerland (Richard 1989, Steiner 1999), Tyrol, and South Tyrol (Unterluggauer et al. 2013) were digitised. The nomenclature (following Bartolucci et al. 2024) and the abundance values were harmonised, resulting in a dataset comprising 128 phytosociological relevés. Abundance values were transformed into Van der Maarel scores (2007), and a cluster analysis (Bray-Curtis similarity; UPGMA algorithm) was performed on the entire database. Characteristic species at the alliance, order, and class levels were identified in accordance with Grabherr and Mucina (1993), integrated by Theurillat et al. (1994), for five different scree and grassland phytosociological classes. The phytosociological analysis across the species' entire range confirmed the existence of distinct clusters, particularly in riverbed and alpine siliceous scree habitats. Among these, a well-defined cluster within the Androsacion alpinae alliance was identified, supporting the proposal of a new and distinctly defined association named Saxifrago bryoidis-Trifolietum saxatilis ass.nova. This new association suggests that alpine siliceous screes should be considered the primary habitat where the species has persisted, while riverbeds represent secondary habitats. These insights into the phytosociological framework of the species will better guide monitoring and conservation efforts for this species of conservation concern.

https://conferenceyoungbotanists.com/abstracts/andrea.mainetti

Talk – Soil-Driven Secrets: How Urban Soils Shape Extracellular Enzymatic Activities and Plant-Microbe Interactions

Anna Gillini[1], Nataliya Bilyera[2], Dalila Trupiano[1], Iryna Loginova[2], Michaela A. Dippold[2], Gabriella Stefania Scippa[1]

[1] Department of Biosciences and Territory, University of Molise, 86090 Pesche, Italy; [2] Geo-Biosphere Interactions, Department of Geosciences, University of Tübingen, Tübingen, Germany

The functioning of urban ecosystems and biodiversity, which are essential to human life and well-being, are under severe threat from anthropogenic pressure and climate change in recent years. According to recent research, biotic and abiotic soil components and plant roots interact underground influencing the biodiversity and ecosystems in a significant but hidden way. A controlled experiment was carried out using young Q. cerris seedlings and three distinct urban soils that were collected from three locations in the city of Campobasso (Molise region), following a specific gradient of vegetation fragmentation and urbanization, in order to provide insight into the function of these nearly unknown interactions in urban environments. Following physicochemical soil analyses, the amount of pollutants in the soil was used to develop a soil quality index (SQI) that linked site fragmentation to soil quality. These soils were then utilized in a rhizobox experiment to grow Q. cerris seedlings for two weeks. After the growth and settling phase, soil zymography was used to map the hotspot development and spatial distribution of the following enzymes: acid phosphatase (P-cycle), β-glucosidase (C-cycle), and leucine aminopeptidase (N-cycle). Analysis of the 2-D zymograms revealed that the soils varied spatially along the urbanisation or soil quality gradient, with the worst quality soils having the highest enzyme activity and hotspot values. Higher enzyme activity and, as a result, soil organic matter turnover were closely related to root activity intensity and could be linked to root exudation and/or rhizodeposition of substrates to modulate plant growth under unfavourable conditions by modifying soil components. Soils from rhizoboxes were collected to determine the composition of microbial communities and to predict their role in the soils. Analyses of bacterial communities using 16S rDNA gene sequencing suggested differences in the rhizosphere and bulk soils between the three sites studied. These findings revealed that soil quality or urbanization influenced not only the shift in extracellular enzyme activity, but also the changes in microbial communities.

https://conferenceyoungbotanists.com/abstracts/anna.gillini37

TALK – Hide and seek: results from monitoring populations of a species prone to prolonged dormancy

Bálint Pacsai[1], Vivien Lábadi[1], Judit Bódis[1]

[1] Hungarian University of Life Sciences, Department of Nature Conservation Biology, Georgikon Campus

The management of protected and rare species populations is frequently planned on the basis of data obtained from censuses, with population size serving as a derived indicator of population condition. This could apply to Fritillaria meleagris, a Eurasian species that is in decline across its range and which serves as a flagship species in conservation in some regions. Estimations of population sizes are typically based on the number of flowering individuals. The objective of our study was to assess the extent of bias in population size estimates based on the number of flowering individuals. Two sets of permanent quadrats were established in populations of Fritillaria meleagris located in wet meadows in western part of Hungary: one in Gyékényes and one in Tüskeszentpéter (with 80 km distance between them). Morphometric characteristics of the plants were recorded on an annual basis between 2017 and 2023, with the specimens then classified according to their age-state categories: juvenile, vegetative, reproductive. Significant differences were identified between the two populations, exhibiting consistent patterns across years. The proportion of individuals flowering at Tüskeszentpéter was notably higher (60.6%) than that observed at Gyékényes (28.9%). The proportion of juveniles at Gyékényes was more than three times that observed at Tüskeszentpéter. The populations were similar in the frequency of prolonged dormancy with about half of the plants appeared aboveground went into dormancy in the following year (and possibly remaining in this state even longer) at both sites. Examination of transitions through dormancy revealed that stasis was the most frequent transition at both sites, however plants at Gyékényes were more likely to step forward an age-state than retrogress following dormancy, whereas at Tüskeszentpéter retrogression was more prevalent than progress. While one- and two-year dormancy were the most common, the maximum potential duration of dormancy remains unknown. Consequently, the mortality estimates were approximate and insufficient to determine the exact population size. The mortality rates observed at Gyékényes and Tüskeszentpéter were approximately 10% and 1-5%, respectively. Given the higher proportion of adult plants at Tüskeszentpéter compared to Gyékényes, an equal number of flowering individuals in the two populations would correspond to a smaller population size at Tüskeszentpéter compared to Gyékényes. These results reinforce the conclusion that the bias of population size estimates based on censuses varies greatly across different populations. They also highlight the need to study the demographic structure of such populations for more reliable population size estimates which can lead to better planning of conservation.

https://conferenceyoungbotanists.com/abstracts/pacsai.balint

TALK – Herbicide Resistance and soil microbial composition

Carlo Maria Cusaro[1], Enrica Capelli[1], Anna Maria Picco[1], Maura Brusoni[1]

[1] Department of Earth and Environmental Sciences, University of Pavia, Via S. Epifanio 14, 27100 Pavia, Italy

The following contribution reports the main results of a research titled "Incidence of resistance to ALS and ACCase inhibitors in Echinochloa species and soil microbial composition in Northern Italy" recently published on Scientific Reports Journal. This contribution is part of the project NODES which is funded by the European Union - NextGenerationEU, Mission 4 Component 1.5 - ECS00000036 - CUP F17G22000190007. Herbicide resistance represents a serious problem for crop management, leading to important yield losses every year. The relation between soil microbial communities and herbicide resistance occurrence is a still poorly known topic. Its investigation would be crucial to better understand potential relapses on agricultural management. The microbiome of soils collected in 32 rice farms located in the Northern Italy (Lombardy) was analyzed, aiming to evaluate the relationship between the microbial composition and the incidence of resistance to acetolactate synthase (ALS) and acetyl-CoA carboxylase (ACCase) inhibiting herbicides in Echinochloa species. A relation between the soil microbiomes diversity and the abundance of weeds survived chemical control was observed. A low microbial diversity was recorded in highly infested paddies (resistant Echinochloa coverage $\geq$ 60%) while a high microbial diversity was recorded in poorly infested paddies (resistant Echinochloa coverage $\leq$ 5%). Fungal communities showed a greater reduction in richness than bacterial ones and a stronger relation with herbicide resistance in paddies where a high incidence of resistant Echinochloa species was observed. In soils with a low microbial diversity, a significant dominance of some bacterial and fungal orders (i.e. Lactobacillales, Malasseziales and Diaporthales) was observed. In general, two different microbial profiles related to the high or low incidence of herbicide resistance by Echinochloa species were identified. The results of this research allow to make hypotheses on the greater or lesser probability of herbicide resistance occurrence based on the composition of the soil microbiome and especially on the degree of biodiversity of the microbial communities. References Cusaro, C.M., Capelli, E., Picco, A.M. et al. Incidence of resistance to ALS and ACCase inhibitors in Echinochloa species and soil microbial composition in Northern Italy. Sci Rep 14, 10544 (2024). https://doi.org/10.1038/s41598-024-59856-0

https://conferenceyoungbotanists.com/abstracts/carlomaria.cusaro01

TALK – The pollination network of Campanula sabatia De Not.

Chiara Bonifazio[1], Mattia Longobardi[1], Silvia Tripi[1], Ian Briozzo[1], Maria Guerrina[1], Gabriele Casazza[1], Gianalberto Losapio[2], Luigi Minuto[1]

[1] Università di Genova; [2] Université de Lausanne; Università degli studi di Milano

Conservation actions, especially with regard to endemic plant species, are often species-based, but it has been long recognized that species conservation initiatives must consider the multitude of ecological interactions in which species are involved, such as those with pollinators. In particular, this work aimed at understanding the role of an endemic species within the pollination network. The target species is Campanula sabatia De Not., endemic to the SW Alps and listed in Annex II of the Habitats Directive. The study area was a site of reintroduction of C. sabatia within Life SeedForce Project. In an area of approximately 500 m2, ten 1 m2 plots were established at a distance of at least 2 metres from each other. Vegetation surveys and direct observation of flower visitors were performed before (2023) and after (2024) reintroduction. After the first summer of observation, in December 2023 five C. sabatia plants per plot were planted in five out of ten plots. Each observed insect was recorded together with the flowering plant visited. During the two field-season, we reached 95 hours of observation and 2056 insects detected. The differences between 2023 and 2024 in terms of alpha, beta and gamma diversity do not appear to be related to the reintroduction of C. sabatia, but rather to a difference in flowering plants due to the peculiarity of the season. However, PLS-DA shows a clear differentiation in the visitors' pool between plots with and without C. sabatia. Our preliminary results suggest that rare species might play a role within the pollination network.

https://conferenceyoungbotanists.com/abstracts/chiara.bonifazio

TALK – Preliminary investigations of the Bryophyte Flora in the Hazel Groves of the Aveto Regional Natural Park (Ligurian Apennines)

Chiara Macolino[1], Claudia Turcato[2], Luigi Minuto[1]

[1] Dipartimento di scienze della terra, dell'ambiente e della vita, Università di Genova; [2] Centro Studi Bionaturalistici

This study investigates the bryological diversity of six hazel groves in the Val d'Aveto Regional Natural Park. The sampling sites were selected between the municipality of San Colombano Certenoli and Mezzanego and they represent both managed and abandoned cultivations. The study of bryophyte diversity is part of a broader floristic characterization of the hazel groves in Aveto Park, aimed at further enhancing these crops, which are already recognized with a cultural and agri-food value. To conduct the investigations, 99 mosses were sampled in three different substrates (soil, rock and bark). In total 47 different taxa were identified, with 5 being new species for the Liguria region and 4 being confirmed records (no information was known after 1968). The bryophytic species richness varied among the six sampling sites, with the lowest diversity observed on bark in all cases. Despite differences in specific composition, the identified taxa suggest similar ecological and chorological conditions for all sites investigated. These findings contribute to increasing knowledge about the bryophytic component of the Ligurian Flora, which is one of the least investigated nationally (Poponessi et al. 2013). The results provided also qualitative information on the bryophytic composition of the Flora in the hazel groves of the Aveto Regional Natural Park.

https://conferenceyoungbotanists.com/abstracts/chiaramacolino.o

TALK – Trait-based study as a conservation tool for protected species: the case study of Trifolium saxatile in the Gran Paradiso National Park

Dario Comunello[1], Andrea Mainetti[2], Silvio Marta[3]

[1] University of Padova, Padova, Italy; [2] Gran Paradiso National Park, Fraz. Valnontey 44, 11012 Cogne (AO); [3] Institute of Geosciences and Earth Resources, CNR, Pisa, Italy

Studies based on functional traits are valuable tools for monitoring the conservation status of plant species. They facilitate the development of ecological models, helping to understand species niche and distribution,and to predict responses to climate change. This study investigated Trifolium saxatile, a species of Community interest (Habitats Directive, Annex II) endemic to the Alps. Our research focused on exploring the intraspecific trait variation of T. saxatile across 10 populations within the Gran Paradiso National Park. We measured vegetative traits such as plant height, length, and number of inflorescences, for 995 individuals. Additionally , leaf traits were measured for 175 individuals and for each population we calculated the CSR strategy.. For each sampling site 11 environmental variables, putatively influencing species occurrence and performances, were collected (elevation, slope, aspect, meso- and microtopography, vegetation cover, and percentages of rockiness and sand, debris, litter and bare soil). Through statistical analyses and ecological modelling, we linked functional traits and the geomorphologic feature of the habitat of the species, aiming to identify the key ecological factors influencing its niche and distribution. Our results suggested that T. saxatile prefers areas with sparse vegetation cover, and a medium-to-high amount of rock and debris. Additionally, CSR classification suggests that T. saxatile favours ruderal and stress-tolerator strategies, although a clear boundary between the two was not evident. Indeed, the populations we analysed tend to lean toward the stress-tolerator strategy, while still maintaining a broad continuum of variability. Altogether, this information seems to suggest a preference for sites with a discrete level of natural disturbance and a scarce competition.This is the first time this preference has been proposed for this species, based on data derived from functional traits and we hypothesize that T. saxatile is not necessarily an opportunistic species. But its ecological niche requires further investigation. Altitude and slope were identified as critical factors for T. saxatile distribution(?) and deserve further analyses in relation to its functional traits. This could provide a better understanding of the distribution of its populations. The approach implemented in the present analysis allows not only assessing the current conservation status of T. saxatile, but provides a valuable benchmark to evaluate the species' ecological plasticity and adaptability, in the context of climate change. By gaining a deeper understanding of its ecological strategies and habitat preferences, local authorities, such as the Gran Paradiso National Park, will improve monitoring and conservation strategies which are mandatory for this species of community interest.

https://conferenceyoungbotanists.com/abstracts/dario.comunello

Talk – Niche variation in endemic Gentiana ligustica between two biogeographical regions

Davide Casalino[1], Ian Briozzo[1], Chiara Bonifazio[1], Maria Guerrina[1], Luigi Minuto[1], Gabriele Casazza[1]

[1] Dipartimento di scienze della terra, dell'ambiente e della vita, Università di Genova

Gentiana ligustica is an endemic species of the Southwestern Alps growing on calcareous rocky grassland, in Alpine and Mediterranean biogeographic regions. Populations in the Mediterranean region are at the warm margin of the species distribution and their conservation status is assessed as “Inadequate”, and the global warming could further negatively affect these populations. The aim of this research is to compare the microenvironmental conditions used by the species in the two biogeographical region investigating plant community and soil. In five sites for each biogeographical region, we performed three floristic relevés in 2x2m plots and we collected three soil samples. We identified alliances and we associated Ellenberg Indicator Values (EIV) to each species to investigate microclimatic conditions. Kruskal-Wallis test and PCA were performed to explore differences between the biogeographical regions. Gentiana ligustica is more abundant in sandy, low depth soils with low nutrients and the soil conditions are similar between the two biogeographical regions. PCA based on EIV shows low differences between the two biogeographical regions, although Mediterranean populations grow under higher variety of ecological conditions. Nevertheless, Alpine populations select significantly higher light intensity. Our results suggest that, despite low differences in microclimatic preferences, Mediterranean populations select shade environment. Further studies on differences in reproductive ecology between the two biogeographical regions will be performed to develop proactive strategies for the conservation species.

https://conferenceyoungbotanists.com/abstracts/davide.casalino

Talk – Long-term Dynamics of Coastal Dune Landscapes and Floristic Diversity: Insights from a Quarter Century of Resurveys in Castelporziano Presidential Estate

Elena Cini[1], Alicia Teresa Rosario Acosta[1], Marco Malavasi[2], Simona Sarmati[1], Silvia Del Vecchio[3], Daniela Ciccarelli[4], Flavio Marzialetti[5]

[1] Department of Science, Roma Tre University, Viale Guglielmo Marconi 446, 00146, Roma, Italy; [2] Department of Chemistry, Physics, Mathematics and Natural Sciences, University of Sassari, Via Vienna 2, 07100 Sassari, Italy | National Biodiversity Future Center (NBFC), Piazza marina 61, 90133, Palermo, Italy; [3] Department of Biological, Geological and Environmental Sciences, University of Bologna, Via Irnerio 42, 40126, Bologna, Italy; [4] Department of Biology, University of Pisa, Via Luca Ghini 13, 56126, Pisa, Italy; [5] Department of Agricultural Sciences, University of Sassari, Viale Italia 39/A, 07100, Sassari, Italy | National Biodiversity Future Center (NBFC), Piazza marina 61, 90133, Palermo, Italy

Coastal dunes are transitional ecosystems situated along sandy shorelines, shaped by steep sea-to-inland environmental gradients. According to the 4th Habitat Report, over 85% of these habitats are classified as having poor conservation status, with a deteriorating trend driven by intense anthropogenic pressures. Monitoring temporal habitat changes is therefore critical to implement effective conservation measures. Traditional methods, such as field resurveys, remain a cornerstone for vegetation monitoring but are both time-consuming and costly. In contrast, in recent years Remote Sensing (RS) has emerged as a promising, cost-effective alternative, offering enhanced data availability and spatial resolution. This study investigates temporal changes in the coastal dune ecosystems of the Mediterranean Protected Area (PA) "Castelporziano Presidential Estate" (Natura2000 code: IT6030084), a strictly regulated zone with limited access. Specifically, we assess floristic and landscape dynamics over a 25-year period using data from 58 resurveyed vegetation plots within land cover classes: Herbaceous Dune Vegetation (HDV), Woody Dune Vegetation (WDV), and Broadleaf Mixed Forest (BMF). The main objective was to determine whether floristic diversity influences landscape dynamics by integrating field and RS data collected during two temporal snapshots (T0: 1998 and T1: 2023). Landscape changes were visualized using chord diagrams, while floristic shifts were evaluated with rank-abundance curves for T0 and T1. Shannon diversity indices were calculated to measure both floristic and landscape diversity within 25 m, 75 m, and 125 m circular buffers around the plots. To explore whether floristic diversity affects landscape dynamics and how these relationships evolve over time, we applied Linear Mixed Effects models. Our results revealed natural encroachment, vegetation succession and a reduction in artificial cover. Floristic analyses highlighted substantial differences between T0 and T1, particularly in WDV, where the dominance of Cistus sp. pl. significantly declined. Models assessing the influence of floristic diversity on landscape dynamics demonstrated strong explanatory power, particularly within larger buffers. Notably, relationships differed between T0 and T1 across all three vegetation units. Landscape diversity exhibited negative trends with increasing species dominance, whereas positive trends were associated with higher species evenness. This study underscores the utility of integrating field and RS data for monitoring temporal changes in Protected Areas. The approach offers valuable insights into the interplay between plant diversity and landscape dynamics and may serve as a foundation for accelerating resurvey efforts and implementing targeted conservation measures.

https://conferenceyoungbotanists.com/abstracts/elena.cini

Poster – Monitoring riparian vegetation from space: developing a cloud-based application in Google Earth Engine

Emilia Pafumi[1], Gabriele Antoniella[2], Saverio Francini[3], Melissa Latella[4], Davide Tognin[5]

[1] Department of Life Sciences, University of Siena, 53100 Siena, Italy; NBFC, National Biodiversity Future Center, 90133 Palermo, Italy; [2] Department for Innovation in Biological, Agro-food and Forest systems (DIBAF), University of Tuscia, Viterbo, Italy; [3] Department of Science and Technology of Agriculture and Environment (DISTAL), University of Bologna, 40126 Bologna, Italy; [4] CMCC Foundation – Euro-Mediterranean Center on Climate Change, Italy; [5] Department of Civil, Environmental and Architectural Engineering, University of Padova, 35131 Padova, Italy

Implementing objective and reproducible tools for vegetation monitoring is fundamental to effective conservation efforts. Ecosystems located at the interface between terrestrial and aquatic environments, such as riparian ecotones, provide essential ecosystem services but are highly vulnerable to anthropogenic pressures. Moreover, inadequate monitoring approaches that can support decision-making processes often hamper their conservation. In this context, satellite remote sensing has the potential to address data gaps by providing information with extensive spatial and temporal coverage. However, the large volume of satellite datasets typically requires significant computational resources and specialized expertise, limiting their usability by non-specialists. To address these challenges, this work aims to develop a user-friendly application for monitoring riparian vegetation over time using freely available remote sensing data. The application has been developed on Google Earth Engine, a cloud-based computing platform that has been increasingly applied for large-scale geospatial analysis in recent years. Development and testing are carried out in a pilot area corresponding to the Bolsena volcanic lake (central Italy). The tool consists of three main modules: (1) selection and pre-processing of the satellite image collection, (2) extraction of water bodies, and (3) identification and quantification of riparian vegetation. Sentinel-2 multispectral imagery is selected as the remote sensing dataset due to its high spatial resolution (10 m) and revisit frequency (5 days). In the first step, the image collection is filtered for a user-defined time range and cloud cover. Subsequently, water bodies are identified based on automatic thresholding of specific spectral indices, such as NDWI. Then, riparian vegetation is identified within a buffer surrounding water bodies using various approaches, including the thresholding of spectral vegetation indices, and the application of automatic image classification techniques based on machine learning. Additionally, the feasibility of discriminating between different types of riparian vegetation will be explored. Ultimately, the tool will be validated using ground truth data collected from the study area, with further testing for generalization to additional sites. The tool will allow the generation of maps and quantitative assessments of riparian vegetation extent and changes over time. Its simple interface will ensure accessibility to a wide range of users, and its cloud-based nature will allow the analysis of large amounts of multi-temporal data without requiring advanced computational resources. This approach will therefore provide critical data to support monitoring, planning and decision-making, and ultimately the conservation of riparian ecosystems, while fostering local community engagement and promoting the social benefits of conserving these vital habitats.

https://conferenceyoungbotanists.com/abstracts/e.pafumi

TALK – Revisiting Pianosa (Italy): how the vegetation of a small Mediterranean island has changed in the last 15 years

Eugenia Siccardi[1], Mariasole Calbi[1], Lorenzo Lazzaro[1], Alice Misuri[1], Bruno Foggi[1], Daniele Viciani[1], Michele Mugnai[1]

[1] University of Florence

The resurvey of historical vegetation plots has become a fundamental methodology in ecological research, providing a unique opportunity to estimate vegetation and environmental change over recent decades. However, conventional techniques such as field surveys are limited in their spatial coverage and lack effectiveness in capturing vegetation change at broader geographical scales. These limitations can be compensated by using satellite data and remote sensing analysis techniques. Here, we propose an approach that integrates ground resurveys of historical data and remote sensing data to assess how vegetation dynamics are influenced by anthropogenic factors, especially land-use change and abandonment of management practices, on Pianosa, a small Mediterranean island. Pianosa island, located in the Tuscan Archipelago (Italy), hosted intense human activity in the form of an agricultural penal colony until the late 1990s when agricultural activities ceased, and the process of land abandonment began. In addition, many conservation measures have been carried out on the island in recent decades, such as the control of alien species or the eradication and restoration of natural habitats. This research aims to evaluate, in this island context, how the different vegetation types present on the island have changed in the last 15 years, both in terms of species and functional composition, and how this change can be interpreted and analysed by remote sensing analysis. The vegetation of Pianosa has been extensively described by Foggi et al (2008), who carried out several vegetation relevés, which were resurveyed in the spring of 2023. The original methodology was followed to revisit a total of 63 georeferenced vegetation plots, ensuring a strong correspondence between the location of the old and new sampling points. Taxonomic and functional turnover was assessed in terms of species and functional traits (leaf area, specific leaf area and plant height) using distance-based ordination techniques. Concurrently, the island's main land cover types were classified utilising a Random Forest model on the two orthophotos of the island closest to the initial and final sampling times. One was captured in 2007 and one in 2023. The accuracy of this categorisation was subsequently determined with an internal validation, and the percentage change in cover of the vegetation types between the 2007 and 2023 data was calculated within a buffer surrounding each plot. The preliminary results show a significant taxonomic compositional shift for all vegetation types considered. The main processes identified as responsible for such changes in species composition are: i) the spread of alien species which colonised and drastically changed the physiognomy of some contexts; ii) a significant encroachment of the grasslands by typical shrub species, with their transition to maquis; iii) a decrease of the abundance of typical rocky cliff species. Changes in the species composition of the vegetation were also identified at the functional level and through remote sensing analysis. These changes are likely attributable to alterations in the vegetation physiognomy.

https://conferenceyoungbotanists.com/abstracts/eugenia.siccardi

TALK – Assessment of heavy metals in soils and their accumulation rates in native plants under anthropogenic and natural pollution in Calabria, Southern Italy

Gilda Perri[1], Ilaria Fuoco[2], Andrea Bloise[1], Carmine Apollaro[1], Mauro Francesco La Russa[1], Giovanni Vespasiano[1], Donatella Barca[1], Domenico Gargano[1]

[1] Department of Biology, Ecology and Earth Sciences, University of Calabria, Via P. Bucci, 87036 Rende (CS), Italy; [2] Department of Biology, Ecology and Earth Sciences, University of Calabria, Via P. Bucci, 87036 Rende (CS) Italy; Institute on Membrane Technology (ITM-CNR), Arcavacata di Rende, CS, Italy

Heavy metals contamination in soils is commonly associated with various sources, both anthropogenic and natural. To mitigate environmental risk in polluted areas, it is crucial to conduct a comprehensive investigation into the origin, type, and concentration of contaminants in soils and in spontaneous plant species in different contexts. In Calabria, there is no data on heavy metal concentrations in soils and plants at dismissed mine sites or on serpentine-derived contamination from serpentine derived-soils. Here, we present the results of quali-quantitative analysis of heavy metals in soils and plants from three distinct locations in the Calabria region: (i) a dismissed arsenopyrite mine site, (ii) a serpentine outcrop, and (iii) an uncontaminated control site, the Botanical Garden of the University of Calabria. We sampled soils and plant materials from a set of spontaneous plant species in common to polluted sites to determine their accumulation rates. Subsequently, we analysed them using ICP-MS. The results showed that concentrations of Co, Cu, As, Cd, and Pb at the mine site, as well as Ni and Cr in the serpentine soil, exceed the legal limits established by Italian law. Among the sampled plants, Asparagus acutifolius, Cistus salviifolius, Dittrichia viscosa, Erica arborea, and Reichardia picroides, collected at the mining site, as well as D. viscosa, A. acutifolius, and E. arborea from the serpentine outcrop, exhibited higher concentrations of various heavy metals compared to the control site. This study provides preliminary information on the capacity of the surveyed species to accumulate heavy metals derived from anthropogenic and natural sources of pollution, thereby offering valuable insights for phytomanagement and the remediation of the contaminated areas.

https://conferenceyoungbotanists.com/abstracts/gilda.perri

TALK – Climate change drives plant compositional changes in alpine snow-bed communities: a 10-year study in the Monte Rosa massif

Ginevra Nota[1], Simone Ravetto Enri[1], Giacomo Marengo[1], Giampiero Lombardi[1], Michele Lonati[1]

[1] Department of Agriculture, Forest and Food Sciences, University of Torino, Largo Paolo Braccini 2, 10095 Grugliasco (TO)

Alpine snow-bed vegetation communities develop in high-elevation (> 2500 m a.s.l.) flat depressions with prolonged snow cover and deep soils rich in organic matter. Long-lasting snowpack protects plant species from freezing damage but also constrains them with a short growing season, leading to the differentiation of snow-bed plant specialists. Climate change is considered an important driver of change for snow-bed communities due to rising air temperatures, earlier snowmelt, and the consequent extension or shift of the growing season. Previous research has shown that most snow-bed species can potentially adapt to such changes, as they have a phenological plasticity able to track snowmelt dates (Crepaz et al. 2024; Quaglia et al. 2020). However, it remains uncertain whether changes in environmental conditions could alter community composition by giving other species a competitive advantage over snow-bed plants. We annually surveyed the botanical composition of seven snow-bed sites (Salicetum herbaceae association) in the Cimalegna plateau (Monte Rosa Massif, NW Italian Alps, 2680-2850 m a.s.l.) over a 10-year period (2015-2024) using the point intercept method on permanent plots. The average temperature and length of the snow-free season during the study period were 5.3 °C and 122 days, respectively, with 2022 showing an anomalous 33-day advancement in the season compared to the average. To investigate the changes in plant composition, the relative abundance of snow-bed, oligotrophic grassland, eutrophic grassland, and scree species (according to their phytosociological optimum), and of individual species were calculated and the trends analyzed with Generalized Linear Mixed Models. Results indicated an overall significant increase in oligotrophic grassland species (+6.9%) and a decline in scree species (-4.2%), while snow-bed and eutrophic grassland species remained stable. Agrostis rupestris was the oligotrophic grassland species showing the highest increase (+3.5%), while Ranunculus glacialis was the scree species declining the most (-1.4%). Noteworthy, the increase in oligotrophic species was more pronounced in the anomalous year 2022, associated with a decrease, although not significant, of snow-bed species. Our findings showed that snow-bed communities are undergoing slow but progressive and directional plant compositional changes towards an increase in grassland species and a reduction of scree species. Such changes likely reflect community response to climate change and more specifically to the advancement and extension of the snow-free growing season. Therefore, we conclude that snow-bed species, despite being able to adapt their phenology to changing environmental conditions, may face competition from grassland species in the long-term.

Crepaz H, Quaglia E, Lombardi G, Lonati M, Rossi M, Ravetto Enri S, Dullinger S, Tappeiner U, Niedrist G. Phenological responses of alpine snowbed communities to advancing snowmelt. Ecology and Evolution 14(7): e11714
Quaglia E, Ravetto Enri S, Perotti E, Probo M, Lombardi G, Lonati M. Alpine tundra species phenology is mostly driven by climate-related variables rather than by photoperiod. Journal of Mountain Science 17(9): 2081-2096

https://conferenceyoungbotanists.com/abstracts/ginevra.nota

Poster – Exploring Morphological Structure and VOC Emissions in Olive Fruits: Potential Interactions with Bactrocera oleae Infestation

Giovanni Spinelli[1], Cosimo Taiti[1], Elisa Masi[1], Luciana Renna[1], Marta Beccaluva[2], Stefano Mancuso[3], Giovanni Stefano[2]

[1] Department of Agricultural, Food, Environmental and Forestry Sciences and Technologies (DAGRI) University of Florence; [2] Department of Biology, University of Florence; [3] Department of Agricultural, Food, Environmental and Forestry Sciences and Technologies (DAGRI) University of Florence, Foundation for the Future of Cities (FFC)

The olive fruit fly (Bactrocera oleae) represents the most significant threat to olive cultivation. Current pest management methods still largely rely on chemical treatments, which are harmful to the environment and subject to increasingly stringent regulations. However, morphological characteristics such as fruit size, firmness, and cuticle thickness play a crucial role in pest resistance. A thicker cuticle may act as a physical barrier against oviposition, while smaller and firmer fruits have been associated with lower infestation rates. Additionally, olive fruits emit volatile organic compounds (VOCs) that influence the behavior of the olive fruit fly, acting as either attractants or repellents. This study aimed to investigate these factors in relation to B. oleae infestation across different olive cultivars and ripening stages, with the goal of promoting sustainable pest control strategies. Four olive cultivars (Arbequina, Canino, Coratina, Nocellara messinese) were analyzed at two ripening stages: early (August) and advanced (November). Samples were collected from the CREA OFA's International Olive World Germplasm Bank, an ideal site for studying the insect's preferences among a diverse range of cultivars. Morphological data and ripening indices were recorded. The degree of infestation by B. oleae was assessed by examining the fruits for insect punctures, categorized into three groups: active, sterile, and dead. Cuticle thickness was evaluated using Nile Red staining, with fruit sections observed under a confocal microscope to obtain data on cuticle thickness and composition. VOCs were analyzed using a Proton Transfer Reaction-Mass Spectrometer (PTR-MS-TOF). Volatile emissions were measured directly from the fruits after simulating insect punctures to identify emission profiles relevant to pest behavior. Larger fruits demonstrated higher levels of infestation but also exhibited a higher proportion of sterile punctures. In contrast, smaller fruits (Arbequina, Canino) showed lower infestation rates. This observation suggests that identifying varieties with small drupes that are nonetheless highly targeted by B. oleae could provide valuable insights into the insect's selection dynamics for oviposition. Nile Red staining revealed that cuticle thickness varies among cultivars and developmental stages. Infested fruits often exhibited thicker cuticles, which likely function as a physical barrier to further infestation, reducing the fruit's vulnerability to injury. The VOC analysis indicated that while the types of VOCs emitted were not distinct among cultivars, there were significant differences in the quantities and distribution of specific compounds. Some substances appeared to be particularly relevant to the insect's behavioral preferences. These results suggest that fruit size, cuticle characteristics, and VOC emissions collectively influence olive susceptibility to B. oleae. Further studies are needed on a broader range of cultivars with comparable drupe sizes and ripening periods to better identify the plant's defense mechanisms.

https://conferenceyoungbotanists.com/abstracts/giovanni.spinelli

TALK – Populations of Lobaria pulmonaria in Contrasting Climates appear Morphologically Similar but Physiologically Different

Giulia Canali[1], Christopher Ellis[2], Paolo Giordani[1]

[1] University of Genoa; [2] Royal Botanic Garden Edinburgh

Lichens form complex symbiotic relationships between a mycobiont, a photobiont, and a pool of microorganisms, enabling them to colonise diverse habitats, including extreme environments. This ecological success reflects a broad evolutionary history and adaptation, alongside various morphological and physiological acclimation strategies. This study investigates the differential responses of two Lobaria pulmonaria populations to identical microclimates. A laboratory experiment simulating acute thermal stress conditions was conducted to assess the species' response. We aimed to observe diverse functional morphology and photosynthetic activity across populations from different macroclimates. Unexpectedly, our findings revealed no statistically significant differences in functional morphological traits. Statistically significant differences were observed for physiological parameters such as water loss rate, faster for thalli from Mediterranean climates and slower for thalli from Oceanic climates. Photosynthetic activity, even though it followed the same trend, was always higher for thalli from Scotland. These responses may reflect the local conditions to which the populations were subjected.

https://conferenceyoungbotanists.com/abstracts/giuliacanali.1992

Poster – Differentiation of ecological niches of Campanula sect. Heterophylla in the Southwestern Alps

Ian Briozzo[1], Chiara Bonifazio[1], Davide Casalino[1], Maria Guerrina[1], Gabriele Casazza[1]

[1] University of Genoa

This study investigates the ecological niche differentiation among several species of the genus Campanula (section Heterophylla), specifically C. sabatia, C. macrorhiza, C. fritschii, C. cochleariifolia, and C. stenocodon, which share similar habitats in the Southwestern Alps. The study aims to examine spatial, climatic, and microenvironmental overlaps among these species to better understand potential competitive dynamics, with a particular focus on C. sabatia, an endemic and vulnerable species listed in Annex II of the Habitats Directive (92/43/EEC). Occurrence data were obtained from the SILENE, LI.BI.OSS., and WIKIPLANTBASE databases, selecting five sites for each species. In each site, three 4 m² plots were installed, and a 100-point contact grid was used to collect microenvironmental data, including rock, gravel, soil, and vegetation cover. Eight uncorrelated bioclimatic variables were analyzed using Kernel-density plots, while climatic niche overlap was calculated using the model proposed by Broennimann et al. (2012). Geographic overlap was evaluated through the convex hull method in QGIS based on distribution data, and microenvironmental overlap was assessed through Principal Component Analysis (PCA). The climatic analysis revealed two main groups: the first, including C. stenocodon and C. cochleariifolia, is characterized by lower temperatures and higher precipitation, while the second, comprising C. sabatia, C. macrorhiza, and C. fritschii, is associated with higher temperatures and lower precipitation. Geographic and climatic overlap showed significant intersections between C. macrorhiza and C. fritschii, C. stenocodon and C. fritschii, and C. cochleariifolia and C. stenocodon. However, despite these overlaps, the PCA revealed significant microenvironmental differences among these pairs of species, highlighting distinct habitat preferences. In conclusion, C. sabatia shows minimal overlap across spatial, climatic, and microenvironmental levels, suggesting a lower risk of interspecific competition. The risk is especially high for C. stenocodon, as its limited distribution falls entirely within the range of C. cochleariifolia, increasing the chance of interspecific crosses and threatening its genetic stability. This highlights the need for conservation actions to prevent hybridization and preserve the genetic diversity of these species in the Southwestern Alps.

https://conferenceyoungbotanists.com/abstracts/ian.briozzo

TALK – Seed Germination Strategies in Salicornia perennans Willd. subsp. perennans: The Role of Salinity, Seed Morphology, and Ecotype

Irene Ventura[1], Mario Fontana[1], Tiziana Lombardi[1]

[1] University of Pisa

Halophytes are natural salt-tolerant plants, which have evolved a variety of physiological and morphological adaptations to survive in saline environments. The mechanisms of salinity tolerance vary among halophyte species but typically include efficient ion regulation, osmotic adjustment, succulence and the sequestration of excess salts in vacuoles to prevent ion toxicity. Halophytes lives and complete their live cycle in habitats, such as salt marshes, inland deserts, salt flats and steppes, where soil are characterized by high sodium chloride content, even higher than seawater. In these habitats, soil surface becomes more saline due to rapid evaporation of water, particularly, during the summer. The success of halophyte populations in these habitats depends on the germination response of seeds, one of the most critical stages in life cycle of halophytes in arid and semi-arid regions. In these regions seed germination usually occurs after the rainy season, which reduced soil salinity surface. Seed germination can be influenced by several factor such as salinity, light, temperature, seed morphotype, but the knowledges about germination of halophytes are still poor. For this work, the germination of Salicornia perennans Willd. subsp. perennans seeds, an annual wild halophyte, was investigated to evaluate the effects of three variables and their interaction on germination parameters: salinity levels, seed morphology, ecotype. Two local ecotypes of S. perennans were selected from salt marshes in Central Italy, Tuscany, and two seed morphotypes—large and small—were separated for the analysis. The experiment exposed seeds to five different salinity levels (0, 88, 176, 350, and 532 mM NaCl), in controlled condition of light and temperature, to assess their impact on germination parameters, including germination percentage (GP), germination index (GI), and time to 50% germination (T50). The results showed that salinity significantly affects the germination percentage of both ecotypes. Higher salinity levels led to a marked decrease in the number of seeds that successfully germinated, according to the literature and the ecological growth conditions of this species. Interestingly, while no significant differences were found in germination rates between the two ecotypes, seed morphology emerged as a critical factor. Larger seeds exhibited a higher germination percentage than smaller seeds, regardless of salt concentration, suggesting that seed size may confer a competitive advantage in germination success under saline stress. These findings align with broader trends observed in other halophyte species, such as Soda inermis Fourr., which also exhibit reduced germination under increasing salinity due to osmotic stress and ion toxicity. The ability of halophytes to tolerate such conditions is an adaptive advantage in saline environments, but extreme salinity levels may still limit germination success. Additionally, these results also demonstrate how seed morphology plays a key role in the germination of this species. the seeds morphology these findings underscore the importance of salinity as a key determinant of germination in S. perennans, while also highlighting the potential influence of seed morphology. Understanding these dynamics is crucial for the conservation and management of saline habitats, as well as for optimizing the cultivation of S. perennans in saline agricultural systems.

https://conferenceyoungbotanists.com/abstracts/i.ventura

TALK – Mount Spundascia's fen: how a microbotanical record sheds light on the last 3000 years of a subalpine landscape's development

Laura Ferigato[1], Giulia Furlanetto[2], Renata Perego[1], Marco Stefano Caccianiga[3], Roberto Comolli[4], Cesare Ravazzi[2]

[1] Laboratory of Palynology and Palaeoecology, CNR-IGAG, Piazza della Scienza 1, 20126, Milano, Italy; [2] Laboratory of Palynology and Palaeoecology, CNR-IGAG, Piazza della Scienza 1, 20126, Milano, Italy; NBFC - National Biodiversity Future Centre (Task 4.4.2 - Dynamic Process Analysis in Protected Areas) Palermo, 90133, Italy; [3] Department of Biosciences, University of Milan, Via G. Celoria 26, I-20133 Milano, Italy; [4] University of Milano-Bicocca, Dept. of Environmental and Earth Sciences, Piazza della Scienza 1, 20126 Milano, Italy

Historical ecology and palaeoecology are essential for understanding the last millennia's vegetation dynamics in relation to environmental changes and human activities, by reconstructing the chain of ecological/anthropogenic events that generated the current vegetation. We analysed co-registered proxies (fossil pollen, charcoal fragments, nutrients), retrieved from a subalpine fen in Valmalenco, Central Alps, to infer the main environmental transformations that led to the current larch-parkland landscape of Mount Spundascia. The primary vegetation was a mixed conifer forest of Pinus cembra, with subordinate Picea abies and Larix decidua. The primary forest was already affected by anthropogenic disturbance in the Final Bronze Age, when fertilized herbs and coprophilous spores indicate the presence pasture activities in the area. Anthropogenic disturbance favoured Larix's expansion. In the Iron and Roman Ages, the forest was exploited for timber and charcoal. The Middle Ages hosted profound environmental changes for the area: from the 11th century the primary forest collapses, gradually substituted by a secondary forest (Pinus mugo, Juniperus). Probably, the primary forest was systematically removed, clearing space for pastures in the area (fertilized herbs' increase) and exploiting charcoal kilns (pollen-slide charcoal's increase), which were found in the study site's surroundings. In the Modern Age, pasture is carried even within the fen, as indicated by high inorganic phosphorus content and coprophilous spores %. Modern pollen spectrum was obtained from moss polsters, revealing the dominance of Pinus mugo's pollen in contemporary vegetation. Though bisaccate pollen grains are notoriously overrepresented, the comparison with the top-core sample, reveals a recent reforestation, led by Pinus mugo and secondly Larix, due to post-WWII abandonment of traditional pasture practices, which are partially still carried in the area.

https://conferenceyoungbotanists.com/abstracts/laura.ferigato

Talk – Morpho-functional characterization of bryophytes from high and low elevation

Leonardo Malvezzi[1], Martina Baccolo[1], Marco Caccianiga[1], Barbara Valle[2]

[1] Department of Biosciences, Università degli Studi di Milano, Milan, Italy; [2] Università degli Studi di Siena, Siena, Italy; NBFC – National Biodiversity Future Center, Palermo, Italy

Functional trait ecology allows to evaluate the ecological characteristics of an organism by analysing a set of parameters: the functional traits. This approach found a significant development also in the field of botany, mainly with respect to terrestrial plants, with the functional application of Grime's CSR model. This allows to conceive a characterization of the functional profile of plant species through the acquisition of few measurements, which can be easily obtained from leaf morphological traits. This method has been successfully applied to vascular plants, including both herbaceous and woody species; in contrast, it has been less or ever applied to non-vascular plants, and to bryophytes in particular. In the present research we selected a set of morphometric parameters with the aim of performing an investigation on mosses through a morpho-functional approach. Our selection of the parameters is partly based on functional traits typically applied to the study of terrestrial plants, adapting them to the morphological structure of mosses. The study includes 11 species sampled in different habitats, from calcareous screes of the Dolomites to low elevation wetlands, including both acrocarpous and pleurocarpous growth forms. The adopted selection of morphometric parameters includes 32 traits obtained through the measurements of different morphological structures, therefore data collecting involved diverse methods. Leaf characters were measured for 10 leaves per species using a light microscope. Stem characters measurements were performed mostly through a digital camera and a stereoscope. Samples' weight was measured at different hydration levels; specific plant area, i.e. the ratio between photosynthetic surface and dry weight, was also measured. Principal Component Analysis (PCA) was conducted on the whole dataset in order to assess the existence of main ecological gradients among the selected species and the effectiveness of variables in describing them. This analysis pointed out two main gradients which revealed a few common trends in the morphometric characters; the first gradient is defined by group of traits which are related to leaf dimensions, while the second one is identified through characters associated with photosynthesising efficiency. These two main gradients are conceptually comparable to those established for terrestrial plants: plant size and leaf economics. The study addressed the effectiveness of a wide variety of morphometric characters, however the number of species which have been taken into consideration is rather limited. Further investigation should focus on excluding the morphometric characters which could result redundant or overly complex, ensuring the acquisition of further measurements from diverse species and habitats, and ultimately allowing to assess morpho-functional responses of bryophytes through more generalized trends.

https://conferenceyoungbotanists.com/abstracts/leonardo.malvezzi

TALK – Photic barriers in a warming world: the crucial role of photoperiod in shaping plant responses to climate change

Martina Tarascio[1], Anna Cazzavillan[2], Lisa Brancaleoni[2], Renato Gerdol[2], Maurizio Cutini[3], Thomas Abeli[1]

[1] University of Pavia; [2] University of Ferrara; [3] Roma Tre University

Photoperiod (the daily duration of light and dark) is a key seasonal signal for plants, influencing physiological and phenological processes such as photosynthetic efficiency, bud burst, flowering, growth cessation, senescence and dormancy. Photoperiod will not change as the climate warms, leading to potential asynchrony in these functionally paired cues. Global mean air temperature increases of up to 4.5 °C are predicted by the year 2100, but even greater warming is projected for middle to high northern latitudes. Despite its importance, there is a lack of extensive literature regarding the role of photoperiod on the response of plant species and communities to the ongoing climate crisis. In this study we reviewed 85 studies addressing the combined effects of photoperiod and climate change on plant distribution, plant traits, plant phenology, plant physiology, evolutionary potential and ecological interactions. Recently, climate change attributable to human influence has been recognized as among the most important contemporary forces driving species' distribution ranges. Our review highlights that plant communities are shifting their ranges northward or to higher elevations in response to climate warming, but photoperiodicity and other non-climatic factors may limit the success of these migrations, as species with highly photoperiod-dependent responses may encounter ”photic” barriers to their movement. Species adapted to different latitudes show variable responses to photoperiod, influencing their migration potential. Different photoperiodic sensitivity of species within a community may alter the competitive ability across species and latitudes in a warmer climate. For example, short-day species that may reach high latitudes through long-distance dispersal events may survive in the new environment but may be unable to flower and reproduce. Changes in flowering time might have negative implications for the survival of these species, as a mismatch between time of flowering and pollinator activity might also occur. Moreover, species that rely on shorter days in autumn for the induction of senescence, might not benefit from improved climatic conditions and a longer growing season at mid latitude. Changes in phenological traits are among the most obvious responses to global warming, yet photoperiod and temperature influence these events in complex ways, with strong variations based on species and latitude. A clear example is represented by the time of bud burst, which represents a compromise between a spring frost avoidance and a sufficiently long growing season. Understanding the role of both photoperiodic and temperature cues on different physiological/phenological traits is therefore crucial to understand how different plant communities and species will be affected by climate change in the near future. This review highlights the importance of disentangling these factors to predict and mitigate the impacts on ecosystems and species as well as underlying the many implications that these have on assisted and natural migrations, the competitive potential of invasive species, agriculture, prediction models, ecosystemic services and biogeochemical cycles.

https://conferenceyoungbotanists.com/abstracts/martina.tarascio

Talk – Floral traits and reproductive ecology of the Mediterranean subendemic orchid Serapias neglecta De Not.

Miriam Bazzicalupo[1], Alex Alberto[2], Maria Guerrina[3], Carla Villa[3], Francesco Saverio Robustelli della Cuna[4], Jacopo Calevo[1]

[1] Royal Botanic Gardens, Kew; [2] Unimont - Universita' degli Studi di Milano; [3] Universita' degli Studi di Genova; [4] Universita' degli Studi di Pavia

Effective conservation strategies require an understanding of a species' reproductive biology to identify intrinsic and ecological factors that influence its persistence. Currently, limited data are available on the biology of Serapias neglecta De Not., a subendemic Mediterranean orchid that is facing local extinctions in Northern Italy and experiencing overall declining trends in Europe. The goal of our work was therefore to collect information on the species' reproductive ecology, investigating which traits could play a role in plant-pollinator interactions, fructification, and seed germination. Field activities were carried out at three sites in Liguria (Italy). We conducted macro- and micro-morphological analyses of the floral tissues; we performed hand-pollination and tested self-compatibility with viability assays and symbiotic germination trials; we investigated the composition of floral VOCs using SFME followed by GC/FID and GC/MS. Seventy-five compounds were identified in the VOC profile, with saturated and unsaturated hydrocarbons dominating the spectrum, including compounds recognized as insect pheromones. Dark spots on the petals, together with the floral tube's depth, mimic the appearance of a bee's nest. Light-reflective elongated trichomes with dome-like protuberances covered the surface of the central labellum. We recorded several classes of secondary metabolites in the floral tissues, including compounds with a putative role in herbivory avoidance. Although we observed accidental autogamy induced by animal visits, no spontaneous self-pollination occurred. Autogamous and geitonogamous pollination led to the production of viable seeds that were able to germinate, but cross-pollination consistently improved seed quality and germination performance. Inbreeding depression was high across all studied populations. We observed no pollination events by hymenopterans during our surveys, but we recorded coleopterans with pollinia on their heads; coleopterans and spiders were seen using the cavity as a resting place or shelter. These findings suggest that S. neglecta mostly relies on pollinators for reproduction and attracts them through a combination of floral traits. The species' declining trends may be linked to a reduced local pollinator population during the flowering period, increased competition from taller grasses, and limited adaptability to changes in habitat management.

https://conferenceyoungbotanists.com/abstracts/m.bazzicalupo

Poster – EXPLORING PATTERNS OF INTRASPECIFIC TRAIT VARIABILITY IN ENDEMIC AND NON-ENDEMIC SPECIES: INSIGHTS FOR CONSERVATION STRATEGIES

Nicola Postiglione[1], Stefano Chelli[1], Giandiego Campetella[1], Roberto Canullo[1], Cristina Gasperini[2], Emmanuele Farris[3], Alfredo Maccioni[3], Francesco Mascia[3], Leonardo Rosati[4], Camilla Wellstein[5], Giacomo Mei[5], Federico Selvi[2]

[1] School of Biosciences and Veterinary Medicine, Plant Diversity and Ecosystems Management Unit, Via Pontoni 5, 62032 Camerino; [2] Department of Agriculture, Food, Environment and Forestry, Applied and Environmental Botany, University of Florence, P.le delle Cascine 28, 50144 Florence, Italy; [3] Department of Chemical, Physical, Mathematical and Natural Sciences, Università degli Studi di Sassari, Via Piandanna 4, 07100 Sassari, Italy; [4] School of Agricultural, Forestry, Food and Environmental Sciences, University of Basilicata, 85100 Potenza, Italy; [5] Faculty of Agricultural, Environmental and Food Sciences, Free University of Bozen-Bolzano, 39100, Bozen, Italy

Most of the plant diversity in temperate forests is found in the understorey, a vital layer for ecosystem functioning that is increasingly threatened by global changes. Conserving understorey diversity and processes is a central objective of the EU biodiversity and forest strategies for 2030. Italian woodlands host a rich endemic flora, comprising 134 taxa, many of which inhabit the understorey. These species are often geographically restricted and highly sensitive to forest management, wildfires and climate change. However, knowledge about their distribution, population dynamics, and ecological roles remains scarce. The FORENDEMICS project aims to investigate the functional traits of endemic forest species to improve ecological understanding and develop effective, targeted conservation strategies. In this study, we employed an innovative trait-based approach to evaluate patterns of intraspecific trait variability in endemic species and their taxonomically closest non-endemic relatives: Crocus etruscus vs. Crocus neglectus, Glechoma sardoa vs. Glechoma hederacea, and Knautia gussonei vs. Knautia drymeia. We sampled four populations of each endemic species across different environmental conditions and compared them with four populations of their non-endemic counterparts. Eleven functional traits were analyzed, spanning above- and below-ground plant compartments: leaf area, leaf mass per area, leaf nitrogen concentration, specific leaf area, flower size, flower mass per area, root nitrogen concentration, specific root length, lateral spread, and bud bank size. These traits capture key strategies related to resource use, sexual reproduction, spatial occupation, and resprouting after disturbance, offering a comprehensive view of species' functional space in relation to their endemic status. Preliminary statistical analyses suggest no consistent patterns in functional trait differences between endemic and non-endemic species. Differences in functional traits appears to occur primarily at the population level, rather than the species level. Environmental factors likely play a more significant role in shaping functional traits, irrespective of endemic status. Further statistical analyses are underway to confirm or refine these initial findings.

https://conferenceyoungbotanists.com/abstracts/nicola.postiglione

POSTER – Understanding the role of bacterial communities associated with the roots of Alnus acuminata: a pathway to improve restoration strategies of degraded lands in Ecuador

Nubia Guzmán[1], Lara A. Quaglini[2], Sarah Caronni[2], Raffaella Ansaloni[3], Rodolfo Gentili[2], Sandra Citterio[2]

[1] Department of Earth and Environmental Sciences, University of Milano-Bicocca, Piazza Della Scienza 1, 20126 Milan, Italy; Azuay Herbarium (HA), University of Azuay, Cuenca, Ecuador; [2] Department of Earth and Environmental Sciences, University of Milano-Bicocca, Piazza Della Scienza 1, 20126 Milan, Italy; [3] Azuay Herbarium (HA), University of Azuay, Cuenca, Ecuador

Land degradation is one of the most concerning issues facing the world today. It is defined as a set of human-induced processes leading to reduction or loss of biological or economic productivity, that result in decreased yields, incomes, food security, and in the loss of vital ecosystem services. Consequently, restoration has become a key strategy to combat land degradation and reverse biodiversity loss. A prerequisite for restoring degraded soils is the identification and proper implementation of suitable technologies. One strategy, to enhance the efficiency of these technologies is to explore plant-microbe interactions. Indeed, the plant symbiotic relationships with bacteria drive key ecosystem processes, lead to a number of benefits such as the promotion of plant growth and the mobilization of nutrients that are not readily available to plants, especially in degraded soils. Alnus acuminata, a native tree of the Ecuadorian Andes, shows great potential like specie to be investigated, due to its remarkable adaptability to various environmental conditions, rapid growth, and ability to colonize disturbed habitats, largely due to its strong association with microorganisms. The aim of this study is to determine the role of bacterial communities associated to the A. acuminata root system in promoting its growth, in order to discover new beneficial microorganisms to be used for an effective restoration of Ecuador degraded lands. Using next-generation sequencing of 16S ribosomal RNA gene amplicons, we investigated the bacterial communities in the bulk soil, rhizosphere and roots-nodules endosphere of A. acuminata growing in a native conserved forest and in a degraded area. The analysis showed that the total number of known bacterial genera in the bulk soil was 357, of which 13 were exclusive to the native forest and 42 to the degraded area. In the rhizosphere, 323 genera were identified, of which 47 were exclusive to the native forest and 19 to the degraded area. Regarding to roots (288 total genera) and nodules (233 total genera), more exclusive bacterial genera were identified in the degraded area, with 116 and 84 respectively, compared to 43 and 62 genera exclusive to the native forest. PCoA analysis revealed a marked difference in bacterial communities between the native forest and the degraded area in the soil-rhizosphere, while endophytic communities exhibited some variation but were not as clearly distinct. Interesting the bacteria community revealed a more abundance of Actinomycetota genera in the degraded areas across bulk soil, rhizosphere and nodule endosphere. It includes strains capable of decomposing recalcitrant organic matter and producing metabolites that promote plant establishment and growth. Additionally, the common presence of the genera Paraburkholderia, Bradyrhizobium and Pseudomonas in the root-nodule endosphere highlights interesting strains for developing microbial consortia for the restoration of degraded high-mountain lands in Ecuador.

https://conferenceyoungbotanists.com/abstracts/naguzman

POSTER – The impact of monoculture tree plantations on biodiversity in the Italian Prealps

Simone Balestra[1], Vanessa Manuzi[1], Erica Ceresa[1], Pietro Gatti[1], Reetta Pirttilahti[1], Gianalberto Losapio[2]

[1] Università degli Studi di Milano; [2] Università degli Studi di Milano; University of Lausanne

Forest ecosystems cover 31% of the global land surface and are subject to a deforestation rate of 13 million ha yr^ (-1). To counteract this trend, several reforestation programs started worldwide. However, these actions raised several problems including the use of non-native species and the poor diversity levels. Furthermore, the long-term effects of reforestation on biodiversity remain poorly documented. Italian history of land management gave us the opportunity to study the long-term effects of reforestation on biodiversity as monocultures of red spruce (Picea abies) were widely planted in northern Italy during the 1920s. We studied the consequences of the spruce plantations on biodiversity of soil fauna and plants. Our focus was on the possible ecological changes triggered by spruce plantations such as soil acidification and canopy cover. We hypothesize spruce monoculture reduces biodiversity at local and regional scales given the non-native range of the spruce and the limestone substrates. We compared plant and soil fauna communities of the spruce monoculture plantations with two other native habitats, including native forests and pastures belonging to two sites in Italian Prealps (Como province). We also measured ecological parameters such as soil properties, ecological indicators, management data and environmental parameters; to extract as much environmental information as possible. We found that spruce monoculture reduces plant diversity in an indirect manner, through the change of environmental conditions such as light input and carbon recycling. We also found a potential negative effect toward arthropod diversity by spruce monoculture, despite our results are still incomplete.

https://conferenceyoungbotanists.com/abstracts/simonebalestra473

TALK – Seasonal dynamics and interspecific variability of photochemical performance in plants from cold-arid Himalayas

Thinles Chondol[1], Xurxo Gago[2], Jaume Flexas[2], Javier Gulías[2], María José Clemente-Moreno[2], Jan Binter[3], Jiří Doležal[1]

[1] Department of Functional Ecology, Institute of Botany, Czech Academy of Sciences, Czech Republic; [2] Research Group on Plant Biology under Mediterranean Conditions, Universität de les Illes Balears (UIB), Ctra. Valldemossa km 7.5, 07122 Palma, Spain; [3] Charles University, Prague, Czech Republic

Plants in extreme environments face heat, cold, resource limitations, and seasonal variations. While they have evolved adaptations to survive, rapid climate change may outpace these adaptations, affecting their performance. Our understanding of how plants in cold-arid regions maintain photochemical performance and net-positive carbon balance is limited, as most studies focus on moist alpine ecosystems. So far existing ecophysiological studies come from lab-grown plants or moist alpine and high-arctic habitats, that do not entirely reflect the conditions of plants from dry and cold high-elevation mountains. This study aims to understand the seasonal dynamics and interspecific variability of the photochemical performance of ten dicot species (310 individuals) from the cold-arid Himalayan region (3100–5300 m asl) measured 4 times throughout the growing season. We used in-situ measured traits and linked them with the seasonal leaf traits. To understand which traits influence plant photochemical performance, we integrated the leaf traits and environmental factors. We expected the photochemical performance to peak during the mid-growing season at the highest elevations, while at the start at the lowest elevations. However, we saw a strong decline in plant performance with the growing season, which is likely because of the fast metabolic activity of young leaves at the start of the growing season. Furthermore, we found significant interspecific variability in resource-use strategies, with seasonal declines in photochemical performance strongly linked to reductions in foliar nutrient content. Our study also revealed the soil moisture to be a crucial factor in determining the plant's photochemical performance however, interspecific differences depending on their adaptive strategies influence if the temperature or soil moisture is limiting. We found that plants from cold moist subnival and alpine habitats are cold-tolerant but limited by soil moisture despite growing in a moist habitat, likely due to the temperature-induced soil freezing during occasional summer snow or sub-zero temperatures. While the plants growing in hot arid steppe and semi-desert habitats are drought-tolerant by having expanded root systems, they are limited by seasonal high temperatures, causing more moisture loss due to evaporative forcing. We infer that unpredictable extreme weather events can cause seasonal stress in plants and influence photochemical performance. These insights contribute to our understanding of plant adaptation strategies in extreme environments and underscore the need for further study into the influence of climate variability on plant functionality in extreme environments.

https://conferenceyoungbotanists.com/abstracts/thinleschondol

TALK – Ecological Characterisation and Invasive Potential of Salpichroa origanifolia in a Meso-hygrophilous Forest Ecosystem

Viola Alessandrini[1], Iduna Arduini[1]

[1] Department of Agriculture, Food and Environment, University of Pisa, 56124 Pisa, Italy

The introduction of invasive alien species represents a significant threat to global biodiversity, altering species interactions and ecosystem processes. Following introduction into a new environment, only 10% of the alien species become invasive. The success of colonisation, stabilisation and subsequent invasive spread is contingent upon a range of factors, including the level of propagule pressure, the functional traits of invasive species, and specific characteristics of the recipient ecosystem. This study explores the invasion process of Salpichroa origanifolia (Lam.) Baill. in the San Bartolomeo Forest (Tuscany, Italy), focusing on the interplay of these three factors. This is the only documented instance of extensive colonisation in an Italian forest. To assess propagule pressure, we documented flowering periods, revealing an extended flowering season (April–October) with a summer regression. Field observations documented consumption of the fruits by birds, foxes and herbivores. We considered vegetative reproduction and light adaptability as functional traits. The species' vegetative reproduction was supported by morphologically distinct rhizomes, collected and classified in different classes. To evaluate light-related functional traits, we measured branch length, leaf area, and biomass under three light conditions in the forest. Results indicated longer branches in high-light environments and larger specific leaf area (SLA) in shade. Anatomical sections revealed shaded leaves exhibiting a less organised anatomical structure. These findings demonstrated a remarkable capacity for adaptation to diverse light conditions through a differentiated allocation of resources. The characteristics of the recipient ecosystem influenced invasion patterns and were defined by vegetation type and abiotic conditions (soil moisture). S. origanifolia was more frequent in Quercus-dominated forests, whereas invasion was reduced in Fraxinus-dominated forests with high soil moisture and undergrowth dominated by Carex spp. The findings demonstrate that S. origanifolia can adapt to diverse light conditions, exhibits high propagule pressure through prolonged flowering, and displays robust vegetative reproduction through a complex system of rhizomes. However, its reduced presence in Fraxinus-dominated forests suggests the influence of abiotic factors (e.g., soil moisture) and biotic competition with large-sized sedges. This highlights the importance of the interplay of the presented factors in shaping invasion dynamics.

https://conferenceyoungbotanists.com/abstracts/viola.alessandrini

POSTER – Combined effect of Hedysarum coronarium-Medicago sativa intercropping on the agronomic parameters of Brassica napus, biodiversity and health soil under water stress

Waad Bousselmi[1], Takwa Gritli[1], Slim ben salah Slim[2], Bacem Mnasri[1]

[1] Laboratory of Legumes, Center of Biotechnology of Borj Cedria (CBBC); [2] Research Unit of-Biodiversity and Resource Development in Mountainous Areas, Higher School of agriculture education of Mateur.

Intercropping with forage legumes offers a wide range of additional benefits, such as significantly higher yields compared to single crops and increased activity and diversity of soil microorganisms. The objective of this study is to investigate the impact of Hedysarum coronarium and Medicago sativa intercropping on the agronomic parameters of Brassica napus and the diversity of soil microorganisms associated with the soil and roots under water stress. To investigate the effect of intercropping Hedysarum coronarium and Medicago sativa on the agronomic parameters of Brassica napus, we conducted during two consecutive years, 2022 and 2023 at the Higher School of agriculture education of Mateur in Bizerte, northwest of Tunisia. Agronomic measurements were taken, including production and growth parameters. To study the diversity of microorganisms, rhizosphere, and root samples of Brassica napus were collected and subjected to sequencing using Illumina MiSeq for a metagenomics approach. At the end of this work, in which we studied the impact of intercropping on the morphological aspect of rapeseed cultivation, we found that: The behavior of Brassica napus intercropping is improved; the growth of Brassica napus is optimized throughout the cycle compared to that obtained in Brassica napus only. This is explained by the fact that Brassica napus can benefit very quickly from an additional source of nitrogen. The optimal condition of the associated Brassica napus in winter output is important to improve grain productivity. Metagenomic analysis showed that the bacterial communities in the roots and rhizosphere of Brassica napus between 2022 and 2023 highlights notable differences and trends. Temporal shifts suggest year-specific environmental factors influencing microbial communities. In conclusion, intercropping is a powerful way to promote a more diversified beneficial bacterial community necessary for rapeseed growth, thus allowing significantly higher yields. Keywords: Intercropping, Brassica napus, Hedysarum coronarium, Medicago sativa. Illumina Miseq.

https://conferenceyoungbotanists.com/abstracts/waadbousselmi4567

TALK – Assessing vegetation changes in coastal dunes: historical plot resurveys in a Mediterranean archipelago

Agnese Denaro[1], Caria Maria Carmela[1], Sperandii Marta Gaia[2], Malavasi Marco[1], Pisanu Stefania[1], Rivieccio Giovanni[1]

[1] Department of Chemical, Physical, Mathematical and Natural Sciences, University of Sassari, Sassari, Italy; [2] Department of Botany and Zoology, Faculty of Science, Masaryk University, Brno, Czech Republic

Mediterranean islands, which are over 10,000, are very important from a biodiversity point of view in term of plant species and vegetation types. They are among the most vulnerable systems particularly along the costal perimeter due to anthropogenic disturbances and global changes. The objective of this study was to monitor dune vegetation dynamics through historical plot resurveys to detect temporal changes in plant communities in the La Maddalena National Park, an archipelago located in the central area of the Mediterranean basin (Sardinia, Italy). In 2023 we conducted a resurvey of six coastal dune sites to monitor vegetation changes and to assess shifts in conservation status. A total of 207 plots, distributed across 40 georeferenced transects encompassing the entire coastal dune systems, were revisited and re-sampled, replicating the methods originally used in 2011. To evaluate the conservation trends, we focused on the dynamics of both characteristic dune species and ruderal (disturbance-adapted) plants, and examined shifts in habitat types. We also analyzed alterations in plant community composition and structure, using dissimilarity indices based on presence/absence and rank-abundance curves. Our findings indicate that over the past 12 years, the coastal dune ecosystems in La Maddalena National Park have undergone significant changes, likely driven by a combination of natural and anthropogenic stressors. This research not only enhances our understanding of vegetation dynamics but also underscores the importance of continuous, long-term monitoring, particularly in vulnerable ecosystems like coastal dunes.

https://conferenceyoungbotanists.com/abstracts/adenaro

TALK – Predicting functional traits of invasive aquatic plants across native and invasive ranges: new advances with DIVE IN MSCA-Global project.

Alice Dalla Vecchia[1], , Roger Mormul[2], Lars L. Iversen[3], Rossano Bolpagni[1]

[1] University of Parma, Department of Chemistry, Life Sciences and Environmental Sustainability, Parma, Italy; [2] Universidade Estadual de Maringá, NUPELIA, Maringá, Brazil; [3] McGill University, Department of Biology, Montreal, Canada

Biodiversity and ecosystems are facing the imperative challenge posed by invasive species responsible for substantial impacts on habitat integrity and ecosystem functioning. Freshwaters are particularly susceptible to invasions, impacting both the functioning and services that these ecosystems provide. Here we present the MSCA-Global DIVE IN project ("Predicting DIVErsity of INvasive aquatic plants") that aims at understanding the mechanisms underlying invasion performance of aquatic plants. With DIVE IN we will determine and predict the spatial range of functional variation of three invasive freshwater plants (Elodea nuttallii, Pistia stratiotes and Trapa natans) in response to environmental conditions. This will be fulfilled in three main steps: description of leaf traits-environment relationships, prediction of trait variation at continental scale, and validation of the observed trends with controlled growth experiments. We will integrate spatial modelling with functional ecology, thereby creating a functional biogeographic framework for studying plant invasions in freshwater systems, thus providing the opportunity to understand functional adaptations across different spatial scales and environmental gradients. Freshwater habitats and invasive aquatic plants do often not follow the consolidated paradigms of terrestrial taxa distribution models, in terms of environmental drivers and realized ecological niches. Therefore, this contribution attempts to highlight gaps and issues of dealing with unique aspects of freshwater ecosystems, by presenting how the DIVE IN project will advance knowledge on the influence of invasive freshwater plants on the functioning of invaded habitats at medium to large scale.

https://conferenceyoungbotanists.com/abstracts/alice.dallavecchia

Talk – The project ACCLIMATE - Acclimation to Climate Change of Lichens in Mountain Alpine Terricolous Environments

Carolina Stringa Basile[1], Matilde Tamburelli[2], Luca di Nuzzo[3], Elisa Beninato[2], Sara Ribotta[2], Andrea Vannini[2], Sergio Favero Longo[4], Elisabetta Bianchi[3], Michele Carbognani[2], Daniele Viciani[3], Alessandro Petraglia[2], Renato Benesperi[3], Paolo Giordani[1]

[1] Dipartimento di Farmacia, Università degli studi di Genova; [2] Dipartimento di Scienze Chimiche, della Vita e della Sostenibilità Ambientale, Università degli studi di Parma; [3] Dipartimento di Biologia, Università degli studi di Firenze; [4] Dipartimento di Scienze della Vita e Biologia dei Sistemi, Università degli Studi di Torino

Climate change significantly impacts the Alps, potentially altering biodiversity and affecting ecosystem functions and services. Species respond to these changes in several ways, including phenotypic acclimation, genetic adaptation, and altitudinal shifts. These responses may be integrated and act at different timescales, with acclimation being observable in the short-medium term. The ACCLIMATE project focuses on testing the acclimation capacity of sensitive species, particularly lichens, to short-term climate changes in alpine ecosystems. Lichens are crucial to alpine environments, sensitive to water availability and temperature changes, making them good indicators of climate change. The project hypothesizes that simulated climate change will reveal significant differences in the acclimation response of lichen species. ACCLIMATE project aims to: develop low-cost technologies for measuring ecophysiological parameters related to the acclimation capacity of species; improve the predictive capacity of process-based models for estimating lichen ecosystem functions by providing measurements of their acclimation to climate change; improve predictive models of the altitudinal shift of species in alpine environments, explicitly considering their physiological acclimation capacity. Manipulative field experiments at the Passo Gavia experimental site (Rhaetian Alps, 2700 m) and laboratory simulations are collecting data on acclimation responses through variation of physiological functional traits, such as photosynthetic efficiency, water content, lichen surface temperature and melanization. These data were obtained by comparing target lichen species under 4 treatments: control (C, no manipulations), warming (W, with Open Top Chambers), drought (D, with Rain-Out Shelters), and warming plus drought (DW, with both ROS and OTC). Ecophysiological data from field and laboratory simulations will be used to parameterize a process-based model to compare current conditions with future climate change scenarios. This model will provide information on the activity period, water retention, and carbon uptake capacity of the examined species. The Gavia experiment will also be integrated with observations of plant, bryophyte and lichen community composition along an altitudinal gradient to relate acclimation capacity to the likelihood of altitudinal shifts in species distribution under future climate scenarios.

https://conferenceyoungbotanists.com/abstracts/carolina.stringabasile

POSTER – Resurveying alpine grasslands in central and southern Apennines

Claudia Zitarelli[1], Maurizio Cutini[1]

[1] Roma Tre University

Alpine ecosystems are considered important hotspots for biodiversity, yet they are among the most susceptible to climate and land-use change and biodiversity loss. Alpine grasslands, in particular, host a complex mosaic of highly specialized communities rich in endemic and rare plants and represent areas of prime conservation value. Changes in structure and composition of ecosystems can severely affect their functioning and the services that they provide, underlining the importance of monitoring ecosystems. Our aim is to track long-term changes in biodiversity and assess environmental change over more than 20 years by resurveying historical vegetation plots originally sampled in some of the most representative summits in central and southern Apennines. Selected plant communities are listed in the Habitats Directive 92/43/EEC as Habitat 6170 (Alpine and subalpine calcareous grasslands) and Habitat 6230* (Species-rich Nardus grasslands, on siliceous substrates in mountain areas and submountain areas in Continental Europe). We will analyze changes in life forms, species richness and diversity. Plant functional traits from dominant species will be measured for a better understanding of plants' ecological strategies. We expect to observe significant changes in community structure and composition and a general decrease in species cover of cold-adapted and specialized species and an upward shift of warm-adapted generalist species, due to the thermophylization process affecting mountain summits.

https://conferenceyoungbotanists.com/abstracts/claudia.zitarelli

POSTER – Leaf trait variability in Mediterranean forest endemics and their divergence from widespread species: a study of 45 taxa and 26 congeneric pairs

Cristina Gasperini[1], Federico Selvi[1], Roberto Canullo[2], Elisa Carrari[1], Stefano Chelli[2], Andrea Coppi[1], Giannantonio Domina[3], Emmannuele Farris[4], Alfredo Maccioni[4], Francesco Mascia[4], Nicola Postiglione[2], Leonardo Rosati[5]

[1] Department of Agriculture, Food, Environment and Forestry, Applied and Environmental Botany, University of Firenze, Firenze, Italy; [2] School of Biosciences and Veterinary Medicine, Plant Diversity and Ecosystem Management Unit, University of Camerino, Camerino, Italy; [3] Department of Agriculture, Food and Forest Sciences, University of Palermo, Palermo, Italy; [4] Department of Chemical, Physical, Mathematical and Natural Sciences, University of Sassari, Sassari, Italy; [5] School of Agricultural, Forest, Food and Environmental Sciences, University of Basilicata, Potenza, Italy

Why endemic species have restricted range size while others, including closely related taxa, have more widespread distribution has been widely discussed, but is still a central issue in ecology and biogeography. Today, it is well established that a variety of historical, ecological, and biological factors can result in a limited dispersal capacity and a restricted distribution range. The Mediterranean flora is especially rich in narrow-ranged endemic species, of which a non-negligible proportion is typical of forest habitats. Recently, Selvi et al. (2023) provided baseline statistics for over 130 forest taxa endemic to Italy, highlighting the currently poor knowledge about their functional characteristics and ecological strategies. Leaf traits play a critical role in plant growth and survival and are essential to understanding the functional space explored by plants in terms of resource use (Wright et al. 2004; Garnier et al. 2015; Niinemets 2020; Niklas et al. 2023). Exploring the functional side of leaves of narrow-ranged endemics can thus provide insights into their resource acquisitive vs. conservative strategies and competitive abilities. In the PRIN project Forendemics context, we focused on key leaf traits in 45 endemic taxa, either herbaceous or woody, sampled across several Italian peninsular and insular regions (one population per species). This allowed us to determine the range of interspecific variability, the position of each taxon within the global leaf economic spectrum as well as their ecological strategies in the CSR scheme. To address the leaf functional divergence to related widespread taxa, we included the trait analysis of 20 congeners of similar forest habitats, resulting in 26 phylogenetically independent contrasts of endemic-non-endemic species pairs. Geographical and environmental variables for each sampled endemic species/population were also accounted for to test their effects on the variation of each trait. Results of these analyses allowed us to advance our understanding of the leaf functional characteristics of narrow-ranged forest endemics, and to test the hypothesis that endemics are mainly characterized by conservative-related traits, such as low SLA and high LDMC, reduced competitive ability and enhanced stress tolerance.

https://conferenceyoungbotanists.com/abstracts/cristina.gasperini

POSTER – The Living Archive: Building a National Seedbank for (threatened) wild plants in the Netherlands based upon scientific principles.

Daan Curwiel[1], Sascha van der Meer[2]

[1] Floron, the Netherlands; [2] Floron

In light of the current biodiversity crisis, which is especially apparent in a strongly urbanised country like the Netherlands, many populations or even entire species have been disappearing from the landscape. Populations have been lost or have become smaller due to processes such as habitat fragmentation and habitat degradation. Resulting in loss of genetic diversity, which in turn can increase the risk of local extinction. To safeguard the standing genetic diversity of populations of wild plant species in the Netherlands a project was launched to collect and store seeds from all indigenous plant species in a National Seedbank. The project, The Living Archive, focusses on collecting and storing seeds of 530 threatened and endangered species which are mentioned on the national Red List (Sparrius et al. 2014). In addition, seeds of other indigenous species are also collected and stored in the National Seedbank. The project started in 2017 and in 2020 two provinces begun professionally collecting seeds of threatened and endangered plant species that are part of their botanical heritage. In 2025 half of all Dutch provinces will be participating in The Living Archive, conserving the genetic diversity of a large number of threatened and endangered wild plant species. To accommodate this project, a procedure for seed collection, processing and storage was created, based on scientific literature. In addition, a collaboration between seed collectors, researchers, local governments and nature conservation agencies was developed to streamline seed collection and processing while also improving communication between the various parties. Harvested seeds are first dried for at least 3 weeks, after which they are cleaned and sorted. Subsequently, half is kept in a humidity controlled refrigerator for germination trials and genetic research and the other half is stored in a different location at -20°C for long term storage. Germination trials have shown that the germination rate of nearly all species did not decline significantly after storage in the humidity controlled refrigerator, for up to six years. Furthermore, seeds from a select number of species have already been used in population reinforcements or reintroduction programmes in the Netherlands, which has shown that these efforts require a long term investment of effort, money and most of all sufficient amounts of seed. Since the start of the project in 2017, seeds of 474 indigenous species, including 276 threatened or endangered species, have been collected in at least one location in the Netherlands. However, a species is only considered completely safeguarded when it has been collected in five different locations on a national level, or three locations on a provincial level, so the work has only just begun.

https://conferenceyoungbotanists.com/abstracts/curwiel

TALK – Reintroduction perspectives for Limonium intermedium (Guss.) Brullo: the only globally “Extinct in the Wild” species of the Italian Flora

Danilo Monari[1], Damiano Trovato[1], Adriana Santanello[1], Francesco Laspina[1], Serena Pannuzzo[1], Martina Salamanca[1], Cristina Blandino[1], Salvatore Cambria[1], Agata Irene Di Paola[1], Antonia Cristaudo[1]

[1] Catania Germplasm Bank, Department of Biological, Geological and Environmental Sciences, University of Catania, Via Empedocle, 58 – Catania, Italy

Limonium intermedium (Guss.) Brullo (Plumbaginaceae) is an endemic chamaephyte originating from Lampedusa (Italy, Sicily), belonging to the L. albidum (Guss.) Pignatti group. It was first discovered in the salty marsh of the south-eastern coast of the island, near the harbour, by the Italian botanist Giovanni Gussone who described it in 1832 as Statice intermedia (1). Subsequently, it was renamed as L. intermedium in 1980 (2). The main population was reported until 1975 by Bartolo et al. (3); later, in 1988, the same Authors stated the destruction of the original habitat due to the construction of the local stadium, with the persistence of only few plants in the surroundings of Vallone Imbriacole. However, in the last Red Lists of Italian Flora it is classified as ”Extinct in the Wild” (EW) (4, 5). As of today, the only existing specimen is preserved in the Botanical Garden of Catania and it was grown by seed samples collected by Salvatore Brullo. The fruits produced by this individual in 2024 were harvested and 81 viable seeds were obtained. A germination protocol was defined, testing different substrates (filter paper moistened with distilled water, 1% and 0.7% agar) and incubating the seeds at 15°C in presence of 12 hours of light. The seedlings were transplanted in cell trays on universal standard soil and the survival rate and growth of the plants was monitored. The aim of this study, conducted at the Seed Bank of the University of Catania, is to develop a protocol for the ex-situ propagation of the species, in order to avert the risk of its extinction. The results obtained, joint with the research of the idoneal habitat on the island of Lampedusa, might lead to a reintroduction project of L. intermedium in its native area. Bibliography 1. Gussone G. (1832). Suppl. Fl. Sicul. Prodr.: 87. 2. Brullo S. (1980). Bot. Not. 133: 283. 3. Bartolo G. et al. (1988). Boll. Acc. Gioenia Sci. Nat. 21: 119-255. 4. Raimondo F. M. et al. (2011). Biogeografia 30: 229-239. 5. Bartolucci, F. et al. (2024). A second update to the checklist of the vascular flora native to Italy. Plant Biosystems, 158(2), 219–296.

https://conferenceyoungbotanists.com/abstracts/danilomonari.2001

Talk – High-resolution species distribution models for two ecologically contrasting, closely related plant species

Domenico Amantea[1], Francesco Cristiano[2], Alessandro Petraglia[2], Domenico Gargano[1]

[1] Department of Biology, Ecology and Earth Sciences, University of Calabria, Via Pietro Bucci, Rende (CS), 87033, Italy; [2] Department of Chemistry, Life Sciences and Environmental Sustainability, University of Parma, Str. dell'Università, Parma (PR), 43121, Italy

Open habitats, such as grasslands, often form complex mosaics, shaped by factors including highly localized ecological conditions, variations in substrates and topography. These settings often express remarkable biodiversity even on very narrow scales; however, these systems are easily threatened by global change components causing fragmentation and disruption of natural systems. High-resolution ecological niche modelling can be crucial in identifying the environmental factors responsible for small-scale patterns of species distribution. Furthermore, these models can be integrated in conservation frameworks for assessing species vulnerability to global change. In this study, we wanted to investigate the ecological niche of two closely related woodrush species, Luzula campestris subsp. campestris and L. calabra (a Calabrian endemism). More specifically, the purpose was to verify the power of high-resolution remote-sensed data in discriminating the spatial envelope of species associated with different environmental conditions (i.e., dry pastures vs. wetlands). To achieve this, we carried out a sampling campaign in Macchia Sacra, a Special Area of Conservation within the Sila National Park (Calabria, Italy) characterized by a complex mosaic of marshlands, wetlands and dry pastures. The sampling process involved the collection of presence records for the two species, as well as vegetation data. For the species distribution models, we used a set of spectral indices derived from Sentinel-2 raw data and UAV-based topographic variables. The analyses on vegetation data confirmed that the two species act as ecological vicariants within the study area. The species distribution models demonstrated high accuracy in distinguishing the niches of the two species, highlighting the potential of RS data for assessing species distribution at high resolutions.

https://conferenceyoungbotanists.com/abstracts/domenico.amantea

TALK – Can 20 year old stored seeds be used for plant translocation? An investigation in the arctic-alpine specialist Viscaria alpina

Fiona White[1], Marco Asnaghi[2], Micol Orengo[2], Thomas Abeli[2], Graziano Rossi[2], Andrea Mondoni[3]

[1] University of Pavia; Free University of Bozen-Bolzano; [2] University of Pavia; [3] University of Pavia; National Biodiversity Future Center (NBFC)

Background The increasing number of threatened plant species requires urgent conservation action. One solution is to translocate plants back to their natural habitat. Many seeds of wild species are stored in dedicated seed banks but there is little information on the suitability of these seeds for plant translocation. There are concerns that stored seeds may produce plants that are not adapted to the current climate. This is especially true in alpine areas where the climate is warming faster than the global average. We used three old (2000 – 2005; 'ancestor') and three recent (2018 – 2020; 'descendant') seed accessions of Viscaria alpina, an artic-alpine specialist, to produce plants which were translocated back to the seed collection site. We monitored plant survival over three years and recorded vegetative, flowering and seed traits. Results Plant survival was high after the third year of translocation (96%) but those producing flowers and the number of flowers per individual decreased. Descendants produced shorter flowering stems than ancestors suggesting plants have evolved to be smaller over 20 years. The number of flowers produced, and the seed mass, number and germination did not differ between ancestors and descendants, indicating these are more conservative traits. Conclusions Plant translocation of an alpine species using old and recently collected seed bank seeds was successful, at least in the short term, demonstrating that seeds at least 20 years old can be used for plant conservation. However, flowering is starting to decline, potentially indicating a reduction in reproductive output. Long-term monitoring is required to determine the success of this translocation. Plants produced from newer seeds were smaller so may have improved drought tolerance, likely in response to the hotter and drier conditions experienced at the study site. Therefore, where possible, we recommend using recently collected seed accessions for plant translocation.

https://conferenceyoungbotanists.com/abstracts/fionajane.white_1

POSTER – REVISITING ELBA ISLAND (ITALY): TAXONOMIC AND FUNCTIONAL VARIATIONS IN THE LAST 20 YEARS

Francesco Ponticelli[1]

[1] Biology department, Universitry of Florence, Italy

Resurveying plant communities is an essential methodology in ecological research. This approach provides a unique perspective to understand how anthropogenic factors, such as land-use changes, the introduction and of invasive alien species, and climate change, have influenced vegetation dynamics. Islands are among the most sensitive and complex ecosystems, where these phenomena have important impacts due to their limited size, high biodiversity, and ecological fragility. Elba Island is the largest island of the Tuscan Archipelago (central Italy), with a long history of mining exploitation followed by increasing tourism pressure, that profoundly shaped its ecosystems. However, in recent decades, a lot of conservation measures have been implemented to protect its natural heritage, including the control and eradication of invasive alien species, and restoration of degraded habitats. Elba also provides an ideal context for analyzing how various vegetation types have evolved over the past 20 years, in terms of floristic and functional composition. The vegetation of Elba has been documented through a series of vegetation surveys carried out in 1992 and 2005, while we have no information on the changes occurred after. The study goal was to evaluate changes in the most relevant vegetation types occurring on Elba Island, such as chestnuts, grasslands, shrublands, dunes and cliffs communities. We revisited fifty-one georeferenced plots in May 2024, recording plant communities replicating the original methodology. This ensured a direct and precise comparison between historical and current surveys. Moreover, we gathered data on three functional traits from databases and calculated taxonomic and functional diversity measures. Finally, we measured between old and new metrics to assess changes in taxonomic and functional composition through time. Preliminary results highlighted changes in the taxonomic composition of chestnuts, grasslands and dune vegetation, while cliffs and shrublands appear to have less significant variations. These changes occurred also from functional point of view, linked to shifts in vegetation structure and physiognomy, as well as adaptations of newly established species in an environment that has undergone ecological modifications. Such changes may be attributed to environmental constraints, including climate change, which acts as a key driver in shaping plant communities composition. These findings provide crucial insights into the ecological transformation processes occurring in insular contexts, where the interplay of natural and anthropogenic factors can generate pronounced effects. Lastly, collected data represents an important knowledge base for managing and conserving natural habitats in this Archipelago, offering valuable guidance for implementing protection and restoration efforts that take ongoing ecological dynamics into account.

https://conferenceyoungbotanists.com/abstracts/francesco.ponticelli

TALK – Effects of global warming on the alpine vegetation of four peaks in the Texel Group, South Tyrol, as part of the GLORIA project

Friederike Westrich[1], Martin Mallaun[1], Brigitta Erschbamer[1], Pau Carnicero[1]

[1] University of Innsbruck

Climate change has a particularly strong impact on alpine vegetation, its distribution and its phenology, as these ecosystems are determined by cold temperatures. Global warming has triggered an increase in species richness at higher elevations, due to upwards migration of less cold-tolerant species. However, this is predicted to set local cryophilic species under extinction debt, due to an increase of competition. To track this trend, the GLORIA monitoring program (Global Observation Research Initiative in Alpine Environments) operates permanent observation plots in 130 study areas worldwide. The study presented here focuses on the GLORIA study area Texel Group (South Tyrol, Central Alps). The study area consists of four monitored summits, ranging from the subalpine to the nival elevation belts. In each summit, four permanent plots and eight sections of the summit area were monitored since 2003, following the standardized protocol of GLORIA. The soil temperature in the four summit aspects is also recorded. Recent comparisons of the monitoring data from 2003, 2011 and 2017 showed that the species number on the three lower summits increased significantly, while the highest summit showed no changes. The data of 2024 revealed a different pattern. The increase in species numbers continues on the two lower summits, but stagnated on the third highest. On the highest summit, Kasererwartl, a rapid increase in species number from eight to 15 occurred over the last seven years. The observed increase in species numbers is significantly correlated with higher annual mean temperatures and warmer winter temperatures. A significant increase of species number was found in all expositions except the northern plots. Kasererwartl showed a significant increase of thermophilic species, and the second highest summit lost the most cryophilic species. In the latter, the new and lost species have a significant difference in the upper elevational distribution range — new species show mostly lower distribution ranges. The significant increase in species with a higher indicator value for temperature and nutrients was found on this summit and also on the highest summit. This data indicates that high summits which have been weakly affected by climate change so far are now experiencing a rapid change in species richness and composition. At the lower summits, a stagnation of species richness or an extinction debt in cryophilic species has not been observed yet.

https://conferenceyoungbotanists.com/abstracts/friederike.westrich

TALK – Inventorying the Tuscan forests for the “Rete Nazionale dei Boschi Vetusti”

Giammarco Dadà[1], Marco Cabrucci[1], Elisa Carrari[1], Federico Selvi[1]

[1] Università degli Studi di Firenze

After the official institution of the “Rete Nazionale dei Boschi Vetusti” (Ministerial Decree 5 April 2023), each administrative Italian region must proceed to the inventory of the forest sites responding to the guidelines and criteria published by the MIPAAF ministry in 2021. Accordingly, the Tuscany Region instituted a research group for the implementation of this task over the regional territory. At present the work has led to the identification of ten forest sites that largely meet the guidelines and criteria, also those given in the official document by the European Commission released in March 2023. This was produced to support the implementation of the EU Biodiversity Strategy 2030, where emphasis is placed on old-growth forests for their strict protection across the EU. Main characteristics requested for the classification as old-growth forest depend on parameters regarding the forest structural characteristics, the presence of native species, the absence of significant human intervention for at least 60 years and a minimum surface of 10 hectares. Among the structural parameters, the presence of large trees (dbh > 50 cm) and habitat trees, either dead or alive, and the amount of dead wood are considered important indicators, as well as the depth of the litter layer. The presence of serial dynamic stages, including forest gaps, and of the different tree regeneration phases are also key elements for a forest to be considered as “old-growth” based on the Ministerial guidelines. Mainly based on field work over the last two years, combined with the study of literature data and historical aspects, our research has led to the identification of 10 forests in Tuscany largely meeting the above requirements, and thus potential candidates for the national network of old-growth forests. These forests are located in both the central-European and the Mediterranean biogeographical regions and include widely different forest types. In this work, we briefly synthetize the methodological steps of the workflow and the characteristics of the ten potential forest sites selected, placing emphasis on plant biodiversity components and Natura2000 habitat types according to the 92/43 EU Directive.

https://conferenceyoungbotanists.com/abstracts/giammarco.dada

TALK – The surprising fungal diversity of biancana badlands

Irene Mazza[1], Elena Salerni[2], Letizia Conti[2], Claudia Perini[3]

[1] Department of Earth and Marine Sciences, University of Palermo, 90123 Palermo, Italy; NBFC, National Biodiversity Future Center, Piazza Marina 61, 90133, Palermo, Italy; Department of Life Science, University of Siena, P. A. Mattioli 4, 53100 Siena, Italy; [2] Department of Life Science, University of Siena, P. A. Mattioli 4, 53100 Siena, Italy; [3] Department of Life Science, University of Siena, P. A. Mattioli 4, 53100 Siena, Italy; NBFC, National Biodiversity Future Center, Piazza Marina 61, 90133, Palermo, Italy

Badlands, somehow meaning “eroded lands difficult to cross”, are multivariate, self-enhancing systems that can be contemplated globally due to its distinctive topography. Among these the Italian badlands, epitomized by calanchi and biancane, are considered a cultural landscape of great interest. The biancane badlands located in the Natura 2000 Network site ”Crete di Camposodo e Crete di Leonina” (Asciano, Tuscany, Italy), part of the well-known “Crete Senesi” complex, are characterized by a series of clay dome reliefs, with whitening color, bare or almost, that arise gently from micropediments. Studied from a geological and botanical point of view, Leonina shows a sparse, mosaiced and dynamic vegetation, plant communities of conservation interest and the protected endemic Artemisia caerulescens subsp. cretacea. The habitats present in the studied area (i.e. pediment, grassland, shrubs, mossy islands), for the first time, have been investigated from a mycological point of view to achieve knowledge about the fungal community, such as presence and diversity of epigeous macromycetes. The study revealed a fungal richness of 180 species, which is surprising compared with the Funga of Tuscan forests. The most represented genus was Conocybe (Bolbitiaceae), 50% of them new entrances for the Sienese Fungarium, often found in the most peculiar habitat of the biancane, the pediment. The most mycodiverse habitat results to be grasslands, followed by pediments. Among the species collected some are of conservation interest such as Hygrocybe mucronella and H. citrinovirens. The latter is an indicator of species-rich semi-natural grasslands and was assessed as “VU” by IUCN due to the loss and degradation of this habitat. The presence of these Hygrocybe species together with Clavaria (3 species), Entoloma (5 species) and Geoglossum (2 species), recognized as environmental quality bioindicators, allow the inclusion of Leonina as an Important Fungus Areas (IFAs). This study on Funga in biancana badlands has added a new aspect to the known Flora, Fauna, geomorphology, and history, from which the uniqueness and fragility of these environments already emerged. This could lead to a wider understanding of the role that whole biodiversity has in the functioning of this vanishing ecosystem and push for conservation action plans.

https://conferenceyoungbotanists.com/abstracts/irene.mazza2

TALK – Past adaptations shape future persistence: climate change responses of orchids in Mediterranean climation regions

Jacopo Calevo[1], Michael F. Fay[1], Kingsley W. Dixon[2], Karl J. Duffy[3]

[1] Royal Botanic Gardens KEW; [2] Curtin University; [3] University of Naples Federico II

Understanding how species respond to ongoing climate change is crucial for their conservation. While extant species have persisted through historical climate cycles and temperature fluctuations, it is not clear how their ranges will be shaped by ongoing rapid rises in mean ambient temperature. We modelled the distributions of 26 Caladenia species native to the Southwest Australian Biodiversity Hotspot. We compared current range extents with past and future climate scenarios using a suite of consensus niche models to assess conservation risks. We also investigated ten species known to hybridize and how ecogeographical isolation will change as a premating barrier in future climates. Under historical warmer climate scenarios (last interglacial period and Holocene climatic optimum) most species had smaller ranges compared with baseline conditions (1970-2000). However, under both moderate and extreme future climate scenarios, only three species experienced range contractions, with the remaining species showing either no range change, or an increase in their range compared with current conditions. In species that hybridize, ecogeographical isolation will potentially increase, thereby acting as a stronger reproductive barrier than under present conditions. As Caladenia species naturally occur in seasonally dry conditions and have evolved in climatically buffered environments already subject to prior epochs of climate change, these results suggest that Caladenia are pre-adapted to survive in elevated temperatures under future climate scenarios. Our model predictions are supported by temperature tolerance experiments on Caladenia huegelii seeds and fungi, long-term demographic studies of key populations, and seasonal fungal metabarcoding data correlated with soil temperature and moisture.

https://conferenceyoungbotanists.com/abstracts/jacopo.calevo

Talk – The vascular flora of Pisa (Tuscany, Italy): towards a citizen science-based monitoring of urban floras

Jacopo Franzoni[1], Brunello Pierini[2], Iduna Arduini[3], Gianni Bedini[1], Stefano Martellos[4], Lorenzo Peruzzi[1]

[1] PLANTSEED Lab, Department of Biology, University of Pisa, 56127 Pisa, Italy; [2] Via Zamenhof 2, 56127 Pisa, Italy; [3] Department of Agriculture, Food and Environment, University of Pisa, 56124 Pisa, Italy; [4] Department of Life Sciences, University of Trieste, 34128 Trieste, Italy

Urban floras are fundamental tools for science-based urbanistic planning, but also starting points for studies concerning the effect of human activities on ecological and evolutionary dynamics in urban environments. Sharing this knowledge with citizens, together with identification tools, may help an active monitoring of urban biotas. Here, we provide the first checklist of vascular plant species occurring in the municipality of Pisa (Tuscany, Italy), by integrating records from previous literature and field observation deposited in the online database Wikiplantbase #Toscana, integrated by observations from iNaturalist. The municipality of Pisa extends for 185.30 km2 within the lower Arno valley, and it encompasses alluvial plains and consolidated sandy dunes near the coasts (the maximum elevation is 4 m a.s.l.) under Mediterranean bioclimatic conditions. Although the landscape of the eastern part of the municipality is deeply anthropized, the western part is included within the Migliarino – San Rossore – Massaciuccoli Regional Park. The established flora (i.e. confirmed native + naturalized and invasive alien taxa) of the municipality of Pisa includes a total of 1,404 specific and subspecific taxa, out of which 112 are alien. Native taxa are +33.3% than predicted from a species-area relationship, whereas alien taxa are +34.9% than expected, attesting for a high floristic richness, but also very high anthropogenic impacts in the territory of Pisa. Among natives, there are taxa of high biogeographical and conservational interest, including 12 species endemic to Italy. For instance, Symphytum tanaicense Steven survives in a small population at the south-western distribution limit of the species range, and it is also listed as Critically endangered in the Red List of the Italian Flora. Interestingly, four taxa reported in the floristic inventory have been described on material originating from the studied area. Among aliens, there are 4 taxa included in the list of invasive alien species of Union concern. The biological and chorological spectra reflect the coexistence of typical Mediterranean and central European habitats in this territory. The vascular flora is quite rich although threatened by anthropic pressures, especially linked to alien invasive species. This inventory will be used in the IDEM FLOS project, which proposes an innovative approach based on citizen science by providing interactive identification tools for a broad public, to discover and monitor the vascular plant species composition in urban areas. Acknowledgements: this work was supported by the Project IDEM FLOS - Funded by the European Union - Next Generation EU — Mission 4, Component 2, Investment 1.4 - CUP H43C22000530001.

https://conferenceyoungbotanists.com/abstracts/jacopo.franzoni

Talk – Forty Years of Change: Assessing Species Dynamics and Conservation Success in Swiss Jura Calcareous Grasslands

Jasmin Lepper[1], Yvonne Willi[1]

[1] University of Basel

Calcareous grasslands are biodiversity hotspots in Europe, yet they have faced dramatic declines due to agricultural intensification, with nearly 95% of extensively managed grasslands lost by the mid-20th century. In the 1990s Switzerland took legal actions in order to protect the unique flora of grassland ecosystems. Despite legal protections established in Switzerland in the 1990s, there is limited knowledge on the effectiveness of these measures in preserving the unique flora of these ecosystems. This study examines long-term vegetation changes in 50 calcareous grassland remnants in the Swiss Jura mountains, utilizing data of former surveys conducted in 1985, 1996, and 2016 to evaluate conservation success and derive recommendations for suitable management of the grassland remnants. By extending the time series with a new survey, we analyse changes in species diversity, the persistence or decline of rare species and shifts in species composition on a local and regional scale and try to link the observed changes to management and landscape structure. Preliminary findings suggest a further decline of habitat specialists and an increase of few dominant generalists. The interplay between landscape structure and management seem to contribute substantially to shifts in species composition and different aspects of diversity that have to be examined further. This research on one hand identifies “winner” and “loser” species of the floristic inventory, on the other hand provides insights into those management practices that support diversity. Our findings will inform sustainable farming and conservation strategies, which are essential for maintaining valuable ecosystems in the face of ongoing environmental pressures. Keywords: biodiversity, conservation, calcareous grassland, time-series analysis

https://conferenceyoungbotanists.com/abstracts/jasmin.lepper

POSTER – MULTI-TAXON MONITORING IN THE STRICT NATURE RESERVE “MONTAGNA DI TORRICCHIO” (ITALY)

Leonardo Salvatori[1], Francesco Chianucci[2], Alessandro Campanaro[3], Alice Lenzi[4], Silvia Gisondi[5], Renato Benesperi[6], Lorenzo Guazzini[6], Luca Di Nuzzo[7], Mirca Zotti; Simone Di Piazza[8]

[1] School of Biosciences and Veterinary Medicine, University of Camerino, Camerino, Italy; [2] CREA - Research Centre for Forestry and Wood, Arezzo, Italy; [3] Council for Agricultural Research and Economics, Research Centre for Plant Protection and Certification, Florence, Italy; [4] Council for Agricultural Research and Economics, Research Centre for Plant Protection and Certification, Florence, Italy; University of Siena, Department of Life Sciences, Siena, Italy; [5] Council for Agricultural Research and Economics, Research Centre for Plant Protection and Certification, Rome, Italy; [6] Department of Biology, University of Florence, Italy; [7] BIOME Lab, Dipartimento di Scienze Biologiche, Geologiche e Ambientali, Alma Mater Studiorum, Università di Bologna, Via Irnerio 42, 40126 Bologna, Italy; [8] Laboratory of Mycology, Department of Earth, Environmental and Life Science, University of Genoa, Genoa, Italy

Global climate changes and the intensification of human activities may threaten biodiversity at various spatial and temporal scales, in turn compromising nature’s contributions to people’s life. Efficient and effective monitoring surveys become pivotal to measure biodiversity changes. We performed a biodiversity investigation applying a multi-taxon approach through the project “Monitoring Integrated Multi-taxon Biodiversity” (MIMTB). We monitored nine plots in the beech forests of the Strict Nature Reserve of ”Montagna di Torricchio” (also part of the International Long Term Ecological Research Network (ILTER)). Sampling lasted from April to October 2024, and we applied standardised protocols for seven taxa: vascular plants, bryophytes, lichens, saproxylic insects, earthworms, soil arthropods, micro- and macro-fungi. We also evaluated the canopy cover and forest structure together with climatic variables such as air humidity and temperature. We aim to: i) infer patterns and drivers of multi-taxon diversity; ii) investigate relationships among the different taxa and between species richness and forest structure; iii) test new approaches and schemes of biodiversity investigations; iv) obtain a checklist of species, also detecting the occurrences of threatened species for conservation purposes.

https://conferenceyoungbotanists.com/abstracts/leonardo.salvatori

Talk – Distribution shift of semi-natural grasslands priority habitats (92/43/EEC) in the European Alps under future climates.

Lucia Doni[1], Geordie Biffoni[1], Gabriele Casazza[1]

[1] University of Genoa

The European Alps are characterised by high environmental heterogeneity and microclimatic diversity which host a great variety of specialised plant species adapt to relatively extreme climates. However, ongoing climatic changes towards warmer temperatures are inducing changes to suitable habitat conditions for biodiversity, with recorded faster rate of change at higher elevations. Consequently, the heterogeneity of alpine habitats is envisioned to be particularly vulnerable to future climatic shift where many species may need to move to follow their suitable climatic conditions. The Alps give home to a variety of priority habitats recognised in the Annex I of the EU Habitat Directive (92/44/EEC) and among those we can find diverse semi-natural grassland habitats known to host a high diversity of plant species and thus play an imperative role in biodiversity conservation. We can expect such habitats, identified as unique for the biodiversity they sustain and of Community Interest, to be affected by increased temperatures due to climate change, and their distribution boundaries to decrease, shift or increase across the Alps. The aim of our study is to predict changes in habitat suitability of five semi-natural grasslands priority habitats, namely 6110*,6210*, 6220*, 6230* and 6240*, by the application of niche-based species distribution models (SDMs). For model predictions, we selected diagnostic plant species for each habitat type of which occurrence data was obtained from GBIF database. We performed principal components analysis to extract the first two axis best explaining species distribution both for 19 environmental variables (CHELSAv.1.2) and six soil variables (SoilGrid) at 1 km resolution. We also included the topographic roughness Index (TPI) to account for topographic heterogeneity. Finally, we used the five variables to run five species distribution modelling techniques (GLM, GBM, ANN, FDA, MARS) to account for model-based uncertainties. Our results show an increased in habitat suitability especially for thermophilous habitats (6210*, 6220*) due to increased temperatures whereas we detected a decreased in habitat suitability for habitats composed by cold tolerant species (6230*). Ultimately, we observed a decrease in habitat suitability for xerophilous habitat (6240*) possibly due to changes in precipitation. However, variations in habitat suitability are not so remarked leading to the assumption that other factors, i.e. advancement of the woods, can greatly affect grasslands.

https://conferenceyoungbotanists.com/abstracts/lucia.doni

TALK – Seed longevity could predicts alpine plant resilience to climate warming

Margherita Tognela[1], Francesco Porro[2], Silvano Lodetti[1], Fiona Jane White[3], Graziano Rossi[4], Veronica Maresca[4], Sergey Rosbakh[5], Andrea Mondoni[6]

[1] University of Pavia, Pavia 27100, Italy.; [2] IGG CNR Pavia, Pavia. Italy; [3] Free University of Bozen-Bolzano, Bozen-Bolzano 39100, Italy; [4] University of Pavia, Pavia 27100, Italy; [5] University of Copenhagen, Copenhagen, Denmark; [6] University of Pavia, Pavia 27100, Italy. National Biodiversity Future Center (NBFC), Palermo 90133, Italy.

Alpine biomes are warming faster than the global average (Auer et al., 2007), altering the physiology, distribution and community composition of alpine plants (Sandvik et al., 2004; Lenoir et al., 2008; Gottfried et al., 2012; Mondoni et al., 2015). Despite this, most existing studies focus more on reporting patterns than on mechanistic explanations of observed changes. In the harsh and highly variable climate of alpine environments, persistence plays an important role in both plant population and community dynamics, allowing plants to withstand or survive unsuitable habitat conditions (Grime, 2002; García & Zamora, 2003; Ozinga et al., 2007). One of the strategies that plants can exploit to persist in situ is to produce long-lived seeds (García & Zamora, 2003; Laiolo & Obeso, 2017). Ecological theory predicts that plants with long-lived seeds should exhibit greater resilience to climate change, but this possibility has not yet been empirically studied. Here, we test the hypothesis that species increasing in abundance tend to produce longer-lived seeds, than species showing a decline. To this end, we used the half-viability period (p50) as a proxy for the seeds' ability to withstand climate-change related stress, estimated through accelerated aging experiments (Newton et al., 2009). Long-term population dynamics were quantified using the non-parametric Cliff's Delta effect size index (Cliff, 1996), calculated from 20 years of plant population monitoring across four Italian target regions of the GLORIA project (Lodetti et al., 2024). The results confirmed our hypothesis, with declining species showing a significantly lower seed longevity, compared to species showing an increase in abundance over the past two decades. These findings provide insights into the mechanisms driving alpine vegetation changes in response to climate warming and enhance predictions of future species composition in montane ecosystems. Furthermore, understanding the role of seed longevity in species persistence can inform conservation strategies, improve vulnerability assessments, and guide restoration efforts in climate-sensitive habitats.

https://conferenceyoungbotanists.com/abstracts/margherita.tognela01

Talk – BioConLobaria: Successful translocations for the conservation of the threatened lichen Lobaria pulmonaria (L.) Hoffm

Marta Agostini[1], Luca Di Nuzzo[2], Renato Benesperi[3], Juri Nascimbene[2], Sonia Ravera[4], Elisabetta Bianchi[3], Patrizia Campisi[4], Alice Delama[3], Silvia Del Vecchio[2], Laura Della Roscia[1], Zuzana Fačkovcová[5], Luana Francesconi[2], Gabriele Gheza[2], Giulia Gualemi[1], Giovanna Pezzi[2], Chiara Rosi[2], Monica Ruffini Castiglione[1], Luigi Sanità di Toppi[1], Luca Paoli[6]

[1] Department of Biology, University of Pisa; [2] Department Biological, Geological, and Environmental Sciences-BiGeA, Alma Mater Studiorum, University of Bologna; [3] Department of Biology, University of Florence; [4] Department of Biological, Chemical and Pharmaceutical Sciences and Technologies, University of Palermo; [5] Department of Pharmacy (DIFAR), University of Genoa; [6] Department of Biology, University of Pisa.

Lobaria pulmonaria (L.) Hoffm is a foliose, broad-lobed macrolichen, also known as the “lung lichen” because of its reticulate upper cortex. The species is distributed in boreal, temperate, mountainous, and oceanic regions of the northern hemisphere, but also in the East and Southern Africa. It prefers old and humid forests with large and mature trees and moderate light intensity, being very sensitive to forest management, environmental pollution and climate change. For such reasons, during the last century L. pulmonaria significantly declined and its conservation may enable to protect other sensitive species and as well as their habitats. BioConLobaria is a conservation project based on lichen translocations and developed along three macro-areas across the Italian Peninsula (Emilia-Romagna, Tuscany and Campania). The main goals are to: 1) evaluate how the season of translocation influences its success and conservation effectiveness, 2) examine the role of population stage in translocation outcomes, 3) assess genetic diversity influence on biodiversity conservation and translocation methods, and 4) explore receptor site suitability to identify factors affecting lichen survival and translocation success. We are simulating seasonal translocations for conservation purposes by transplanting the model species (young and adult fragments of thalli) from control sites into 1) mature, undisturbed oak/chestnut/beech forests and 2) disturbed environments (such as logged sites with isolated trees of the same forest types) during spring, summer, autumn and winter. We are focusing our attention on early and long-term responses, accounting morpho-physiological traits of the lichen, such as growth rates, water holding capacity, photosynthetic performances, chlorophyll contents, and other biochemical assays, before and after the translocation. At the same time, for each experimental condition, we are registering micro-climatic parameters and the hydration of the thalli using data-loggers. The initial results reveal differences in growth rates, water-holding capacity, photosynthetic performances, and chlorophyll content across experimental conditions, influenced by population stage, translocation season, and forest type.

https://conferenceyoungbotanists.com/abstracts/marta.agostini

Talk – Long-term Dynamics of Understory Plant Diversity in Italian Forest Ecosystems: Trends and Drivers

Maura Francioni[1], Simone Di Piazza; Mirca Zotti[2], Anna Andreetta[3], Stefano Carnicelli[4], Francesco Chianucci; Nicola Puletti[5], Zuzana Fačkovcová; Paolo Giordani[6], Alessandro Bricca[7], Martina Pollastrini; Filippo Bussotti[8], Giorgio Brunialti; Luisa Frati[9], Giandiego Campetella[1]

[1] School of Biosciences and Veterinary Medicine, University of Camerino, Via Pontoni 5, 62032, Camerino; [2] Department of Earth, Environment and Life Sciences, University of Genova, Corso Europa 26, 16132, Genova; [3] Department of Chemical and Geological Sciences, University of Cagliari, S.S. 554 bivio per Sestu, 09042, Monserrato, Cagliari; [4] Department of Earth Science, University of Florence, Piazzale delle Cascine 15, 50144, Firenze; [5] CREA, Research Centre for Forestry and Wood, viale Santa Margherita 80, 52100, Arezzo; [6] Department of Pharmacy, University of Genova, Viale Cembrano, 4, 16148, Genova; [7] Faculty of Agricultural, Environmental and Food Sciences, Free University of Bozen-Bolzano, Bolzano, Italy; [8] Department of Agricultural, Food and Environmental Sciences, University of Florence, Piazzale delle Cascine 28, 50144, Florence, Italy; [9] TerraData environmetrics, Italy

Forest ecosystems are widely distributed across Europe and are under threat from global changes. Understory vascular plants represent the predominant component of plant biodiversity and are influenced by multiple factors, including climate, soil characteristics, and canopy structure. Given the variability of environmental factors and the successional dynamics of vegetation, long-term monitoring is crucial for studying changes in plant communities. Species responses often exhibit temporal delays relative to environmental changes. Despite the growing number of studies employing the “resurvey” approach, this method often provides a static representation of communities at two distinct points in time, limiting the ability to comprehensively capture community dynamics. Our study is based on frequent resampling of 31 permanent plots 50m X 50m within the ICP Forests LII network (ConEcoFor), classified into four biomes present in Italy, over a 24-year period (1999–2023). The study aims to assess: (i) temporal trends in plant diversity (alpha and beta) and (ii) the climatic, edaphic, and forest structural drivers of plant diversity. Climate data on daily mean temperature and total precipitation were extracted from the E-OBS dataset provided by the Copernicus Climate Change Service and used to calculate climate indices for the reference period. Soil variables (pH, NH4, SO4, K, NO3) and forest structure parameters (canopy and shrub cover, and defoliation degree) were directly measured in the field. Linear mixed models were employed, with years considered as a “fixed factor” for the first objective, and environmental variables for the second objective. Plots were included as a “random factor”. The analyses revealed a reduction in species richness in nemoral biomes (beech and deciduous oak forests) and the boreal biome (spruce forests), in contrast to the Mediterranean biome (holm oak forests), which showed no significant temporal trends. However, the lack of trends in species richness in the Mediterranean biome conceal a significant species turnover. The parameters influencing species richness include structural variables, soil pH, aridity indices, and precipitation variability, with different roles and importance depending on the biome considered. After many years of data collection, the ICP Forests monitoring sites reveal significant changes in plant diversity across Italian forests. These changes require further exploration from a functional perspective and using a multi-taxon approach.

https://conferenceyoungbotanists.com/abstracts/maura.francioni

Talk – The giant hogweed on the Alps: niche dynamics of a burning invasive alien plant across the alpine region

Raffaele De Matteis[1]

[1] Univeristà degli Studi di Milano-Bicocca

Giant hogweed (Heracleum mantegazzianum Sommier & Levier; Apiaceae) is an invasive plant, native to the Caucasus and introduce to Europe in the 19th century, where it has spread thanks to its adaptive traits and frequent cultivation. It can have negative impacts on ecosystems and even public health, due to severe burnings caused by its toxic sap. Therefore, its management is mandatory in the EU (EU regulation n.1143/2014). Understanding its ecology in Europe should be paramount for such purpose, but studies are few. For example, there is a lack of knowledge for the Alps, an area where H. mantegazzianum is not evenly distributed, with sharp differences going southward and westward. In this study, we investigate the reasons of such differences, to understand if they are mainly due to climatic or environmental limits. We analysed the ecological niche of the species and its dynamics across different sectors: north and south, east and west. A PCA-based method was used to test the differentiation of niches in ecological space, defined by climatic and environmental terms. Niche dynamics across the sectors were described following the COUE framework. The analyses showed differences and shifts southward and westward, mainly regarding climate. Climatic factors explain most variance along the PCs, especially air and soil winter temperatures, together with summer and winter rainfalls. Focusing on climatic niche dynamics between north and south, the niches are mostly stable, but they do not fully overlap, and they are not similar. In the south, the species shifts to conditions absent in the north, with lower annual rainfall and warmer winters. For the dynamics from east to west, the niche stability is low as the alien expands to new conditions westward, with drier, warmer winters. Following the shifts, the analyses indicate that H. mantegazzianum should occupy warmer, drier conditions in south-western Alps. There, the species is less spread than elsewhere on the chain, likely due to unsuitable novel climatic conditions. This may be caused by a lack of sufficiently cold and wet winters, needed to break seed dormancy. Conversely, environmental niche dynamics are highly stable, with irrelevant shifts: the species does not occupy sites with novel soil or land cover characteristics anywhere. Even if they have a marginal role, the variance determined by such factors is mostly explained by urban cover, soil organic carbon and pH. In conclusion, differences in the distribution of H. mantegazzianum across the Alps are mainly due to climate. Even if this analysis would require further small-scale integrations, its results should be considered in the management of the species in the EU.

https://conferenceyoungbotanists.com/abstracts/raffaele.dematteis_1

TALK – Predicting the Future Distribution of Alpine Lichens under Climate Change Scenarios

Sara Ribotta[1], Elisa Beninato[1], Carolina Stringa Basile[2], Luca Di Nuzzo[3], T'Ai Gladys Whittingham Forte[1], Andrea Vannini[1], Alessandro Petraglia[1], Paolo Giordani[2], Renato Benesperi[3], Daniele Viciani[3], Michele Carbognani[1]

[1] Università di Parma; [2] Università di Genova; [3] Università di Firenze

Understanding the impact of climate change on biodiversity is crucial, particularly in alpine ecosystems where lichens serve as key bioindicators. This study focuses on three terricolous lichen species: Cetraria islandica, Nephromopsis nivalis, and Solorina crocea, chosen for their representation of a wide elevational gradient in alpine habitats and their distinct ecological niches. C. islandica thrives in alpine and subalpine zones on nutrient-poor soils. N. nivalis, a characteristic high-elevation species, is predominantly found in extreme alpine environments above the treeline, where it is adapted to dry, snow-covered habitats. S. crocea typically occupies mid-to-high altitudes, favouring moist, shaded areas near snowbeds. Using occurrence data (1980–2024) and bioclimatic variables (1 km resolution), including snow-related metrics (Snow Cover Days, Snow Water Equivalent), we developed species distribution models (SDMs) to project their potential distributions under future climate scenarios (MPI-ESM; SSP126, SSP370, SSP585) for 2011–2040, 2041–2070, and 2071–2100 time periods. Spatial cross-validation and ensemble modelling (GLM, RF, BRT, MDA, FDA) ensured robust predictions, with evaluation metrics including AUC, TSS, and the Boyce Index. Results reveal significant shifts in suitable habitats and species-specific trends in range changes. Notably, C. islandica may exhibit a geographical shift in its climatically suitable areas, N. nivalis could experience habitat fragmentation, and S. crocea might face minor changes in its distribution. Furthermore, N. nivalis appears to be the only species that, under some scenarios, could experience habitat expansion, whereas C. islandica and S. crocea are projected to suffer habitat loss. These findings underscore the urgency of monitoring alpine habitats and implementing targeted conservation strategies. For instance, higher altitude protected areas may become critical for the survival of fragmented N. nivalis populations, while C. islandica may require active interventions, such as assisted migration, to cope with the shifts of suitable areas. Additionally, community-level conservation strategies, considering both vascular plants and cryptogams, will be essential for maintaining existing vegetation diversity in alpine regions. The broader ecological implications of these shifts stress the need for adaptive management strategies that take into account not only species distribution but also the ecosystem services provided by lichens, such as nutrient cycling and soil stabilization. Future work aims to incorporate dispersal dynamics and community-level data to take into account biotic interactions between vascular plants and cryptogams for a comprehensive understanding of vegetation responses to climate change. These insights underline the urgency of conservation strategies tailored to mitigate biodiversity loss in alpine regions.

https://conferenceyoungbotanists.com/abstracts/sara.ribotta

Talk – Farmland ponds as unique ecosystems for plant diversity across diverse pondscapes

Silvia Cannucci[1], Emanuele Fanfarillo[1], Simona Maccherini[1], Gianmaria Bonari[1], Claudia Angiolini[1], Tiberio Fiaschi[2], Emilia Pafumi[1], Francesco Mascia[2], Leopoldo de Simone[2], Rossano Bolpagni[3]

[1] Department of Life Sciences, University of Siena, Via P.A. Mattioli 4, 53100 Siena, Italy. NBFC, National Biodiversity Future Center, 90133 Palermo, Italy; [2] Department of Life Sciences, University of Siena, Via P.A. Mattioli 4, 53100 Siena, Italy; [3] Department of Chemistry, Life Science and Environmental Sustainability, University of Parma, Parco Area delle Scienze 11/a, 43124 Parma, Italy

Wetlands are some of the most vulnerable habitats in the world. Permanent farmland ponds, nestled within heavily human-modified landscapes, are potential elements of naturalness but remain insufficiently studied. This is particularly true for the Mediterranean region where farmland ponds are fundamental in supporting freshwater biodiversity though strongly affected by management practices inducing changes in environmental heterogeneity and consequently of the diversity hosted by ponds. We assessed the plant diversity in response to different pondscape contexts and we defined the spatial scale hosting the higher level of plant biodiversity of farmland ponds in central Italy. We carried out vegetation surveys in 45 farmland ponds located in three areas of Tuscany, along a pondscape agriculturaldisturbance gradient. We found that species richness and composition of plant communities varied along the gradient of disturbance of pondscapes. In the most disturbed pondscape, aquatic plant communities had the lowest species richness, with the highest presence of species well adapted to disturbed environments. Conversely, more natural pondscapes tended to host a higher richness of aquatic species, with helophytes being particularly abundant in the less disturbed pondscape. Although the degree of disturbance of the pondscape significantly affected species richness and composition, the pond identity which contributes to the uniqueness of the ponds and the water-land gradient, had a stronger influence. Our findings suggest that higher plant diversity is hosted at a local scale while at the landscape scale, where greater biodiversity is preserved in ponds located in areas where agricultural activity occurs at a moderate level.

https://conferenceyoungbotanists.com/abstracts/silvia.cannucci2

TALK – Fungi in Multi-Taxon Analysis: the experience of PRIN project MultiForDiv

Silvia Giusto[1], Simone Di Piazza[1], Paolo Giordani[2], Zuzana Fačkovcová[2], Giorgio Brunialti[3], Luisa Frati[3], Stefano Chelli[4], Giandiego Campetella[4], Roberto Canullo[4], Marco Cervellini[4], Maura Francioni[4], Anna Andreetta, Stefano Carnicelli[5], Francesco Chianucci[6], Nicola Puletti[7], Mirca Zotti[7]

[1] Department of Earth, Environment and Life Sciences, University of Genova; [2] Department of Pharmacy, University of Genova; [3] TerraData environmetrics, Spin-off Company of the University of Siena; [4] School of Biosciences and Veterinary Medicine, University of Camerino; [5] Department of Chemical and Geological Sciences, University of Cagliari; [6] Department of Earth Science, University of Florence; [7] CREA, Research Centre for Forestry and Wood

Temperate forests across Europe provide vital ecosystem services, including carbon storage, water regulation, and habitat provision. However, these forests face significant threats due to global changes, such as climate shifts and human-induced disturbances. Biodiversity conservation is a central goal of national and international policies, yet many aspects of forest diversity, particularly those of understorey plants, fungi, included lichenized fungi (or lichens), remain poorly understood. These organisms are crucial for ecosystem functioning and highly sensitive to environmental and anthropogenic pressures on both short, - and long-term scales. The aim of the project is to understand patterns and drivers of multi-taxon forest diversity (lichens, vascular plants, fungi, etc.) of the Italian forests, through the sites belonging to the International Co-operative Programme on Assessment and Monitoring of Air Pollution Effects on Forests LII network. This study focuses on the functional diversity of soil fungi, key players in nutrient cycling and forest resilience. Soil samples from various italian plots were collected and analyzed using dilution plating to quantify and identify fungal strains. Functional traits, such as xerotolerance, thermotolerance, and solubilization of phosphates, were assessed to explore their ecological roles and responses to environmental variables. To understand patterns and drivers of multi-taxon diversity, we integrated data on microclimate conditions, soil properties, forest structural characteristics, and lichenized fungi diversity. This functional approach, which goes beyond traditional species-based indicators, recognizes the diverse ecological roles that different species play. So far, a total of four plots have been sampled, with 1018 colony forming units counted, corresponding to 121 morphotypes. The results aim to provide a more comprehensive understanding of forest biodiversity, supporting conservation strategies and sustainable forest management in the face of global change. This research was carried out within the framework of the PRIN 2022 MultiForDiv Project cod 2022A42HL4.

https://conferenceyoungbotanists.com/abstracts/silvia.giusto

POSTER – The Impacts of Climate Change on Coastal Wetlands in Mediterranean Regions

Silvia Macis[1], Alba CUENA-LOMBRAÑA[1], Michela MARIGNANI[1]

[1] Department of Life and Environmental Sciences, University of Cagliari, Viale S. Ignazio, 13, 09123 Cagliari (CA), Sardinia, Italy

Climate change poses an increasing threat to natural habitats in Mediterranean climate regions, particularly affecting coastal wetlands, whose vulnerability is well documented but still under-researched. Accordingly, although it is recognized that Mediterranean ecosystems such as coastal wetlands are at risk, specific studies on the effects of climate change on their specific ecological dynamics remain limited. To address this gap, we conducted a systematic review of literature gathered from Scopus and Web of Science (WoS), encompassing publications from January 1992 to November 2024. Our analysis aimed at categorizing studies based on climate change factors, environmental impacts, methodological approaches, and geographic scale. From a total of 826 articles initially screened, 70 specifically addressed the effects of climate change on Mediterranean coastal wetlands, with 96.6% focusing on the Mediterranean Basin. Key climate change factors identified included sea level rise (SLR), salinity, increased temperatures, extreme events, altered precipitation, and drought. SLR emerged as the most studied factor, whose impact affects generalized wetland systems, soil, vegetation, and coastal human heritage. Secondly, the effects of salinity, which is closely associated with SLR, were highlighted as significantly influencing plant and animal communities, disrupting freshwater habitats, and degrading soil health. Rising temperatures were mainly correlated with the detriment of biological and physical processes, particularly vegetation and wildlife, while extreme events such as heatwaves, floods, and storms were reported as factors exacerbating damage across ecosystems. Conversely, precipitation and drought received comparatively less attention despite their critical role in shaping wetland hydrology and vegetation responses. The reviewed studies highlighted uneven research efforts, with a predominant focus on specific climate factors and their interactions with generalized wetland systems, often neglecting more targeted assessments of agriculture, soil, and human heritage. Methodologically, these studies employed diverse approaches, including modelling, IPCC scenario analyses, experimental works, and observational research, with scales ranging from local to regional. Our findings underscore the pressing need for integrated management strategies that address the interconnected impacts of SLR and salinity, both of which are exacerbated by rising temperatures and increased evapotranspiration. Such integration is crucial for mitigating cascading effects, including reduced freshwater availability, salt accumulation in soils, eutrophication, and shifts in species composition. Identifying vulnerable species and understanding species-specific adaptations is essential for devising effective conservation strategies. Globally, the concentration of research within the Mediterranean Basin contrasts with the relative paucity of studies on coastal wetlands from other Mediterranean climate regions worldwide. Expanding research to these regions would offer valuable insights into shared vulnerabilities and adaptive responses, enabling a more holistic understanding of global Mediterranean ecosystems. Future research should adopt interdisciplinary approaches to address underexplored issues, particularly the socio-ecological impacts on human heritage, agriculture, soil, and vegetation. Mediterranean coastal wetlands are undergoing profound changes reflecting global climate change patterns. Therefore, considering the expected profound changes to coastal wetlands due to climate change, effective conservation and management should require a comprehensive perspective that integrates multiple climate factors and their cumulative impacts.

https://conferenceyoungbotanists.com/abstracts/silvia.macis2

Talk – Native Seeds for ecological restoration: Improving the seed supply chain with technology, training and Community Engagement

Simone Pedrini[1]

[1] Curtin University

The degradation and destruction of natural habitats, with consequent loss of biodiversity and ecosystem services, is one of the major global challenges of the 21st century. Recently, the UN launched the Decade for Ecosystem Restoration, a global initiative to reverse the current trend of ecosystem degradation. A key component of ecosystem restoration is the use of native seeds. Unfortunately, in Western Australia, as is the case for most regions of the world, native seeds are usually not available in the quantity and diversity required; seed quality is usually unknown, seed price very high (>1,000 $/kg), and successful seed establishment in the field meagre (> 10%). Our research team at Curtin University has been working closely with native seed suppliers and users to tackle the major issues that are currently crippling the local native seed supply chain. We are developing and testing technological solutions with seed suppliers to improve various steps of the seed supply chain, such as cost-effective seed quality testing, seed processing, seed use, and seedling establishment. A crucial element of the project is engagement with local First Nation groups and developing and delivering seed training to upskill and empower Aboriginal rangers to become leaders in the restoration economy.

https://conferenceyoungbotanists.com/abstracts/simone.pedrini

TALK – Micro-scale plant diversity in traditional wood pastures

Thuy Hang Le[1], Stefan Zerbe[2], Adrian Indreica[3], Alessandro Bricca[2], Gabriel Tofan[3], Johann Nikolaus Janssen[4], Gianmaria Bonari[5]

[1] Stefan Zerbe, Adrian Indreica, Alessandro Bricca, Gabriel Tofan, Johann Nikolaus Janssen, Martin Sauerwein, Gianmaria Bonari; [2] Free University of Bozen-Bolzano; [3] Transilvania University of Brasov; [4] Leibniz University Hannover; [5] University of Siena

Wood pastures are characterised by open grasslands with isolated solitary trees. They create diverse micro-environments beneath tree canopies that influence plant communities. However, the impact of micro-environmental gradient variation below tree canopy on plant diversity has not been adequately addressed yet. This research investigates the influence of solitary tree canopies on plant community diversity and composition in Romanian wood-pasture systems. We conducted stratified random sampling at 30 sites in Transylvania, involving 360 plots along a micro-gradient of tree canopy projections—from under to outside—as a proxy for varying shadow conditions. Data on solitary tree structures, species cover, plant traits and ecological variables were collected. We found distinct shifts in vascular plant community composition along micro-environmental gradients from under the canopy to outside areas, primarily due to changes in light availability and nutrient conditions. Decreasing light availability reduces species and functional diversity in line with the filtering effect of canopy cover. Lastly, the establishment of seedlings of woody species under the canopy projection suggested a reduction of competition with grassland species and a facilitation process exerted by adult trees. Solitary trees play a crucial role in creating favourable conditions for shade-tolerant and woody species within wood pastures. Our findings underscore the importance of solitary trees in promoting different plant communities at a micro-environmental gradient. We suggest the application of patchy management of wood pastures with scattered maintenance of woody species and simultaneous cutting of shrubs at places to prevent succession in case of abandonment.

https://conferenceyoungbotanists.com/abstracts/thuyhang.le

POSTER – Tree Monoculture Plantations Decrease Plant Diversity in the Italian Prealps

Vanessa Manuzi[1], Simone Balestra[1], Pietro Gatti[1], Gianalberto Losapio[2]

[1] Department of Biosciences, University of Milan; [2] Department of Biosciences, University of Milan and Institute of Earth Surface Dynamics, Faculty of Geoscience and Environment, University of Lausanne.

On one hand, afforestation and reforestation can contribute to mitigate climate change impacts via carbon sequestration. On the other hand, these actions can also have counteractive effects on ecological systems by negatively affecting biodiversity. However, the long term consequences of afforestation and reforestation for biodiversity are poorly understood. We address the long-term, centennial impact of afforestation and reforestation policies dated 1920s in Italian Prealps. Afforestation and reforestation actions were implemented with tree monoculture of spruce (Picea abies). We conducted a comparative study examining plant community composition and functional diversity along with environmental factors (i.e., luminosity and ground surface temperature) among spruce monoculture plantations, native deciduous mixed forests, and pastures. Our results reveal the long-lasting impact of afforestation and reforestation on biodiversity. Spruce monoculture plantation decreases plant species richness by 39 % and 56 % as compared to native mixed forest and pasture, respectively. Likewise, the diversity of plant functional forms decreases in spruce plantation as compared to mixed forests and pastures. Although luminosity and ground surface temperature do not vary from mixed forests to spruce plantations while they substantially change in pastures, we found a positive relationship between plant diversity and these two environmental factors. Our research provides novel evidence that tree monoculture plantations negatively impact biodiversity still one hundred years after reforestation. As biodiversity loss and climate change are two interwoven processes, they must not be treated separately. Solution: For what concerns future afforestation and reforestation programs, we recommend that they include biodiversity-driven actions and address win–win solutions, for their effectiveness in climate change mitigation would otherwise be compromised.

https://conferenceyoungbotanists.com/abstracts/vanessa.manuzi

POSTER – CAROLINA PROJECT: PRELIMINARY RESULTS OF TAXONOMIC AND FUNCTIONAL PLANT DIVERSITY

Virginia Amanda Volanti[1], Eugenia Siccardi[2], Andrea Coppi[2], Andrea Scartazza[3], Eleonora Peruzzi[3], Maurizio Sarti[4], Francesca Bretzel[3], Serena Doni[3], Leonardo Latilla[5], Michele Mattioni[6], Birhane Gebrehiwot Tesfamariam[6], Olga Gavrichkova[6], Lorenzo Lazzaro[2]

[1] University of Florence, Firenze, Italy;; [2] University of Florence, Firenze, Italy; [3] Istituto di Ricerca sugli Ecosistemi Terrestri, Consiglio Nazionale delle Ricerche, Pisa, Italy; [4] Istituto di Ricerca sugli Ecosistemi Terrestri, Consiglio Nazionale delle Ricerche, Porano, Italy; [5] 4Istituto di Ricerca sugli Ecosistemi Terrestri, Consiglio Nazionale delle Ricerche, Montelibretti, Italy.; [6] Istituto di Ricerca sugli Ecosistemi Terrestri, Consiglio Nazionale delle Ricerche, Porano, Italia

Grasslands represent species-rich plant communities in Europe and their loss is one of the primary causes of terrestrial biodiversity depletion in the Mediterranean Basin. In Italy the abandonment of agro-pastoral activities has an important role in this process, leading to the wood encroachment and loss of grasslands cover. Furthermore, one hypothesis is that grazing makes the system climate-resilient by diversifying the ecological niches. The project CAROLINA (ClimAte Resilience Over Landuse change In semi-Natural grAsslands) aims to explore the potentiality of the grassland's extensive management under different climate conditions in terms of biodiversity conservation and C sequestration and to examine changes in ecosystem resilience to climate change with land-use variation. The study took place in 3 sites located in different climatic zones of Italy: alpine pastures with moist cool climate (Pieve Tesino, TN), Mountain-Mediterranean pastures (San Rossore, Massaciuccoli, PI) and Mediterranean pastures with warm and dry climate (San Venanzo, Orvieto, TR). The project foresees a double approach used to evaluate the impact of grazing abandonment and climate change: a manipulation experiment and a chronosequence approach. During 2024, portions of grasslands in San Rossore and San Venanzo sites have been excluded from grazing through the installation of fences and portions of these areas are object of climate manipulation with structures that lead to a reduction of precipitation, to simulate the future climate trends. Between May and June 2024, we conducted the first floristic vegetation surveys and measurements of functional traits in the areas subject to climate manipulation in San Rossore and San Venanzo and in the chronosequence areas in Pieve Tesino. The preliminary analyses carried out concern taxonomic and functional diversity. Species richness is significantly higher at San Venanzo and there is no significant difference between the 3 manipulative layers, exclusion of grazing and reduction of rainfall, exclusion of grazing and control, in terms of diversity. The analysis of functional indices shows that functional richness has similar values in the same treatments of different sites. Other indices such as Rao's quadratic entropy, functional divergence, functional dispersion are significantly higher in San Rossore. At Pieve Tesino, the plant community in the chronosequence corresponding to pasture and the first stages of wood encroachment is typical of grasslands. Species richness is similar among these 3 stages, then drops in wood areas, where we observed a shift towards typical understory communities. Functional diversity reflects the taxonomic trend, but it was not possible to fully complete the surveys this year, so the analyses obtained are preliminary and will be finalised during the second year of the project. The data collected and analyses carried out in the year 2024 are at the zero point and need to be supplemented and compared with surveys and measurements of functional traits that will take place in 2025.

https://conferenceyoungbotanists.com/abstracts/virginiaamanda.volanti

POSTER – Marsh gladiolus flowers prefer to bloom in forests rather than in meadows - Reproductive characteristics of forest and meadow populations in Hungary

Vivien Lábadi[1], Sándor Csete[2], Bálint Pacsai[1], Judit Bódis[2]

[1] Hungarian University of Agriculture and Life Sciences, Institute for Wildlife Management and Nature Conservation AND Hungarian University of Agriculture and Life Sciences, Festetics Doctoral School;
[2] Hungarian University of Agriculture and Life Sciences, Institute for Wildlife Management and Nature Conservation

The endangered status of the marsh gladiolus (Gladiolus palustris Gaud.) is reflected in its status as a species of Community interest (EU Habitats Directive). Although it has been on the European Red List since 2011 (as Data Deficient), its populations tend to decline. Although significant part of the global population is located in Hungary, few information have been published on these populations yet. The original habitats of the species may have been open forests but nowadays the largest Hungarian populations are found in secondary meadows. For species that reproduce by seed, as Gladiolus does, understanding their reproductive characteristics is essential to determine the viability of a population. Our studies focused on the differences in reproductive characteristics between the meadow and forest populations of Gladiolus palustris. We selected sample sites in that three regions where the species occurs, both in meadows and forests in 2024: in Balaton-felvidék and in North Kiskunság one-one meadow and one-one open forest population; in South Kiskunság three meadow populations. We recorded the proportion of vegetative and reproductive individuals in 1x1 m random quadrats, and some characteristics of flowering individuals randomly selected in the populations: plant height, number of flowers, number of fruits. The results showed that the proportion of flowering individuals varied in the populations studied. It was higher in forest populations (66–73%) than in meadow populations (27–62%). The height of flowering individuals was larger in more closed habitats. Within the forest populations there was a statistically confirmed difference in mean height between the Balaton-felvidék (69.20 ± 9.92 cm) and the North Kiskunság (60.82 cm ± 11.43) populations. There was no significant difference in mean height between the three meadow populations of the South Kiskunság region. Both the average number of flowers and the fruit set of individuals were found to be significantly dependent on the habitat (meadow or forest) and also on population. In the meadow populations of South Kiskunság the average lower individuals produced on average fewer flowers (2.40–4.00). This was inversely related to the reproductive success (58%–70%), where the average fruit set was also highest. The average number of flowers was higher in the forest populations (4.60–5.90), however the fruit set was lower (21%–54%). In the meadows of Balaton-felvidék and North Kiskunság, the mean height and the mean number of flowers of the replicates are in between. To summarise the reproductive success of Gladiolus palustris, the meadow populations of South Kiskunság had the highest fruit set, but the average number of flowers was lower. On the other hand, in the forest population of Balaton-felvidék the average number of flowers was higher and the fruit set was also relatively high. Unfortunately, only two forest populations remain in Hungary, and one in which the number of individuals is critically low. In the case of Gladiolus palustris, forest habitat loss may be a serious limiting factor, but the species quite successfully adapted to meadow habitats, allowing it to survive.

https://conferenceyoungbotanists.com/abstracts/vivilabadi98

POSTER – PHOTOSYNTHETIC PHENOTYPE OF TWO CICHORIUM INTYBUS L. CULTIVARS: THYLAKOID ULTRASTRUCTURE, PHOTOCHEMISTRY AND CARBON ISOTOPIC ANALYSIS

Angela Martina[1], Matteo BALLESTRIERO[1], Elena MARROCCHINO[1], Lorenzo FERRONI[1]

[1] Department of Environmental and Prevention Sciences, University of Ferrara, Ferrara, Italy

Red chicory (Cichorium intybus L., Asteraceae) is an important winter crop widely cultivated in Northern Italy. The Chioggia Precoce and Treviso Precoce varieties are the most common chicories grown along the eastern coast of Emilia Romagna. These cultivars, shaped through empiric selection methods, show notable differences in the shoot morphology, including leaf orientation, suggesting the selection of distinct morpho-functional photosynthetic phenotypes. To investigate this hypothesis, a combination of chloroplast ultrastructure analysis, chlorophyll a fluorescence measurements, and δ13C isotopic ratio analysis was performed. The research was conducted on plants grown in neighboring fields along the Ferrara coast, with samples collected between December 2023 and January 2024. Chloroplast shape and thylakoid organization were different between the two varieties. In Chioggia, chloroplasts were generally elliptical with a well-organized thylakoid system; in Treviso, they were more globular with highly variable thylakoid architectures, even within the same cell, including elongated single thylakoids, grana of varying sizes, and distinctive ”thylakoid circles”. While the two cultivars did not differ with respect to the thylakoid appression degree, Treviso had grana with a wider stacking repeat distance (SRD) than Chioggia. Chioggia, on the other hand, displayed greater granum cross-sectional irregularity (GSI), reflecting a tendency for thylakoid disks to slide laterally (Mazur et al. 2021). Photochemical parameters, measured in the field with Handy-PEA and MultispeQ devices, indicated a lower efficiency in Treviso than Chioggia. However, interestingly, δ13C isotopic analyses of roots, stems, and leaves showed similar or slightly more favorable values in Treviso (More et al., 2022). In conclusion, the photosynthetic phenotyping of Treviso and Chioggia chicory likely reflects specific adaptations developed during the varietal selection process (Barcaccia et al., 2016). Whether these adaptations are linked to the special characteristics of the coastal environment will be assessed in comparative studies with similar varieties from other regions.

https://conferenceyoungbotanists.com/abstracts/mrtngl1

TALK – Living on the edge: How Lunularia cruciata thrives on polluted mining waste

Antonio De Agostini[1], Pierluigi Cortis[1], Francesco Saverio Robustelli della Cuna[2], Francesca Soddu[3], Cristina Sottani[2], Dario Nicola Tangredi[4], Francesco Guarino[4], Annalena Cogoni[1], Andrea Vacca[5], Cinzia Sanna[1]

[1] Department of Life and Environmental Sciences, University of Cagliari, Cagliari, Italy; [2] Environmental Research Center, Istituti Clinici Scientifici Maugeri IRCCS, Pavia, Italy; [3] Neuroimmunology Laboratory, IRCCS Mondino Foundation, Pavia, Italy; [4] Department of Chemistry and Biology "A. Zambelli", University of Salerno, Fisciano, Italy; NBFC National Biodiversity Future Center, Palermo, Italy; [5] Department of Chemical and Geological Sciences, University of Cagliari, Monserrato, Italy

The tailings dump of Barraxiutta (Sardinia, Italy) is heavily contaminated by heavy metals leading to minimal plant colonization. However, wild populations of the liverwort Lunularia cruciata (L.) Dum. thrive on these polluted soils. This study investigates the mechanisms underlying the presence of L. cruciata in this extreme habitat by comparing the contaminated population with a control population from a pristine environment. Analyses focused on: (i) pollutant content, assessed through ICP–OES of acid-digested plant tissues; (ii) photochemical efficiency, evaluated using the Normalized Difference Vegetation Index (NDVI) and chlorophyll fluorescence assays; and (iii) the profile of biogenic volatile organic compounds (BVOCs), characterized via GC-MS analysis of thalli extracts obtained by steam distillation followed by the separation of the organic and aqueous phases through diethyl ether extraction. The results confirmed significant contamination in L. cruciata growing on polluted soils by Fe, Al, Zn, Pb, Cu, and Cd. Despite this, photosynthesis remained remarkably efficient. NDVI measurements showed no significant differences in photosynthetically active light absorption between control and contaminated populations, indicating that the absorbed light was effectively utilized in photosynthesis. Chlorophyll fluorescence assays further revealed that, while heavy metals negatively affected the PSII antenna complex, the maximum quantum yield of PSII (Fv/Fm) remained stable and comparable to controls. This indicates that the chloroplast membranes in contaminated L. cruciata remain intact and fully functional, allowing the plant to maintain photosynthesis at levels considered optimal for bryophytes. Concerning the possible explanation for a perfectly preserved photosynthetic machinery in such a harsh habitat, this could be found in the sesquiterpene fraction being more than doubled in contaminated L. cruciata and by the positive correlation of total sesquiterpenes with increasing concentration of Cu, Fe, Pb and Zn in contaminated L. cruciata thalli. Sesquiterpenes are volatile isoprenoids (VIs) which are known for playing a crucial role in stress resistance in plants facing high light, extreme temperature, drought, oxidizing atmosphere, and heavy metals (Vickers et al., 2009). In this case, increased sesquiterpenes may stabilize cellular membranes and prevent oxidative damage thanks to their antioxidant properties, both adverse effects linked to heavy metal toxicity in plants. In the present contribution a role of VIs, particularly sesquiterpenes, is proposed in the mitigation of the adverse effects of heavy metals in bryophytes. Such an adaptive strategy might be related to the inherent ability of liverworts to synthesize and store a great variety of protective VIs. In conclusion, within this study new knowledge was gained on the role of VIs in non-vascular plants copying with adverse environmental conditions and environmental pollution. Vickers, C., Gershenzon, J., Lerdau, M. Loreto, F. A unified mechanism of action for volatile isoprenoids in plant abiotic stress. Nature Chemical Biology 5, 283–291 (2009).

https://conferenceyoungbotanists.com/abstracts/antonio.dea

TALK – Pathogenic susceptibility in microplastic-exposed crops: the case of Solanum lycopersicum var San Marzano nano

Beatrice Chiavacci[1], Ivan Baccelli[2], Sihem Fodil[2], Cristina Gonnelli[1], Ilaria Colzi[1]

[1] Department of Biology, University of Florence, Florence, Italy; [2] Institute for Sustainable Plant Protection, National Research Council, Sesto Fiorentino, Italy

Plastic has become a pervasive presence in our daily life; used in all industrial sectors and commercialized in the most diverse forms, its production rates are growing year by year. Due to this, the dispersion of this material in the environment becomes inevitable and its exposure to physical, chemical and biological processes leads to micro- and nano-plastics formation (MPs, particles diameter < 5 mm and $\leq$ 100 nm, respectively). The harmfulness of these polymers depends on the particle size with the smaller as the more toxic. Despite the recent increasing attention on the fate of MPs in the soil-plant system, the effect that their accumulation in the soil generates on disease resistance mechanisms of plants has never been investigated. Since agriculture is moving towards sustainability targets, it appears impelling to understand how soil pollution with MPs may affect the plant innate immune system. Enhanced pathogen susceptibility, for instance, would have consequences in terms of crop losses and increased use of plant protection products. The project “MINACROP - The dark side of MIcro- and NAno-plastics in the soil: impact on CROP physiology and pathogen resistance” (PRIN2022) aims at filling this gap by investigating at the physiological and phytopathological level the effects of MPs on the model crop species Solanum lycopersicum var. San Marzano Nano. To address this issue, two of the most widely dispersed plastic polymers in the environment and in agricultural soils, polyvinyl chloride (PVC) and polyethylene terephthalate (PET), were chosen, based on the ecologically realistic MPs levels found in these areas. Plant seedlings were exposed to three different MPs concentrations (0.5, 1.0 and 1.5 % w/w , size range 40-50 μm) and grown in pots for 14 days under controlled conditions. At the end of the treatment period, before harvesting, photosynthetic efficiency and pigment content analysis were performed. Then, plants were sampled and biometric traits and elemental composition were evaluated. The effects of MPs contamination on the susceptibility of S. lycopersicum to two different pathogens (Botrytis cinerea and Pseudomonas syringae pv tomato DC3000) were evaluated after infection. MPs-exposed plants showed a higher fresh and dry weight, even though not significantly. Photosynthetic efficiency was not considerably altered after 14 days, except for the minimal chlorophyll fluorescence parameter, consistently with a relevant MPs dose-dependent reduction of chlorophyll and flavonoid levels observed in all the plastic treatments. Despite the short exposure period, all MPs concentrations impacted on the ionomic profile of plant shoots. Interestingly, plants treated with higher MPs concentrations exhibited a significant increased P. syringae cell growth in infected leaves, while B. cinerea induced larger lesion diameter only in PET treated samples. The obtained results indicate that soil contamination with MPs has negative impacts on the disease resistance against S. lycopersicum pathogens. Despite the lack of detectable adverse effects on plant growth, the alterations that MPs induced in the plant physiology resulted in a higher susceptibility to pathogens infections which may have a negative impact on tomato crop health, productivity and quality.

https://conferenceyoungbotanists.com/abstracts/beatrice.chiavacci

Talk – Effects of acoustic vibration on Olea europaea cv "Leccino"

Bruno Bighignoli[1], Giulia Mozzo[1], Marta Beccaluva[2], Giovanni Stefano[2], Luciana Renna[1], Riccardo Mori[3], Elisa Masi[1], Cosimo Taiti[1], Stefano Mancuso[3], Diego Comparini[1]

[1] Department of Agriculture, Food, Environment and Forestry (DAGRI), Università degli Studi di Firenze, Viale delle Idee 30, Sesto Fiorentino (FI), Italy; [2] Department of Biology, Università degli Studi di Firenze, Via Micheli 3, 50121, Florence, Italy; [3] Department of Agriculture, Food, Environment and Forestry (DAGRI), Università degli Studi di Firenze, Viale delle Idee 30, Sesto Fiorentino (FI), Italy; Fondazione per il Futuro delle Città (FFC), Via delle Cascine 35, 50144, Florence, Italy

In recent years, the study of the effects of mechanical vibration treatments on plants has attracted increasing interest. Acoustic vibrations have been observed to trigger various plant morphological traits as well as numerous physiological and genetic responses. Although it is still unclear how plants perceive and transduce these stimuli, many studies report their sensitivity to different vibrations including recordings of natural sounds (e.g., running water, insect chewing) and artificial sounds as mono-frequency stimulation. To date, the vast majority of these studies have been conducted on horticultural or herbaceous plants, usually over short periods, while research on arboricultural trees has been very limited due to several factors, mainly for the long-life cycle and their woody tissues. In this work, we investigated the effects of low-frequency (120 Hz) acoustic vibrations on the tree Olea europaea L. cv "Leccino" over a six-month period. Our results showed that plant morphology, gas exchange, and leaf structures were affected by the vibrations. Plants subjected to vibration exhibited lower levels of photosynthetic activity and stomatal conductance than the control group. Furthermore, vibration-exposed plants showed a thickening of the upper and lower cuticles at the leaf level, distortion of the cells composing the palisade layer, and a decrease in chlorophyll levels within the mesophyll compared to the control group. These findings demonstrate that vibrations can modulate plant morphology and physiology, highlighting the need for further studies to understand the mechanisms behind these changes at the signalling and molecular level. Additionally, further research is required to determine whether these leaf-level modifications influence infield plant resistance to abiotic and biotic stresses. Adopting preventive control strategies such as this could contribute to the development of more sustainable agricultural practices, reducing the need for chemical treatments and external inputs.

https://conferenceyoungbotanists.com/abstracts/bruno.bighignoli

POSTER – Challenged (by) parasites: Acclimation kinetics of a plant-plant-pathosystem

Charline Gennat[1], Susann Wicke[1]

[1] Organismal Plant Interactions Group, Westfälische Wilhelms-Universität Münster, Institute for Evolution und Biodiversity, Münster, Germany

Plants are constantly exposed to diverse biotic and abiotic stresses, which vary in both duration and intensity. To survive, they have developed sophisticated acclimation mechanisms that involve changes in gene expression, metabolism, and physiology. While much research has focused on single stressors, plants in natural environments often encounter multiple simultaneous stresses, resulting in interactions that can either amplify or mitigate their overall impact on plant survival and adaptation. This study investigates the effects of combined stresses on Arabidopsis thaliana, integrating abiotic stresses (cold, heat, and high light) with biotic stress caused by parasitism from the holoparasitic plant Phelipanche ramosa. Physiological responses, such as photosynthetic efficiency and reactive oxygen species (ROS) levels, were analyzed in conjunction with transcriptomic data to elucidate acclimation mechanisms. The role of plastid-mediated stress responses was further examined using Arabidopsis mutants deficient in genes involved in acclimation (cp31a, cp29a, cp29b). Additionally, the research explored how the loss of photosynthesis in Phelipanche ramosa influences its response to abiotic stresses. This dual-stress pathosystem provides a unique framework for studying the interplay between host and parasite under environmental challenges. The results reveal that parasitism modifies the host's stress acclimation responses, with Arabidopsis mutants displaying varying resilience to abiotic stresses. For example, cp31a mutants exhibited heightened sensitivity to cold, while parasitized wildtype and cp29a mutants demonstrated improved resilience to heat. Intriguingly, Phelipanche ramosa employed distinct survival strategies depending on the host genotype and stress conditions, activating both conserved and unique acclimation genes under cold stress. These findings highlight the complexity of stress interactions and provide new insights into the adaptive strategies of plants and their parasites under environmental stressors. This research underscores the importance of studying combined stress responses to deepen our understanding of plant resilience and adaptation in the context of a changing environment.

https://conferenceyoungbotanists.com/abstracts/charline.ge

Poster – Analysis of vascular cambium response to drought and heat stress through integrated omics approaches to identify tolerance mechanisms and key factors in forest resilience strategies

Chiara Pezzuto[1], Dalila Trupiano[1], Antonello Montagnoli[2], Alessio Giovannelli[3], Gabriella Stefania Scippa[1]

[1] Department of Bioscience and Territory, University of Molise, Pesche, Italy; [2] Laboratory of Environmental and Applied Botany, Department of Biotechnology and Life Science, University of Insubria, Varese, Italy; [3] CNR-IRET, Sesto Fiorentino, Italy

Climate change is a severe global threat. Studies show that forest biomass continues to be one of the most sustainable solution to sequester a significant amount of anthropogenic carbon and mitigate the rise of global temperature. The vascular cambium is thought to play a role in biomass production, with its activity potentially being influenced by environmental changes. Despite its importance, the regulatory mechanisms controlling the vascular cambium activity are still not fully understood. Therefore, a greater knowledge - especially about the influence of stress factors on plant secondary growth - is crucial. Our research aim is to analyze the response of poplar (Populus nigra) to the combination of heat and water stress. Specifically, the investigation is performed on seed-grown poplar plants under two different temperature and watering conditions in two separate climate rooms. Due to the several differences between root and stem, the vascular cambium is collected from both organs. Integrated omics approaches will be conducted to acquire an overview of the vascular cambium response to environmental stresses. In detail, the transcriptomic, hormonomic and metabolomic data will be integrated to pinpoint the molecular factors and biomolecules specifically involved in (i) the stem and root response to the stress combinations, and (ii) during growth phases . The information, all together, will be used to construct models to successfully predict the impact of climate change and to improve forest resilience. Furthermore, this knowledge could be applied to select genotypes better adapted to global warming and climate change that our planet is increasingly observing with greater speed.

https://conferenceyoungbotanists.com/abstracts/c.pezzuto

POSTER – Regulation of the Golden2-like 1 (GLK1) transcription factor

Christopher Großmann[1], Kerstin Kaufmann[1]

[1] Plant Cell and Molecular Biology, Humboldt-Universität zu Berlin, Institute of Biology, Berlin, Germany

GLK1, a member of the Golden2-like transcription factor family, plays a fundamental role in regulating chloroplast development, photosynthesis, and overall plant growth. Its activity is tightly controlled at multiple levels, including transcriptional, post-transcriptional, and post-translational regulation. Transcriptionally, GLK1 expression is modulated by various environmental cues, like light intensities and temperature. In addition, hormonal signals, and developmental stages play also a role in GLK1 transcriptional regulation, indicating its versatile responsiveness to diverse stimuli. Analysis of transcription factor binding sites revealed that the GLK1 promoter can be divided into three mayor cis-regulatory regions as defined by an open chromatin status. These regions act as hubs for transcription factor binding, with many transcription factors binding to more than one region. To unravel the regulatory regions contributing to developmental, environmental and retrograde-signaling controlled regulation of GLK1, Cas9-based promoter deletions were generated. Stable transgenic lines expressing either promoter or promoter variant-Luciferase fusions, as well as translational fusions with the GLK1 promoter and the genomic locus fused C-terminally to the LUC gene are used to further dissect these environmental signaling pathways.

https://conferenceyoungbotanists.com/abstracts/christopher.grossmann

TALK – Investigating below-ground plant-bacteria interaction through the analysis of volatile compounds released by bacteria and roots

Claudia Russo[1], Cristiana Rizzi[1]

[1] University of Milano-Bicocca

Plants are naturally associated with beneficial microorganisms that play a crucial role in their growth and health. In particular, bacteria inhabiting the root endosphere and rhizosphere promote the growth of the host plants, increase their stress tolerance and protect them from pathogens. In addition to those already present in seeds, specific bacterial strains are recruited by seedlings during growth, forming dynamic endophytic and rhizospheric communities that are shaped by environmental conditions. Many factors are known to contribute to this biological interaction, but the mechanisms of communication between plants and bacteria in the soil, that underlie the root colonization process, are still poorly understood. The aim of this study is to identify the volatile compounds emitted by roots and bacteria in soil and to shed light on their role as signaling molecules mediating plant-bacteria communication aimed at establishing specific endophytic and rhizospheric communities during seedling growth. To this end, we filled a rectangular aluminium pot (60 cm long) with autoclaved sand, sowed Brassica juncea seeds at one end, and inoculated a consortium of selected plant growth-promoting bacteria (PGPBs) in the centre of the pot. A distance of 10 cm was left between the inoculated area and the plant growth area. A system of Teflon tubes exploring the soil and channeling emitted VOCs into a glass vial was set up for each of the following three zones of the pot: the plant area (PA), the inoculated area (IA), and the area at the opposite end to the plants with only sandy soil (SA). We then identified the volatile compounds released by both roots and bacteria over time. VOCs in the vials were trapped by solid phase microextraction (SPME) and analyzed by gas chromatography-mass spectrometry (GC-MS). To assess potential VOC-mediated migration of bacteria in the soil, at the same times as the VOC analysis, we sampled soils in the three pot areas PA, IA and SA, and in the areas between PA and IA (PA-IA) and between IA and SA (IA-SA). The bacteria community in each soil sample was determined by high-throughput 16S rRNA gene Illumina sequencing. The seed community and the established root endophytic and rhizospheric bacterial communities at the end of the experiment were also analysed using the same technique. Preliminary results showed that during the first 24 h after sowing, when most seeds germinate and radicles elongate, VOCs detected in PA were totally different from those in IA. At this stage bacterial DNA was found only in the IA area, although a small amount was also detected in PA probably due to seed endophytes. During the subsequent stages bacterial DNA was also detected in PA-IA, IA-SA and SA suggesting a migration of PGPBs from the centre to the ends of the pot. Accordingly, the similarity of emitted VOCs increased between the different areas. Only the results of ongoing NGS analyses will allow to understand whether B. juncea modulates its root microbiota, interacting with soil bacteria, and whether the emitted volatile compounds are involved in this process.

https://conferenceyoungbotanists.com/abstracts/claudia.russo1

Talk – Optimisation of an Analytical Method for VOC Sampling in the Rhizosphere Using HS-SPME and GC-MS

Cristiana Rizzi[1], Claudia Russo[1]

[1] University of Milano - Bicocca

The rhizosphere is a hub of chemical interactions crucial for plant growth, nutrient cycling, and plant-microbe communication. Volatile organic compounds (VOCs) emitted by plant roots and microorganisms in the rhizosphere play a significant role in these interactions. Despite their importance, sampling and analysing these VOCs remains challenging due to their low concentrations, variability, and the complex matrix of soil and root exudates. This study focuses on the set up of an analytical method for the sampling and analysis of VOCs from plant roots and soil bacteria. We investigated two complementary sampling strategies: (1) direct extraction from roots and bacteria by using liquid nitrogen and (2) time-resolved monitoring of VOCs emitted in soil by roots and bacteria. While cryogenic root extraction provides a comprehensive inventory of stored VOCs, time-resolved monitoring is non-invasive strategy that focuses on monitoring VOCs in soil, emitted by the intact potted plant or bacteria over time and that provides real-time data on signal molecules actively involved in plant-microorganism interactions. The optimization of the laboratory experiment was designed to evaluate parameters critical to the development of the analytical method for VOC monitoring using headspace solid-phase microextraction (HS-SPME) coupled with gas chromatography-mass spectrometry (GC-MS). The experimental system utilized Sorghum bicolor and Brassica juncea plants grown in pots using in the second approach perforated Teflon tubes installed within the soil, allowing for the efficient collection of VOCs emitted in the bulk and rhizosphere soil. These tubes were connected to a vial where the SPME fiber was exposed for sampling. This design minimized contamination and enabled consistent sampling from the complex soil-root environment. Key variables influencing method performance were identified, including SPME fiber type (e.g., polydimethylsiloxane, carboxen, or divinylbenzene coatings), sampling temperature, equilibration time, and desorption conditions. Multiple fibers with different coatings were tested to maximize VOC capture efficiency across a range of volatilities and polarities. The two phase fiber CWR-95/PDMS was selected. The exposure time of the SPME fiber and the extraction temperature were optimized to balance sensitivity and reproducibility. VOC sampling was evaluated at two-time intervals—1 hour and 24 hours—and under different temperature conditions, including ambient temperature, 40°C, and 60°C. Increasing the temperature during sampling significantly enhanced the extraction of VOCs by promoting volatilization, thereby enabling the detection of a broader spectrum of compounds. To balance the need for ecological relevance and analytical efficiency, it was decided to conduct sampling at ambient temperature for a prolonged duration of 24 hours. This approach yielded VOC profiles comparable to those obtained with shorter sampling times at elevated temperatures, while better representing the dynamics of VOC emissions under natural conditions. Results indicated that this experimental system provides a robust framework for studying VOC emissions from plant roots and their interactions with rhizosphere microorganisms. Understanding the pathways by which microorganisms and plants synthesise VOCs could be a key to studying the complex multi-trophic interactions that influence and improve plant health. Such information could also be useful in increasing the ability of plants to degrade organic pollutants often found in urban soils.

https://conferenceyoungbotanists.com/abstracts/cristiana.rizzi

Talk – Essential oil from rhizome and leaf of Peucedanum ostruthium W. D. J. Koch: comparative micromorphological and phytochemical analyses

Cristina Danna[1], Antonella Smeriglio[2], Domenico Trombetta[2], Martina Imbesi[2], Laura Cornara[1]

[1] Department of Earth, Environment and Life Sciences (DISTAV), University of Genova, Corso Europa 26, 16132 Genova, Italy; [2] Department of Chemical, Biological, Pharmaceutical and Enviromental Sciences (ChiBioFarAm), University of Messina, Viale Ferdinando Stagno d'Alcontres 31, 98166 Messina, Italy

Peucedanum ostruthium W. D. J. Koch (Apiaceae family) is a perennial rhizomatous herbaceous species growing in alpine environments. The plant, known as masterwort, is renowned in traditional medicine since Middle Ages and referred in historical and recent ethnobotanical studies (1). Several pharmacological research have investigated the plant extracts, especially focusing on the rhizomes rich in coumarins, while few studies are available regarding the essential oil (EO) of P. ostruthium (2–4). We collected the species in Aosta Valley and studied both the rhizome and the leaf from a micromorphological and phytochemical perspectives. Anatomical features focusing on the oil ducts, in which the EO is formed, were elucidated through Light, Fluorescence and Scanning Electron microscopy. Secretory ducts, typical of the Apiaceae family, were found in both leaves and rhizomes, present in the latter in greater quantity and size. In the cross sections stained with Fluorol Yellow, the secretory channels and their contents reacted with a strong yellow-green fluorescence due to the presence of terpenoids. The EOs from both parts were obtained through hydro-distillation and the phytochemical profiles were acquired through GC-FID and GC-MS analyses. Phytochemical analyses highlighted a very different phytochemical profile of the EO depending on the part of the plant from which it was isolated, with the one obtained from the rhizome being much richer. Specifically, the EO isolated from P. ostruthium leaves showed the sesquiterpene β-caryophyllene as the most abundant compound (21.58%) followed by β-selinene (13.95%), humulene (α-caryophyllene, 13.82%), germacrene (10.33%), naphthalene (6.82%) and espatulenol (6.65%). On the contrary, the EO isolated from the rhizome showed the monoterpene D-limonene as the most abundant compound (28.01%) followed by sabinene (19.01%), α-phellandrene (11.56%) and terpinene-4-ol (5.44%). These substantial phytochemical differences could also reflect a different behaviour of the two EOs from a biological point of view. For these reasons, studies are currently underway to evaluate the antioxidant, anti-inflammatory and antimicrobial activity. 1. Danna C, Poggio L, Smeriglio A, Mariotti M, Cornara L. Ethnomedicinal and Ethnobotanical Survey in the Aosta Valley Side of the Gran Paradiso National Park (Western Alps, Italy). Plants. 2022;11(2). doi:10.3390/plants11020170 2. Carron C, Simonnet X, MC Cardell JH, Héritier J, Carlen C. Sélection d 'un écotype d 'impératoire (Peucedanum ostruthium (L .) W . D . J . Koch). 2020;52(2):96-103. 3. Cisowski W, Sawicka U, Mardarowicz M, Asztemborska M, Luczkiewicz M. Essential oil from herb and rhizome of Peucedanum ostruthium (L. Koch.) ex DC. Zeitschrift fur Naturforsch - Sect C J Biosci. 2001;56(11-12):930-932. doi:10.1515/znc-2001-11-1202 4. Garzoli S, Iriti M, Vitalini S. Chemical composition, antiradical and phytotoxic activity of the essential oil from Peucedanum ostruthium W.D.J.Koch leaves. J Phytomolecules Pharmacol. 2022;1(2):88-95. doi:10.56717/jpp.2022.v01i02.011

https://conferenceyoungbotanists.com/abstracts/cristinadanna95

TALK – Orange Peel Waste-Derived White-Rot Fungus Digestate: A Promising Approach to Enhance Plant Resistance against Botrytis cinerea

Erika Bellini[1], Riccardo Lorrai[2], Andrea Tonanzi[2], Simone Ferrari[2]

[1] Dipartimento di Biologia, Università di Pisa, Via Luca Ghini 13, 56126, Pisa; Dipartimento di Biologia e Biotecnologie "Charles Darwin", Sapienza Università di Roma, p.le Aldo Moro 5, 00185 Roma; [2] Dipartimento di Biologia e Biotecnologie "Charles Darwin", Sapienza Università di Roma, p.le Aldo Moro 5, 00185 Roma

Agriculture requires an intensive application of pesticides to protect plants from harmful organisms. However, excessive use has led to environmental pollution and increased pathogen resistance. The use of plant elicitors is an environmentally friendly strategy that enhances plant resistance by triggering immunity. We developed a green protocol to produce elicitors from agro-industrial waste by exploiting the white-rot fungus Phanerochaete chrysosporium. Interestingly, the culture filtrates exhibited only weak antifungal activity against Botrytis cinerea, suggesting their primary mode of action is through elicitation of plant defenses rather than direct pathogen inhibition. To evaluate their efficacy, we treated Arabidopsis thaliana seedlings with Pasteur-sterilized filtrates and examined the expression of defense-related genes: PHYTOALEXIN DEFICIENT 3 (PAD3), PATHOGENESIS-RELATED 1 (PR-1), and PLANT DEFENSIN 1.2 (PDF1.2). In addition, adult plants sprayed with the filtrates were analyzed for callose deposition, a hallmark of immune responses, and their resistance to B. cinerea was assessed. The results showed that the filtrate: i) upregulated PAD3 expression in seedlings, ii) promoted callose accumulation in treated leaves, and iii) significantly enhanced resistance to B. cinerea. Further investigation revealed that the resistance mechanism is dependent on the jasmonic acid pathway but independent of ethylene signaling. Plants carrying mutations in CORONATINE INSENSITIVE1 (COI1) failed to respond to the filtrate, while ETHYLENE-INSENSITIVE PROTEIN 2 (EIN2) mutants exhibited responses comparable to wild-type plants. Moreover, weekly applications of the filtrate progressively increased resistance in a dose-dependent manner. HPAEC-PAD analysis identified oligosaccharides in the filtrate, compounds known to act as immune activators in plants. Finally, we demonstrated that commercial Solanaceae crops, including tomatoes, eggplants, and peppers, benefited from filtrate treatments, showing enhanced resistance to pathogens without compromising yield. This approach highlights the potential of utilizing agro-industrial waste to develop sustainable plant protection strategies.

https://conferenceyoungbotanists.com/abstracts/erika.bellini

Talk – Sprouting ability of Sonchus arvensis at different growth stages

Fanny Defant[1], Lena Ulber[1], Bärbel Gerowitt[2], Sabine Andert[1], Doreen Gabriel[1]

[1] JKI (Federal Research Centre for Cultivated Plants); [2] University of Rostock

Sonchus arvensis L. (perennial sow-thistle) is a perennial weed in the Asteraceae family. It is native to Europe and widespread to America and Asia. Common in arable fields, it often becomes problematic for crop production, especially in Northern Europe and Northern Asia. In recent years, a problematic spread of S. arvensis towards the Southern Europe has been observed. Sonchus arvensis forms a compact plant rosette and produces yellow flowers, yielding numerous seeds after pollination. It also propagates via vegetative roots, thereby forming plant clones. In arable fields, soil tillage fragments these roots, spreading the plant further. These root fragments, known as ramets, contribute significantly to its distribution. Environmental conditions such as light and temperature also affect the sprouting capacity, development and growth of S. arvensis. The aim of this study was to analyse the effect of temperature and photoperiod on the sprouting ability of S. arvensis at different growth stages. Knowledge on the ability of the plant to sprout from the ramets can help to optimise management strategies for S. arvensis. The experiment was conducted at the JKI (Federal Research Centre for Cultivated Plants) in Braunschweig, Germany in 2024. At different growth stages of S. arvensis, ramets were collected from three field populations. The developmental stages for root collection were: rosettes, flowers, seed heads, wilting, and after frost. During sampling, roots were classified into those developed in the previous year (old roots) and those developed in the current year (young roots). All roots were cut into 5 cm ramets, potted at a depth of 2.5 cm and kept in growth chambers. The sprouting ability was tested under three different temperature (6°C, 15°C, and 24°C) and two photoperiod regimes (16h light/8h dark and 8h light/16 dark). In addition, pots with ramets were also placed outdoors to assess the impact of natural temperature and photoperiod. The time of re-sprouting (shoot emergence) was recorded, followed by weekly assessments of the plant developmental stage and number of leaves. A final assessment took place after accumulating 720 degree-days and included an assessment of the following parameters: fresh and dry weight of the aboveground biomass, planted ramet and newly formed roots. Preliminary results for the experiment will be presented. These will provide information on the sprouting ability of S. arvensis throughout the growing season and the impact of temperature and photoperiod on the sprouting capacity over the year. It can be shown that the developmental stage must be considered when modelling the sprouting capacity of S. arvensis, as the base temperature also changes throughout the year.

https://conferenceyoungbotanists.com/abstracts/fanny.defant

Poster – Microscopy coupled with DNA barcoding-based analysis as diagnostic tools to identify toxic plants

Federica Betuzzi[1], Camilla Micaletti[1], Elena Capuzzi[1], Enrico Bajona[2], Jessica Frigerio[3], Laura Cornara[1]

[1] Department of Earth, Environment and Life Sciences (DISTAV), University of Genoa, Corso Europa 26, 16132 Genova, Italy; [2] Department of Agricultural, Food and Forest Sciences (SAAF), University of Palermo, Viale delle Scienze 4, 90128 Palermo, Italy; [3] Department of Biotechnology and Biosciences, University of Milano-Bicocca, Piazza Della Scienza 2, 20126 Milan, Italy

Plant poisoning can be related to the: (i) misidentification between edible and toxic wild herbs due to morphological similarities; (ii) contamination of crops by weeds; (iii) use of toxic plants in traditional herbal medicine. Species belonging to Solanaceae family contain tropane alkaloids and are often involved in human poisoning. For example, in southern Italy, leaves of Mandragora autumnalis Bertol. can be confused by inexpert pickers with those of Spinacia oleracea L., Borago officinalis L., Beta vulgaris L., and accidentally collected for culinary uses. Moreover, M. autumnalis can grow near cultivated fields, so its leaves can be mechanically harvested and occasionally present in commercial frozen vegetables. Despite its known toxicity, mandrake root and rhizome are present in herbal market stalls of Morocco for their aphrodisiac properties or as cold remedy. However, this practice is potentially dangerous for public health. In particular, the presence of mandrake is sometimes indicated in artisanal “Thè Royal du Maroc”, a typical beverage of the Maghreb area. Since mandrake is used in form of root cut to prepare this herbal tea, its botanical identification is very difficult even for experts. Moreover, some species are used as a substitute for or to counterfeit mandrake, such as Alpinia officinarum Hance, Acorus calamus L., Withania somnifera (L.) Dunal, Sceletium tortuosum L. Considering this, we carried out a micro-morphological characterization of mandrake leaves and rhizome to identify their diagnostic features. The leaves were compared with those of spinach and beet, while the rhizome was compared with those of A. officinarum, A. calamus and an unknown rhizome found in an artisanal sample of “Thè Royal du Maroc”. Species-specific primers were designed for A. officinarum, A. calamus, and M. autumnalis with the aim of identifying these species within the “Thè Royal du Maroc” mixture. The primer pairs were designed based on specific marker standards of DNA barcoding (matK, psbA-trnH) and initially tested on pure samples to verify their efficiency. Results showed that mandrake, spinach and beet leaves had distinguishing features such as different kinds and distribution of covering and glandular trichomes. Instead, the rhizome fragments present in the herbal mixture called “Thè Royal du Maroc” showed anatomical characteristics very similar to those of A. officinarum, such as numerous vascular bundles scattered throughout the cortex and stele, without any particular orientation. These bundles were collateral endarch and surrounded by a bundle sheath. On the contrary, mandrake rhizome had a structure typical of other Solanaceae members, showing a thin layer of cork surrounding the cortex, a phloem region, a radiate xylem, and a central pith with scattered groups of intraxylary phloem. Regarding the DNA barcoding-based analyses, an amplicon was obtained for leaf mixes of the target species created in the laboratory but not for “Thè Royal du Maroc”, suggesting that in dried rhizomes DNA can be degraded. Microscopy is a first tool for identifying toxic plants in complex mixtures. DNA barcoding is useful for confirming or not the presence of certain species, but its effectiveness depends on DNA quantity and quality and plant material.

https://conferenceyoungbotanists.com/abstracts/federica.betuzzi

TALK – Which crown defoliation level may be considered a threshold for severe physiological impairment in Quercus ilex L.? ? Results of a two-year field study in a Mediterranean forest

Francesca Alderotti[1], Antonella Gori[2], Francesco Ferrini[2], Mauro Centritto[3], Cassandra Detti[4], Diana Vanacore[4], Cecilia Brunetti[5]

[1] National Research Council of Italy (CNR), Institute for Sustainable Plant Protection, Via Madonna del Piano 10, 50019 Sesto Fiorentino (FI), Italy; [2] University of Florence, Department of Agriculture, Food, Environment and Forestry, Viale delle idee 30, 50019 Sesto Fiorentino; Florence, Italy; [3] National Research Council of Italy (CNR), Institute for Sustainable Plant Protection, Via Madonna del Piano 10, 50019 Sesto Fiorentino (FI), Italy.; [4] University of Florence, Department of Agriculture, Food, Environment and Forestry, Viale delle idee 30, 50019 Sesto Fiorentino; Florence, Italy.; [5] 1 National Research Council of Italy (CNR), Institute for Sustainable Plant Protection, Via Madonna del Piano 10, 50019 Sesto Fiorentino (FI), Italy

The increase in drought and aridity occurrence and intensity is likely causing the rising incidence of Quercus ilex L. (holm oak) mortality, one of the most widespread oak species dominating the Mediterranean landscape. Hydraulic dysfunction and carbohydrate depletion are key traits involved in the physiological processes linked to tree vitality. In this field-study, xylem embolism and non-structural carbohydrates (NSCs) availability in adult trees facing harsh environmental conditions were monitored with the objective of identifying the threshold of a physiological impairment rising the risk of tree mortality. To this end, xylem embolism and NSCs limitations associated with different levels of holm oak crown defoliation were evaluated. Percentage loss of hydraulic conductivity (PLC), xylem water potential (ψx) and NSCs (starch and soluble sugars, SS) were seasonally monitored for two years in non-defoliated (CL1), moderately defoliated (CL2) and severely defoliated (CL3) holm oak trees within a Mediterranean forest located in Southern Tuscany (IT). Increased crown defoliation was associated with higher PLC and lower ψx and NSC availability, with significant differences among the defoliation classes mainly observed in the summer and autumn seasons. Non-lethal xylem embolism (PLC $\cong$ 50%) reduced carbon uptake in summer and autumn in CL2 and CL3 defoliated trees, but not in spring, when lower SS availability was not associated with hydraulic damages. Over the two years of investigation, the physiology of CL2 trees deteriorated to the level of CL3 ones. Interestingly, we observed delayed starch reserve recovery in CL2 and CL3 trees, occurring in winter rather than in autumn as observed in non-defoliated CL1 trees. Therefore, we suggest the absence of autumn NSC recovery after summer drought as a sign of incipient holm oak mortality. In conclusion, our research shows that moderate holm oak crown defoliation may conceal severely damaged tree physiology, leading to PLC,ψx and NSCs values similar to those of severely defoliated trees in subsequent phases.

https://conferenceyoungbotanists.com/abstracts/francesca.alderotti

TALK – Silene latifolia: a striking thallium facultative hypertolerant and hyperaccumulating species

Gaia Regini[1], Isabella Bettarini[1], Marco Dainelli[1], Beatrice Chiavacci[1], Ilaria Colzi[1], Federico Selvi[2], Antony van der Ent[3], Cristina Gonnelli[1]

[1] Department of Biology, Università degli Studi di Firenze, Via Micheli 1, Florence 50121, Italy; [2] Department of Agriculture, Food, Environment and Forest Sciences, Università degli Studi di Firenze, P. le Cascine 28, Florence I-50144, Italy; [3] Laboratory of Genetics, Wageningen University and Research, Droevendaalsesteeg 1, Wageningen 6708 PB, The Netherlands

Thallium is the most toxic element known to mankind: its harmfulness is mainly due to the chemical similarity of Tl+ to K+, that leads to interferences with K-dependent biochemical processes. This feature and its current and historic release into the environment make it an emerging environmental pollutant of concern. Thallium is not only toxic, but also economically valuable, and therefore novel and, if possible, nature-based methods for extraction from contaminated land or wastes are desirable, including phytomining, using hyperaccumulator plants. These plants have the extraordinary ability to accumulate metal(loid)s in their above ground-tissues, far exceeding soil concentration. Facultative hyperaccumulation is a rare phenomenon reported from a small number of widespread species in which most populations are metal sensitive, but some populations are metal tolerant and hyperaccumulating. Silene latifolia is such as facultative hyperaccumulator for thallium, and in this study, we examined population-specific thallium tolerance and accumulation trait in two metallicolous and two non-metallicolous populations. The metallicolous populations were one from Saint-Laurent-le-Minier (France), a Tl-rich mine dump, and one from Valdicastello Carducci (Italy), a geochemically anomalous area with natural high Tl concentration in soil, while the non-metallicolous accessions were from two non-contaminated sites: Barraux (France) and Montenero (Italy). Seeds were sown in peat soil and then plantlets were transferred to hydroponics. After a 7-days pre-culture period, samples were exposed to a growing series of TlNO3 concentrations (0, 2.5, 5, 30, 60 µM) for seven days. Leaf area and root length increment were calculated, chlorophyll a fluorescence, indices of leaf pigments and Tl concentration in both shoots and roots were measured. The results reveal that the non-metalliferous populations accumulated up to 1000 and 2000 µg g-1 d.w., exceeding the limit of toxicity for normal plants (20 µg Tl g-1 d.w.) and suggesting a remarkable basal Tl tolerance of Silene latifolia. Still, non-metallicolous populations were negatively affected by Tl and had a growth reduction of 50–70 % at the highest thallium dose level. On the other hand, the metallicolous populations greatly exceeded the non-metallicolous ones, displaying thallium hyper-tolerance and hyperaccumulation, attaining up to 7000 and 14,000 µg Tl g-1 d.w. in the shoots at the highest thallium dose level in hydroponics (60 µM), while had minimal growth reductions. Moreover, metallicolous populations preserved photosynthetic activity and had higher ionome stability under thallium treatment, in addition to a positive correlation between thallium and sulphur in their shoots. This study revealed a striking ecotypic response in thallium tolerance/accumulation in Silene latifolia. It also opens research perspectives to identify Tl root-based transporters and detoxification mechanisms. Its potential use in phytomining should be further investigated too, through tests in real life conditions on Tl-contaminated soils.

https://conferenceyoungbotanists.com/abstracts/gaia.regini

POSTER – Optimization of enzymatic digestions on tomato seeds to recover proteins and peptides

Giorgia Benati[1], Maura Ferri[1], Annalisa Tassoni[1]

[1] Department of Biological, Geological, and Environmental Sciences, University of Bologna, via Irnerio 42, 40126 Bologna Italy

The present work is part of the AgriLoop EU project, which aims at promoting sustainable agricultural production by valorizing its by-products. Specifically, the goal of this study is to successfully extract proteins and peptides from tomato seeds for potential use in food or other applications based on the biological activities of the extracts. The excessive consumption of animal-based proteins and the use of plant proteins predominantly as animal feed for meat production is proved to be environmentally unsustainable, and this research seeks to offer an eco-friendly alternative. Initially, seven proteases and five cell-wall hydrolytic enzymes were tested at different concentrations on dried and grounded tomato seeds. The resulting digestates were analyzed for protein content, but also for reducing sugars and polyphenols contents. After identifying the best enzymes, a two-step approach was tested, starting with the best cell-wall hydrolytic enzyme followed by one of the best proteases. However, this method did not significantly improve protein yield with respect to the use of proteases alone. SDS-PAGE was performed to gain an overview of the molecular weight distribution of the proteins and peptides extracted. When treated with proteases, tomato seeds exhibit a high proportion of low molecular weight peptides. To further refine the protocol and try to improve the peptide yield and pool, additional trials were conducted. Enzymatic digestions were also applied to: precipitated proteins from tomato seeds, autoclaved and sonicated fresh seeds and defatted ones. An optimization of the extraction conditions was also performed by lowering the incubation temperature and the addition of hydration and sonication steps. Based on the results of protein content the best approach selected was protease treatment with either Papain, Bromelain, Protamex or Trypsin using a lower incubation temperature. The evaluation of antioxidant activity of the extracts using ABTS assay is ongoing. Further steps include peptide sequencing and the assessment of additional biological activities to better characterize the extracts and gain a deeper understanding of the benefits of the extracted peptides.
This project has received funding from the European Union's Horizon Europe research and innovation programme under the grant agreement No. 101081776, the UK Research and Innovation (UKRI) fund under the UK government's Horizon Europe funding guarantee, the Swiss State Secretariat for Education, Research and Innovation (SERI) and from the National Key Research and Development Program supported by the Ministry of Science and Technology of the People's Republic of China (No. 2023YFE0104900). Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of neither of the aforementioned Funding authorities. Neither the European Union, the United Kingdom, the Swiss Confederation or the People's Republic of China nor the European Commission, UKRI, SERI or NKRDPC can be held responsible for them.

https://conferenceyoungbotanists.com/abstracts/giorgia.benati2

Poster – MicroRNA-induced regulation of wheat (Triticum aestivum L.) root architecture and function

Giorgia Tonielli[1], Alessia D'Agostino[2], Gabriele Di Marco[2], Gerardo Pepe[2], Adelaide Teofani[2], Chiara Pontecorvi[2], Manuela Helmer Citterich[2], Antonella Canini[2], Angelo Gismondi[2]

[1] 1Department of Biology, University of Rome Tor Vergata, Via della Ricerca Scientifica 1, 00133 Roma, Italy 2 PhD program in Cellular and Molecular Biology, University of Rome Tor Vergata; [2] 1

Wheat (Triticum sp.) is one of the most cultivated crops in the world, providing about 20% of the total calories in the human diet. Unfortunately, in the next decade, the increasing worldwide food demand and the present climate change issues have made insufficient the current grain yield rate. In recent years, the attention of scholars has been focused on promoting the root system architecture (RSA) of this species to improve its access to nutrients and productivity. However, to date, no study has investigated the role of miRNAs in the regulation of Triticum aestivum RSA. Thus, the aim of the present contribution was to investigate the cellular and molecular processes mediated by miRNAs which may determine the root growth in wheat seedlings (Altamira variety), to reach a better comprehension of the phenomena linked to the developmental biology of this species and to favour the design of novel biotechnological approaches able to promote its yield and quality. An initial transcriptomic approach was applied on roots from wheat seedlings grown at different timings (4 and 8 days after seeding, henceforth DAS). The bioinformatic analysis revealed a modulation at these stages of some molecular pathways already known in the literature and associated to RSA (e.g., calcium ion transport and homeostasis, cell wall structure, defense and pathogen response, redox balance). Interestingly, the results also evidenced an upregulation of genes involved in abscisic acid production. To have a better overview on the expression of miRNAs during wheat root growth, a miRNome differential expression analysis was carried out at the same DAS. The results of this analysis revealed the potential modulation of different pathways mediated by microRNAs associated with RSA (e.g. calcium ion transport, cell wall macromolecule catabolic processes, defense response), confirming the evidence obtained by transcriptomics. These findings directed our attention to two specific microRNAs, miR398 and miR397b-5p, which have not yet been studied in wheat root development. Their respective targets—Cu/Zn SOD (Cu, Zn Superoxide Dismutase, involved in detoxifying superoxide anions) and Laccase 2 (a multi-domain cupredoxin oxidoreductase involved in lignification and secondary cell wall biosynthesis)—are known to be regulated by distinct transcription factors activated by ABA. The expression analysis of miR397b-5p and miR398 and their targets in wheat roots at different growth stages (i.e., 4, 6, 8, 10 and 12 DAS) revealed a down regulation of both miRNAs during the root development, while the level of transcript for Laccase 2 remained stable and that of Cu/Zn SOD accumulated. These data would suggest a different regulatory mechanism for the two miRNAs on their respective targets (i.e., inhibition of translation and degradation of the mRNAs). To better define this context, spectrophotometric activity assays were performed for both these enzymes, confirming the putative key function of the two investigated miRNAs on their targets. Lastly, to provide a more general overview of this kind of regulation the transcript level of other Laccases and antioxidant enzymes was monitored. All this preliminary evidence opens new perspectives on the role of the miRNAs in wheat RSA.

https://conferenceyoungbotanists.com/abstracts/giorgia.tonielli

POSTER – Impact of Acoustic Vibration on Rhizobium-Legume Symbiosis

Giulia Mozzo[1], Bruno Bighignoli[1], Marta Beccaluva[2], Diego Comparini[1]

[1] Department of Agricultural, Food, Environmental and Forestry Science and Technology (DAGRI), Università degli Studi di Firenze, Viale delle Idee 30, Sesto Fiorentino (FI), Italy.; [2] Department of Biology, Università degli Studi di Firenze, Via Micheli 3, 50121, Florence, Italy.

Recent studies suggest that low-frequency acoustic vibrations can affect various biological processes, root apparatus development, seed germination, microbial activities, and plant growth. These innovative approaches offer a potentially effective method for enhancing agricultural practices. Considering the rhizobium-legume symbiosis is sensitive to external factors, this study investigated the effect of low-frequency acoustic vibrations on the interaction. The symbiosis between rhizobia and legumes is essential for the implementation of sustainable agriculture due to its contributions towards synthetic fertilizer reduction dependency. The mechanisms involved in this mutualism are highly complex involving nodulation factors, receptors, infection threads plant responses, and nutrient exchange, which help boost soil fertility, crop resilience to climate change, biodiversity conservation, and, ultimately, high yields without exhausting the natural resource base. In our experiment, the acoustic vibrations were tested on Medicago sativa when inoculated with its symbiotic partner Rhizobium meliloti, putting together four groups of treatments-inoculated and non-inoculated plants under acoustic vibrations with respective controls. The results indicated significantly increased root growth, nodule number and weight, and plant biomass through acoustic vibrations. These findings indicate that low-frequency acoustic vibrations can be an innovative abiotic method to promote rhizobia-legume symbiosis and hence foster sustainable agricultural development. The work is a starting point into some of the aspects of mechanical mechanisms to maximize the plant-microbe interaction advance in sustainable agriculture.

https://conferenceyoungbotanists.com/abstracts/giulia.mozzo

Talk – Nitric Oxide role in rice root formation and development exposed to viable and autoclaved mycorrhizal spores

Giulia Raffaele[1], Marilena Ronzan[2], Emanuela Del Dottore[3], Barbara Mazzolai[3]

[1] Istituto Italiano di Tecnologia & Università di Napoli Federico II; [2] Istituto Italiano di Tecnologia; [3] Istituo Italiano di Tecnologia

Nitric oxide (NO) is a reactive nitrogen species involved with various signalling processes in the plant responses to biotic stresses. Nowadays, it is evident that NO is accumulated during the interaction with rhizobia bacteria (Berger et al., 2020) and arbuscular mycorrhizal fungi (Martínez-Medina et al., 2019). However, its specific role remains unclear. This study aims to elucidate the role of NO in the early stages of the interaction between Oryza sativa L. and Rhizophagus irregularis (MUCL 41833), focusing on its influence on the formation and development of large lateral roots, which are preferentially colonised during the AM symbioses (Chiu et al., 2022). Experiments were conducted using a treated group with viable and autoclaved spores, as well as a control group. Three replicates of the experiment were carried out. Nitric oxide was detected through DAF-FM specific dye seven days post-inoculation. The NO endogenous signal was located in the root primordia and the internal tissues of the large lateral roots in the treated group with viable spores, whereas it was not detected in the roots of the autoclaved spores and control group. These results suggest that nitric oxide plays a role in the development of the root primordia and large lateral roots following arbuscular mycorrhizal fungi perception. Further research will be essential to determine the nitric oxide signal pathways and clarify its interaction with other molecules during the mycorrhizal pre-symbiotic phase. Bibliography BERGER, A., GUINAND, S., BOSCARI, A., PUPPO, A. & BROUQUISSE, R. (2020) Medicago truncatula Phytoglobin 1.1 controls symbiotic nodulation and nitrogen fixation via the regulation of nitric oxide concentration. New Phytologist 227, 84–98. CHIU, C.H., ROSZAK, P., ORVOŠOVÁ, M. & PASZKOWSKI, U. (2022) Arbuscular mycorrhizal fungi induce lateral root development in angiosperms via a conserved set of MAMP receptors. Current Biology 32, 4428-4437.e3. MARTÍNEZ-MEDINA, A., PESCADOR, L., FERNÁNDEZ, I., RODRÍGUEZ-SERRANO, M., GARCÍA, J.M., ROMERO-PUERTAS, M.C. & POZO, M.J. (2019) Nitric oxide and phytoglobin PHYTOGB1 are regulatory elements in the Solanum lycopersicum – Rhizophagus irregularis mycorrhizal symbiosis. New Phytologist 223, 1560–1574.

https://conferenceyoungbotanists.com/abstracts/giuliaraffele1996

POSTER – Asparagus officinalis L.: a food plant model for monitoring heavy metal contamination in fields bordering roadways in the Ferrara province (Italy)?

Marcello Bigoni[1], Angela Martina[1], Lorenzo Ferroni[1], Elena Marrocchino[1]

[1] University of Ferrara, Department of Environmental and Prevention Sciences, Ferrara, 44121, Italia

The expansion of road networks has intensified environmental contamination, particularly through the deposition of metallic xenobiotics into agricultural soils, posing critical challenges to food safety ecosystem sustainability, and public health. Elements such as Pb, Cd, Cr, Ni are of particular concern owing to their persistence, bioaccumulative nature and capacity to transfer through trophic levels, impacting both ecosystem integrity and public health. Soil contamination arises from both geogenic and anthropogenic sources, with industrial and agricultural activities serving as predominant contributors. Metals from vehicular emissions, fertilizers, and wastewater irrigation exacerbate soil contamination near roadways. In the Ferrara province, where extensive roadway systems intersect agricultural landscapes, assessing the impact of such contamination is essential to safeguard the quality of agroecosystems and agricultural products. Among crops, the geophyte Asparagus officinalis L. (Asparagaceae) can be an interesting model to monitor metal contamination. Its rhizomes and roots are exposed for several years to the potential presence of metal contaminants in the soil, which can be transferred to the edible turions. In the study, six sampling locations were chosen in agricultural zones in the inland, close or not to Ferrara, or in the coastal strip, which is traversed by the state road SS309 Romea. In the entire territory, asparagus cultivation complies with the “Asparago Verde di Altedo” PGI specification, which allows for a defined set of varieties. Such variability can be informative on the role of genotype in influencing metal absorption rates and distribution within plant tissues. Cr, Ni, Pb, Cd, V and Cu were analysed in soils and turions. Soils underwent preliminary screening using X-ray fluorescence (XRF) for semi-quantitative assessment. Elemental contents in soils and turions were then analysed by inductively coupled plasma mass spectrometry (ICP-MS). The elemental concentrations were evaluated against regulatory benchmarks including Italian legislation DM 46/2019 and European Regulation (EU) 2023/915, which establish safety thresholds. Pb and Cd concentrations in all soils and turions were well below regulatory limits. The concentration ratio turion/soil indicated a selective accumulation of Cu and Ni, but also Cd, but not Cr and V. However, the latter two elements in turions were close or above reference values because of relatively high concentrations in soils. Particularly, Cr, Ni, and V confirmed their natural relative abundance in Ferrara province soils, as is well documented in the literature. Data did not allow evidence of consistent patterns as related to the field proximity to roads, most probably because of metal accumulation specificities of the cultivars. However, the site located near the town emerged for higher levels of metals in soils and turions. An effective use of asparagus as a plant system to monitor heavy metal enrichments in soils should therefore take into consideration particularly (i) the evident selectivity of element uptake and accumulation, also related to different cultivars, and (ii) the geochemical background of a certain soil, which can make it difficult to discern potential anthropogenic enrichments.

https://conferenceyoungbotanists.com/abstracts/bgnmcl

TALK – Deciphering plant-microplastic interactions in freshwaters through Spirodela polyrhiza: towards phytoremediation applications

Marco Dainelli[1], Sara Falsini[1], Stéphanie Boutet[2], Ilaria Colzi[1], Andrea Coppi[1], Massimiliano Corso[2], Giovanni Stefano[1], Sandra Ristori[3], Cristina Gonnelli[1], Alessio Papini[1]

[1] Department of Biology, University of Florence, Via Micheli 1, 50121 Firenze, Italy; [2] Université Paris-Saclay, INRAE, AgroParisTech, Institut Jean-Pierre Bourgin (IJPB), 78000 Versailles, France; [3] Department of Chemistry, University of Florence, Via della Lastruccia 3, Sesto Fiorentino, 50019 Firenze, Italy

Microplastics (MPs, 1 µm – 5 mm) pose a growing threat to ecosystems, as evidenced by the substantial efforts made by the scientific community in recent years to investigate their presence in the environment and their toxic effects on living organisms. Nonetheless, resolving this issue must be a priority, with the search for new technologies to address this goal at the forefront. This research aimed to investigate how MPs interact with the floating freshwater plant Spirodela polyrhiza with a focus on evaluating its potential, along with that of its exudates, for mitigating these emerging environmental pollutants. Manufactured blue-fluorescent spherical MPs with diameter between 1 and 5 µm were used to prepare N-medium with a particle concentration of 0.05 g L-1, which was then administered to S. polyrhiza colonies for one week under controlled conditions (MP+S). The experimental setup also included two control conditions: N-medium without plants but containing MPs at 0.05 g L-1 (MP), and growth medium with S. polyrhiza but without MPs (S). The presence of particles did not affect plant growth in terms of frond number and total frond area, and no differences were observed between the treatment and control group (S) in fresh and dry weight at the end of the week of exposure. In addition, tissue accumulation of macro- and micronutrients, measured using X-ray fluorescence (XRF), was not affected by the presence of MPs. The number of items in solution and their area were analyzed at the end of the experiment using optical light microscopy. 400 particles were measured, and their sizes were categorized into classes. In the control condition (MP), smaller particles predominated, with a significant number in the 0-10 µm² class. In contrast, particles in the treatment condition (MP+S) were less abundant in the smaller classes and more prevalent in larger ones, indicating aggregation in the presence of S. polyrhiza. The treatment condition showed a significantly lower number of items, suggesting particle adsorption by the roots and underside of the fronds, confirmed by confocal microscopy analysis. The binding force of the MPs on S. polyrhiza was strong, as a large quantity of them remained on the surfaces even after washing and incubation for 4 days in an MP-free medium. The Zeta potential of particles was also measured at the start and end of the test: control MPs remained stable at -17 mV, while those incubated with plants showed a less negative value of -11 mV. These effects on the behaviour of particles in solution in the presence of S. polyrhiza were thought to result from the exudation of specific compounds by the plant-root system. To investigate this, compounds were analyzed using LC-MS/MS untargeted metabolomics, yielding preliminary data that identified specific metabolic features exuded only in the presence of MPs. Validating their role in particle aggregation and surface adsorption could have potential biotechnological applications in the phytoremediation of freshwater systems.

https://conferenceyoungbotanists.com/abstracts/marco.dainelli

TALK – Unrevealing the Role of Epidermal Patterning Factor-Like Peptides in the Root Nodule Symbiosis.

Mariel Isidra Arellano[1], Manoj Kumar-Mahto[1], Luis A. López-Villagómez[1], Miriam Bazzicalupo[1], Katharina Schiessl[2], Giles E.D. Oldroyd[3], Oswaldo Valdés-López[4], Caspar Chater[1]

[1] Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3AE, U.K.; [2] Sainsbury Laboratory, University of Cambridge, 47 Bateman Street, Cambridge CB2 1LR, UK.; [3] Sainsbury Laboratory, University of Cambridge, 47 Bateman Street, Cambridge CB2 1LR, UK. and Crop Science Centre, Department of Plant Sciences, University of Cambridge, 93 Lawrence Weaver Road, Cambridge CB3 0LE, UK.; [4] Laboratorio de Genómica Funcional de Leguminosas, Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México, Tlalnepantla 54090, México.

In response to nitrogen starvation, legumes can establish symbiosis with nitrogen-fixing bacteria, such as rhizobia. Host legumes form new organs called nodules, inside which rhizobia fix atmospheric nitrogen in exchange for photoassimilates. Root Nodule Symbiosis (RNS) allows legumes to grow in soils with low nitrogen availability. This symbiosis is mediated through complex pathways involving transcription factors, hormones, and peptides. Peptides play an important role in regulating different stages of RNS. Epidermal Patterning Factor Like peptides are positive regulators of stomatal development in diverse land plant species. EPFL peptides are also important in stress tolerance, mainly drought. In this study, we demonstrated that Epidermal Patterning Factor Like peptides play an essential role in nodule development. Spatiotemporal expression analysis revealed that EPFL genes are transcriptionally active during nodule formation. Additionally, downregulating EPFL genes negatively affects nodule development. Finally, EPFL synthetic peptides in Medicago roots have a positive effect on nodulation; plants develop more and larger nodules. These data suggest that EPFL peptides might play a determinant role in the nodulation process. The involvement of these stomatal-associated EPFs in M. truncatula-rhizobial responses raises tantalizing questions about shared or divergent mechanisms and evolutionary relationships in nodule development programs across legumes. This study also opens new biotechnological applications using synthetic peptides to improve the nodulation and resilience of plants under different abiotic stresses.

https://conferenceyoungbotanists.com/abstracts/c.isidra

POSTER – Urban stress and plant adaptation: exploring the morphological, genetic and physiological changes in Populus alba"

Marta Beccaluva[1], Tommaso Gabbriellini[2], Luciana Renna[3], Federico Vita[4], Stefano Mancuso[5], Giovanni Stefano[2]

[1] 1. Department of Biology, Università Degli Studi Di Firenze, via Micheli 3, 50121, Florence, Italy; 2. Department of Architecture, Università degli studi di Firenze, Via della Mattonaia, 8 - 50121 Firenze, Italy; 3. Fondazione per il Futuro delle Città (FFC), Via di Novoli, 10, 50127 Florence, Italy.; [2] Department of Biology, Università Degli Studi Di Firenze, via Micheli 3, 50121, Florence, Italy; [3] Department of Agricultural, Food, Environmental and Forestry Sciences and Technologies (DAGRI), Università Degli Studi Di Firenze, Viale delle idee 30 Sesto fiorentino (FI), Italy.; [4] Dipartimento Di Bioscienze, Biotecnologie E Ambiente (Dbba), Università degli Studi di di Bari; [5] Department of Agricultural, Food, Environmental and Forestry Sciences and Technologies (DAGRI), Università Degli Studi Di Firenze, Viale delle idee 30 Sesto fiorentino (FI), Italy. Fondazione per il Futuro delle Città (FFC), Via di Novoli, 10, 50127 Florence, Italy.

Cities are the greatest visible sign of human impact on the Earth's ecosystem. Due to their dense population, transport networks, energy use and increased impermeable surface cover, they radically affect the carbon cycle, as well as the state of the atmosphere and climate. While comprising merely 3% of the Earth's surface area, urban areas are accountable for a substantial 70% of global CO2 emissions. CO2 is the most worrying greenhouse gas (GHG) due to its rapid increase in concentration in the atmosphere (from the 280 ppm about 150 years ago to the current 420 ppm). Cities are also characterised by other stress conditions such as higher temperatures, increased surface water and rainwater runoff and pollution. The environmental parameters variation mentioned above ensure that urbanisation has great impact on the environment, ecosystem processes and the ecology of all organisms. Despite numerous studies on the subject, we still know little about how urbanisation affects the organisms' evolution in general and plants in particular. Plant life is highly dependent on the environmental conditions in which they grow, so any prolonged stress generates an adaptive and subsequently evolutionary response on their part. In this context, our research aims to exploit plant adaption in urban areas where CO2 concentration has been reported to be higher than the extra-urban area. To evaluate the evolutionary rates of plants in Florence city, where high CO2 levels could accelerate the effects of positive selection on key adaptive strategies, we carried-out biochemical, microscopy and genetic analyses on Populus alba grown in urban and non-urban areas. Through more physiological approaches, we wish to determine how higher CO2 concentrations influence the photosynthetic processes. As the activity of the RuBisCO enzyme is sensitive to changes in CO2 concentrations, rubisco's activity is measured by a high-throughput enzyme essay applied to our model species sampled inside and outside the city. Moreover, to compare chloroplast genomes, given their key role in photosynthesis, we use molecular and genetic tecniques to analyse genome size, structure, gene content and sequence mutations at protein level. Using confocal microscopy, we determine how urban enviroment models the morphological structure of photosyntetic tissues and leaf cuticle. In the end, to assess the impact of the urban environment and the adaptation strategies adopted at the cellular level we use Trasmission Electron Microscopy. The proposed approach will deepen our understanding of the physiological responses of plants to urban climatic and environmental conditions. Furthermore, this research will introduce innovative methodologies for assessing the health of urban vegetation and implementing effective conservation strategies.

https://conferenceyoungbotanists.com/abstracts/marta.beccaluva

POSTER – Evolution of fleshy fruits in Myrtaceae: initial impressions in the subgenera of Syzygium

Nayara Machado[1], Káthia S. M. Mourão[1], Eve J. Lucas[2]

[1] Universidade Estadual de Maringá; [2] Royal Botanic Gardens

The Myrtaceae family, included in the Myrtales order, exhibits great diversity, particularly in the Neotropical region. Traditionally, the family's classification has been based on anatomical characters, especially reproductive ones such as flowers, fruits, and embryos. Currently, phylogenetic proposals are based on molecular analysis. However, we believe that more characteristics, such as variation in the anatomy of the fleshy fruit (homoplastic in Myrtaceae), could be relevant to understanding phylogenetic patterns or in the context of the heterogeneous distribution of diversity across genera. The aim of this study is to perform a comparative analysis of the pericarp anatomy of species found in lineages that exhibit fleshy fruits (Syzygieae, Myrteae, Xanthomyrteae,), with the goal of understanding the evolution of this trait in the family. Initially, floral buds and fruits from five species present in different subgenera of the Syzygieae tribe were processed according to standard anatomical techniques, sectioned using a rotary microtome, and analyzed under an optical microscope. Our results so far show a certain homogeneity in the presence and location of secretory cavities, idioblastic crystals of the druse type, and vascular bundles among the species and subgenera analyzed, except for Syzygium claviflorum (Subgenus Perikion), which exhibits a circular arrangement of short fiber bundles in the mesocarp. The compitum, a structure that did not show a consistent pattern among the species analyzed so far, is one of the characters that will be further examined at a later stage due to its importance in the relationship between the number of ovules and viable seeds. Further studies, expanding the number of species from other tribes, are ongoing to better understand the diversification of fleshy fruits in the family and the relationship between patterns for this structure.

https://conferenceyoungbotanists.com/abstracts/naypequeno

TALK – Biostimulants in action: enhancing nickel phytoextraction in Odontarrhena decipiens (Nyár.) grown in serpentine soil

Pablo Carril[1], Gaia Regini[2], Donatella Fibbi[3], Alessio Papini[4], Cristina Gonnelli[2], Ilaria Colzi[2]

[1] Department of Biology, Università' degli Studi di Firenze, Via Micheli 1, Florence 50121, Italy; [2] Department of Biology, Università degli Studi di Firenze, Via Micheli 1, Florence 50121, Italy; [3] G.I.D.A. S.p.A, Via di Baciacavallo 36, 59100 Prato, Italy; [4] Department of Plant Biology, Università degli Studi di Firenze, Via La Pira 4, Florence, Italy

Nickel is a highly-demanded metal in the industrial sector, primarily due to its role in the production of lithium-ion batteries, stainless steel and nickel alloys. However, conventional methods of Ni extraction often lead to soil erosion due to the overuse of both heavy machinery and harmful chemicals, posing serious threats to the environment. In this context, agromining, i.e. the use of plants to extract trace elements from contaminated soils and to recover them from the plant biomass, offers a promising solution for the recovery of Ni from contaminated substrates, such as soils, sediments, and even activated sludge from wastewater treatment plant. In particular, hyperaccumulators from the Odontarrhena genus are specialized plants growing on serpentine soils (highly rich in Ni levels) with a remarkable capacity to accumulate extraordinarily high levels of Ni in their aboveground tissues, making them ideal candidates for agromining applications. However, since Ni accumulation depends on several factors, especially high and fast plant biomass production and soil health, it is crucial to adopt effective and sustainable strategies to maximize phytoextraction efficiency with low ecological impact. In this context, organic amendments are well-known to improve soil structure, reduce soil erosion and supply essential nutrients. Hence, by enriching the soil with organic matter, these amendments not only could support the growth of hyperaccumulator plants, but also enhance their ability to extract metals from the soil while creating a healthier ecosystem that can sustain both plant growth and metal recovery over time. In the present study, we carried out a 60-day pot experiment to evaluate the efficacy of two biostimulants - spirulin, i.e. the dried biomass produced from the cyanobacterium Athrospira platensis, and wood distillate (WD), a by-product of the pyrolysis of plant biomass - on enhancing both plant growth and Ni accumulation in Odontarrhena decipiens (Nyár.). Plants were grown in serpentine soil and treated with varying concentrations of spirulin (0.1%, 0.5%, and 1% (m/v)) and wood distillate (0.1%, 0.2%, 0.3%, and 0.5% (v/v)), which were applied in three different forms: foliar spray, fertirrigation and a combination of both. Compared to non-treated plants, O. decipiens fertirrigated with spirulin at 1% and with WD at 0.5% exhibited a significant increase in both plant fresh weight (over 50% in both cases) and dry weight (50% and 38% increase, respectively), suggesting a key role for both biostimulants in increasing plant growth and overall biomass production. Regarding the Ni accumulation, application of 0.1% WD increased plant leaf Ni content by 45%, indicating that both WD-mediated biomass increase and Ni accumulation improvement were not directly correlated. On the other hand, application of 1% spirulin showed the highest leaf Ni accumulation, which increased significantly compared to non-treated plants, suggesting a dual role for this concentration in boosting both plant biomass and phytoextraction capacity. The present findings not only contribute to the understanding of agromining as a sustainable metal recovery approach, but also underscore the viability of incorporating biostimulants into agromining strategies to maximize metal recovery while potentially promoting ecological restoration of contaminated areas.

https://conferenceyoungbotanists.com/abstracts/pablo.carrillvaglini

Talk – Urban wastewater phytoremediation by autochthonous microalgae in winter season: indoor and outdoor trials

Pierluigi Giacò[1], Elisa Benà[1], Sara Demaria[1], Costanza Baldisserotto[1], Giulia Zanotti[2], Simonetta Pancaldi[3]

[1] Department of Environmental and Prevention Sciences, University of Ferrara, C.so Ercole I d'Este, 32, 44121 Ferrara, Italy; [2] HERA SpA – Direzione Acqua, Via C. Diana, 40, 44044 Cassana (Ferrara), Italy; [3] Department of Environmental and Prevention Sciences, University of Ferrara, C.so Ercole I d'Este, 32, 44121 Ferrara, Italy; Terra&Acqua Tech Laboratory, Technopole of Ferrara University, Via Saragat, 13, 44122 Ferrara, Italy

Water scarcity and water pollution are two of the major problems that humanity is going to face shortly. Water is mostly consumed by agriculture, industry, and housing, which then release wastewater (WW) into the environment. These effluents generally are rich in organic matter, nitrogen (N), and phosphorus (P), and their release into the environment can bring to loss in river quality, sediment contamination, and even eutrophication. Even if depuration is performed, WW treatment plants (WWTPs) are still considered a point source of pollution. Microalgae are gaining increasing attention for WW depuration thanks to their ability to remove pollutants from the wastewater (WW) with simultaneous production of biomass enriched in nutrients and other molecules of interest. As environmental conditions change widely geographically and throughout the year, sites and seasons specific tests are needed. We performed two site-specific prototype-scale experiments to test the ability of a previously isolated microalga to efficiently depurate prototype-scale volumes of WW during winter, when the environmental conditions are not optimal for microalgal growth. Two different setups were tested, one indoor and one outdoor. For both cultivations, dry biomass production, photosystem II maximum quantum yield (Fv/Fm), pigments concentrations were monitored. N and P removals were evaluated along with nutrient concentration in biomass. In addition, Escherichia coli concentration was monitored to evaluate the microalgal disinfection potential of the effluent. Interestingly, cells grown outdoor underwent severe photoinhibition for the first days, but then they adapted to the new growth conditions. Despite the absence of significant growth in both indoor and outdoor conditions, N was largely removed from the medium with the highest result recorded outdoor (almost 70%). No P removal was recorded, although P content in biomass increased both indoor and outdoor, meaning that multiple processes could be happening at the same time. Moreover, a huge decrease in E. coli content was recorded in both conditions, suggesting potential for effluent disinfection. Project funded under PR-FESR EMILIA ROMAGNA 2021-2027 (CUP F37G22000200003).

https://conferenceyoungbotanists.com/abstracts/gciplg

TALK – Enhancing plant resistance to Botrytis cinerea using Cylindrotheca closterium extract

Saverio Savio[1], Erika Bellini[2], Riccardo Lorrai[3], Chiara Frezza[4], Serena De Santis[4], Fabio Sciubba[5], Simone Ferrari[3], Roberta Congestri[1]

[1] Department of Biology, University of Rome 'Tor Vergata', Rome, Italy; [2] Department of Biology, University of Pisa, Pisa, Italy; [3] Department of Biology and biotechnologies "Charles Darwin", Sapienza University of Rome, Rome, Italy; [4] Department of Industrial, Electronic and Mechanical Engineering, Roma Tre University, Rome, Italy; [5] Department of Environmental Biology, Sapienza University of Rome, Rome, Italy

The reliance on chemical pesticides in agriculture poses significant risks to environmental and human health, prompting stricter regulatory measures that limit synthetic agrochemicals and promote organic crop production. This shift has driven interest in developing bio-based plant protection solutions. Microalgae, including cyanobacteria, have emerged as a promising source of bioproducts for diverse applications, such as pharmaceuticals, nutraceuticals, bioenergy, aquaculture, and more recently, agriculture. Owing to their wealth of bioactive compounds, including phytohormones, vitamins, carbohydrates, amino acids, and exopolymeric substances, microalgae are gaining attention for their potential as plant biostimulants, enhancing growth and resilience to stress. In this study, we explored the potential of the field isolated marine diatom Cylindrotheca closterium (Ehrenberg) D.M. Williams & Round as a source of bioactive compounds with protective effects against plant pathogens. C. closterium was mass cultivated in indoor photobioreactors under controlled conditions (25 °C, irradiance of 80 μmol photons m-2 s-1 and 12:12h L/D cycle), and the biomass, harvested at the stationary phase, was extracted using a green extraction protocol to obtain an aqueous cellular extract. Then, the diatom extract was tested for its ability to enhance plant defense against Botrytis cinerea, a notorious fungal pathogen that causes grey mold and severe yield losses in a variety of plants. Arabidopsis thaliana plants treated with a foliar spray of the diatom extract exhibited significantly increased resistance to the fungal pathogen Botrytis cinerea. This resistance was attributed to the activation of plant defense mechanisms and the prevention of fungal spore adhesion on leaf surfaces. Contact angle analysis revealed that the extract reduced surface hydrophobicity in a dose-dependent manner, making leaf surfaces more hydrophilic and less conducive to fungal attachment. The protective effects of the diatom extract extended beyond A. thaliana to crops such as Solanum lycopersicum (tomato), Solanum melongena (eggplant), and Capsicum annuum (bell pepper), with an approximate 80% reduction in lesion incidence across all tested species. Gene expression analyses confirmed the extract's role in inducing plant immune responses. Additionally, the chemical composition of the extract was characterized using FTIR and NMR spectroscopy. This study highlights the potential of microalgae-derived extracts as sustainable, eco-friendly alternatives for enhancing plant resistance to pathogens, providing a versatile tool for improving crop protection in an environmentally responsible manner.

https://conferenceyoungbotanists.com/abstracts/saverio.savio

TALK – Disentangling Intra-annual Tree Growth Responses to Hydro-Climatic Conditions: Insights from Quantitative Wood Anatomy in Peatlands

Silvia Piccinelli[1], Johannes Edvardsson[2], Christophe Corona[3], Lenka Slamova[3], Veiko Lehsten[2], Markus Stoffel[3]

[1] Franklin University Switzerland; [2] Lund University, Sweden; [3] University of Geneva, Switzerland

Peatland dynamics, influenced by climatic and hydrological fluctuations, play a crucial role in regulating carbon storage capacity and methane emissions, thereby affecting feedback processes on climate change. Persistent draining conditions driven by increasing air temperature, drought and evapotranspiration, promote soil aeration and peat mineralization boosting tree establishment, which further lower water-table levels, and eventually cause an increase in greenhouse gas emissions. Conversely, peatland tree growth is hindered by either excessively dry or waterlogged conditions, which lead to water stress in trees or limit nutrient uptake due to anoxia and soil acidity, respectively. Despite recent research efforts, dendroecological studies focused on peatland trees remain scarce, impairing a successful application in hydro-climatic reconstructions. To address this gap, we sampled and analyzed 13 Pinus sylvestris trees at Mycklemossen peatland in southern Sweden, selecting three 63-year-long chronologies: ring width (RW), radial cell-wall thickness (CWTrad) and radial diameter (Drad). While daily air temperature, precipitation and estimated water-table data were correlated with RW, xylem traits were assessed at an intra-seasonal resolution, by dividing each ring into five equal-width sectors and computing five chronologies per trait. Our results provide significant, albeit variable, hydro-climatic responses among wood parameters, with the strongest signal detected for temperature in CWTrad and Drad, resulting in i) a positive correlation during the beginning of the growing season for CWTrad (March-May, S3-4), and ii) a negative correlation during spring and summer for Drad (March-August, S4). While growth responses to water-table were absent in RW chronologies, a significant influence was observed in the earlywood formation of both Drad and CWTrad during summer of the previous year of ring formation (July-August, S1-3), with negative and positive correlations, respectively. Moreover, a variable but significant positive effect of precipitation was detected in CWTrad, though not visible in RW. Our novel findings offer a crucial advancement in dendroecological research, confirming the value of QWA analyses over RW, allowing for more accurate hydro-climatic reconstruction models in peatland environments, extremely needed in the actual context of global change.

https://conferenceyoungbotanists.com/abstracts/spiccinelli

TALK – Unveiling the biosynthetic potential of lichens: a comparative genomic analysis of secondary metabolite diversity in ascomycetes

Anna Pasinato[1], Laura Maglione[1], Garima Singh[2]

[1] Department of Biology, University of Padua; [2] Department of Biology, University of Padua; Botanical Garden of Padua

Lichens, a symbiotic association between a fungus and one or more photobionts, have been considered a rich source of secondary metabolites, owing to the diverse array of bioactive compounds identified from the fungal partner. However, this assumption has not been systematically tested. Directly comparing the chemical diversity of organisms is challenging when using secreted metabolites as a metric, as metabolite secretion is influenced by spatial and temporal cues as well as life stages. Genome mining for biosynthetic gene clusters (BGCs), however, provides an excellent proxy for assessing the biochemical potential of these organisms. In this study, we analyzed 374 genomes of Ascomycete fungi, comprising 136 lichenized and 238 non-lichenized taxa, to compare their biosynthetic potential. Using the automated pipeline antiSMASH, we identified all biosynthetic gene clusters (BGCs) present in these genomes. To assess whether there was a significant difference in biosynthetic potential between lichenized and non-lichenized fungi, we conducted a pairwise t-test. Additionally, we performed a randomization test with 100 samples, using 10,000 replicates, to further validate the results and account for potential sampling variability. We identified 13,687 BGCs, majorly belonging to four classes: polyketide synthase (PKS), terpene, non-ribosomal peptide synthase (NRPS), ribosomally synthesized and post-translationally modified peptide (RiPP), and hybrid BGCs. We found that that lichenized fungi harbor a higher number of BGCs compared to non-lichenized fungi, with a notable enrichment in PKS gene clusters. To further investigate the relationship between phylogeny and BGC richness, we compared closely related lichenized and non-lichenized fungi within the classes Dothidiomycetes, Eurotiomycetes and Lichinomycetes. In Dothidiomycetes and Eurotiomycetes, lichenized fungi exhibit levels of BGC enrichment comparable to those observed in the largest lichenized fungal class, Lecanoromycetes. Notably, Lichinomycetes display a general reduction in BGCs regardless of lifestyle. This class is characterized by smaller genome sizes, which likely contribute to a significant reduction in their secondary metabolite gene content. We propose that the multispecies complex lifestyle of lichens may have driven the diversification of biosynthetic genes in this group of fungi. This study highlights the influence of both lifestyle and evolutionary lineage on BGC richness and provides compelling evidence positioning lichens as promising candidates for biotechnological exploration of their secondary metabolite potential.

https://conferenceyoungbotanists.com/abstracts/anna.pasinato

POSTER – The Mystery of Blue Flowers: Sequencing and Analysis of the Cornflower Genome

Chiara Dassow[1], Boas Pucker[2]

[1] SynBio2024-Team, Plant Biotechnology and Bioinformatics, Institute of Plant Biology & BRICS, TU Braunschweig, 38106 Braunschweig,Germany; [2] Plant Biotechnology and Bioinformatics, Institute of Plant Biology & BRICS,TU Braunschweig,38106 Braunschweig,Germany

Blue flower colouration in plants has fascinated researchers for centuries and remains a subject of great interest in plant biology. The most prominent mechanism responsible for blue flower colouration is the usage of an anthocyanin, delphinidin. Only a few species have been described to have blue flower colouration due to the formation of a metal ion complex and no genetic data seems available. An example of this is the cornflower (Centaurea cyanus). In this study, we employed Oxford Nanopore Technology (ONT) to sequence the cornflower genome, providing a comprehensive framework for genetic exploration. The sequencing data were used to assemble a high-quality reference genome sequence, enabling the detailed analysis of gene networks associated with pigment biosynthesis and metal ion complexation. Basecalling was performed with Dorado, and long reads were corrected with HERRO. The assembly had a genome size of 721 Mbp, 391 contigs, an N50 of 16.35 Mbp and a BUSCO score of 98.8 %. Structural annotation was achieved with GeMoMa with a total number of 28,763 genes. A customized annotation pipeline was applied to identify the key genes for the flavonoid biosynthesis pathway, shedding light on the molecular processes that govern this unique colouration. Our results highlight specific genes implicated in the biosynthesis of anthocyanins (e.g. bHLH42:CC08661, ANS: CC18886, F3H: CC10283) and specific transferases that are critical for the linkages of side chains to the flavonoid structure, which are needed for the formation of the metal ion complex (e.g. Glycosyltransferase: CC25081, Malonylglycosyltransferase: CC12466). This research not only advances our understanding of the genetic and molecular basis of blue flower colouration but also provides a valuable genomic resource for future studies on the cornflower and related species. The elucidation of these mechanisms has implications for fields ranging from ornamental horticulture to synthetic biology, where recreating or enhancing blue pigmentation remains a significant challenge.

https://conferenceyoungbotanists.com/abstracts/c.dassow

TALK – First steps towards conservation of endemic Salvia in Italy with population genomics

Chiara Paleni[1], Cristina Puricelli[1], Camilla Pieri[1], Silvia Manrique Urpì[2], Larissa De Paola[3], Aureliano Bombarely[4], Martin Kater[1], Carla Lambertini[5]

[1] Museo Orto Botanico di Brera e Erbario, MOBE, Università degli Studi di Milano, Milan, Italy; [2] Instituto Universitario de Conservación y Mejora de la Agrodiversidad Valenciana, COMAV, Universitat Politècnica de València, Valencia, Spain; [3] Groningen Institute for Evolutionary Life Sciences, GELIFES, University of Groningen, Groningen, The Netherlands; [4] Instituto de Biologia Molecular y Celular de Plantas, IBMCP (CSIC-UPV), Valencia, Spain; [5] Dipartimento di Bioscienze, Università degli Studi di Milano, Milan, Italy

The Salvia genus is well known in botanical gardens for its long, shared history with humans, as medicinal, culinary and aromatic plants; but while domesticated plants like kitchen sage (S. officinalis) and rosemary (S. rosmarinus) enjoy great popularity, their wild relatives are less known. Around 20 species of Salvia grow natively in Italy, of which S. pratensis, one of the most common, is closely related to endemic taxa whose classification has been debated in the past (S. ceratophylloides, S. saccardiana, S. haematodes, S. pratensis subsp. bertolonii). In this project we investigated the geographic distribution of genetic diversity in Salvia populations via a sampling campaign in the entire peninsula, thanks to a network of contributors coordinated by the Botanical Garden of Brera (coming from other botanical gardens, institutions, or individuals). The aim of the study is to create a phylogeny for the genus supported by genome-wide data and verify whether there is genetic isolation between different taxa of the pratensis group that corroborates their species status, to finally develop genetic markers to identify endemics more easily. The long-term goal of the project is to develop ex situ collections that adequately represent the genetic diversity present in natural populations. The collection of dry leaf samples was analysed with the Genotyping-By-Sequencing (GBS) method, which allows to obtain thousands of markers distributed all over the genome. The S. pratensis genome was sequenced and assembled with PacBio HiFi data to serve as a reference and annotated with information on gene locations and function. The results on 155 samples, 14 taxa show separation between the endemic taxa and S. pratensis, which is split in three lineages: one lineage in Northern and Central Italy; S. saccardiana in sympatry but clearly genetically isolated from S. pratensis in Veneto; and a lineage including samples identified as both S. haematodes and S. pratensis coming from southern Italy. Subspecies bertolonii is instead clustering within S. pratensis. Moreover, different levels of ploidy were seen inside the Salvia genus and separation was seen between other groups of related species (S. verbenaca and S. clandestina; S. argentea and S. desoleana, an endemism of Sardinia). More analyses are in progress to include additional samples from the range of S. saccardiana and other populations and species. The results from this project will give a clearer idea of the evolution of this genus in Italy and help identify morphologically similar species with genetic data. The project is a case study for the use of second and third generation sequencing applied to study and conservation of biodiversity in an Italian botanical garden and in nature.

https://conferenceyoungbotanists.com/abstracts/chiara.paleni.97

Talk – Adaptation to ash dieback disease in natural populations of European ash

Dario Galanti[1], Connor Tyler[2], Angela Biro[2], Daniel Wood[2], Richard Buggs[3], Richard Nichols[4], Laura Kelly[3]

[1] 1 Plant Health and Adaptation, Royal Botanic Gardens, Kew, Richmond, UK. 2 School of Biological and Behavioural Sciences, Queen Mary University of London, Mile End Road, London, UK.; [2] 1; [3] 1,2; [4] 2

Natural tree populations are exposed to increasing threats from biotic and abiotic stressors. One recent case with large predicted ecological and economic consequences is ash dieback, a fungal disease currently decimating ash (Fraxinus excelsior) populations in the UK and northern Europe. Although there is some evidence that European ash populations are already adapting to the disease via selection on standing genetic variation, it is still unclear if this process will be fast enough to conserve populations. Also, it is unclear if novel genetic variation could be generated at a rate fast enough to make it available to selection. To investigate these questions and predict the future prospects for ash populations in northern Europe, we undertook a large whole genome sequencing effort to screen three UK populations (~930 trees) for genetic variants associated with resistance to the disease. We investigated this via Genome Wide Association, using different phenotypes such as visual assessments of disease damage and the quantification of fungal DNA load on the trees. Here we present these preliminary results and discuss comparisons with previous findings and plans for future investigations. Related to the latter, we assigned pedigrees including several parent-offspring pairs that will allow us to 1) look for alleles changing in frequency due to selection on standing genetic variation and 2) track the formation of de-novo variants since the arrival of the epidemic. In particular, we are interested in the role of novel Structural Variants (SVs), introduced by processes such as transposable element activity and recombination that have the potential to quickly generate large amounts of novel genetic variation. With this in mind, we are currently generating long read sequencing data from assigned parents and their offspring, to investigate SV formation and selection in the new generation of ash trees.

https://conferenceyoungbotanists.com/abstracts/d.galanti

TALK – Exploring rhizobacteria-induced molecular pathways in Solanum lycopersicum

Giulia Ghirardello[1], Rosalba Cipriani[1], Sebastiano Nigris[1], Barbara Baldan[1]

[1] Università degli Studi di Padova

Plants cohabit and interact with diverse soil microorganisms, that are archaea, bacteria, fungi, and protists, which form the root microbiota. These communities play a pivotal role in enhancing plant growth through improved nutrient uptake, immunity, and stress tolerance. Here, we examine the role of bacterial species isolated from a commercial compost (SESA s.p.a.) on Solanum lycopersicum cv. Micro-Tom growth and health. Firstly, we identified six main bacterial species from the culturable microbiota of the compost, belonging to Bacillus, Kocuria, Glutamicibacter and Microbacterium genera. Tests for their plant growth-promoting traits revealed their capacity to solubilize phosphorus, produce siderophores and synthesise auxin. The tomato seedlings were grown in vitro and inoculated with single bacterial species to investigate the early plant responses to colonisation through molecular and microscopic techniques. RTqPCR and RNAseq analysis of the plant transcriptome highlighted a specificity in the expression profile of genes representing pathways involved in plant-microbe interplays, such as flavonoid biosynthesis and ethylene production, as well as the immunity system related to the different bacterial species. Moreover, the bacteria expressing fluorescent-tag proteins enabled their tracking through tomato plant tissues and organs by confocal microscopy. Finally, a preliminary analysis of the metabolomic profile induced in tomato root and shoot tissues and exudates shows the signalling molecules and metabolites produced by the interaction. This study contributes to deciphering the molecular signalling behind the interactions between plants and beneficial bacteria in the context of the promotion of sustainable agriculture practices proposed by the European Union within the EU Sustainable Goals 2030.

https://conferenceyoungbotanists.com/abstracts/giulia.ghirardello

TALK – Genomic and phylogenomic analyses of Bradyrhizobia associated with Tuber magnatum

Jacopo Vujovic[1], Simone Graziosi[1], Benucci Gian[2], Federico Puliga[1], Mirco Iotti[3], Antonella Amicucci[4], Gregory Bonito[2], Alessandra Zambonelli[1]

[1] Università di Bologna; [2] Michigan state University; [3] Università degli studi dell'Aquila; [4] Università di Urbino

The white truffle (Tuber magnatum Picco) is the most prized truffle, but cultivating it on a large scale remains challenging compared to other valuable Tuber species. Moreover, the mycelium of T. magnatum has not been successfully cultivated until recently, posing significant challenges in experimental settings. In our recent work Graziosi et al. 2024, we identified beneficial interactions between T. magnatum mycelium and Bradyrhizobia. These interactions enable the successful in vitro growth of T. magnatum mycelium. Both the isolated T. magnatum and the associated bacteria showed a mutual dependency on modified Woody Plant Medium (mWPM). Neither the bacteria nor the T. magnatum mycelium could grow independently on mWPM. Phylogenetic analyses using 16S rRNA, glnII, recA and nifH genes revealed that these bacterial strains are a monophyletic group, distributed across five subgroups. These strains belong to a previously undescribed lineage within the Bradyrhizobium jicamae supergroup of the Bradyrhizobium genus. In this study, we sequenced the genomes of two bacterial strains (17.3.1;41.3.2), which were associated with the most vigorous T. magnatum isolate (TMG5072). Using Element AVITI system we generated 150 bp paired-end reads. Phylogenomic analyses, conducted with over 400 single-copy orthologous genes conserved in bacteria (BUSCO), confirmed the placement within the B.jicamae supergroup. These strains are positioned in a new sister clade alongside the recently described species B. roseum. The ongoing analysis of the first two sequenced genomes aims to explore the metabolic potential of these bacteria, focusing on understanding their potential role in promoting the in vitro growth of T. magnatum, particularly in relation to carbohydrate and nitrogen metabolism. Establishing stable T. magnatum mycelial cultures and gaining a deeper understanding of the associated bacteria could lead to the development of new biotechnologies for cultivating the white truffle. Furthermore, this knowledge may provide a foundation for further studies on the biology of this species. Graziosi, S., Puliga, F., Iotti, M., Amicucci, A. & Zambonelli, A. (2024) In vitro interactions between Bradyrhizobium spp. and Tuber magnatum mycelium. Environmental Microbiology Reports, 16(3), e13271. https://doi.org/10.1111/1758-2229.13271

https://conferenceyoungbotanists.com/abstracts/jacopo.vujovic2

POSTER – The LIFE Seedforce project: a comprehensive genotyping initiative to assist the conservation of endangered Habitat Directive plant species

Paloma Perez-Bello Gil[1], Fabio Marroni[1], Emanuele De Paoli[1], Valentino Casolo[1], Giuseppe Fabrini[2], Lara Dixon[3], Roberta M. Ceriani[4], Luciano di Martino[5], Blanka Ravnjak[6], Joseph Buhagiar[7], Gianluigi Bacchetta[8], Antonia Cristaudo[9], Gabriele Casazza[10], Cristina Salmeri[11], Mariacristina Villani[12], Sara Magrini[13], Costantino Bonomi[14]

[1] Dipartimento di Scienze AgroAlimentari Ambientali e Animali, Università degli Studi di Udine, Udine, Italy; [2] Dipartimento di Biologia Ambientale, Sapienza Università, Rome, Italy; [3] Conservatoire botanique national méditerranéen de Porquerolles, Hyères, France; [4] Centro Flora Autoctona della Lombardia, Parco Monte Barro, Galbiate, Italy; [5] Ente Parco Nazionale della Majella, Guardiagrele, Italy; [6] University of Ljubljana, Biotechnical faculty, Botanic Garden, Ljubljana, Slovenia; [7] Universita' ta' Malta, MSIDA, Malta; [8] Centro Conservazione Biodiversità (CCB), Dipartimento di Scienze della Vita e dell'Ambiente, Università degli Studi di Cagliari, Cagliari, Italy; [9] Università degli Studi di Catania, Catania, Italy; [10] Università degli Studi di Genova, Genova, Italy; [11] Università degli Studi di Palermo, Palermo, Italy; [12] Centro di Ateneo Orto Botanico dell'Università di Padova, Padova, Italy; [13] Università degli Studi della Tuscia - Dipartimento di Scienze Ecologiche e Biologiche, Viterbo, Italy; [14] Museo delle Scienze (MUSE), Trento, Italy

We present the approach and preliminary results of the LIFE Seedforce project (LIFE20 NAT/IT/001468), which aims to improve the conservation status of 29 endangered native plant species in Italy, Malta, France and Slovenia (https://lifeseedforce.eu/en/). Assessing genetic diversity of populations is an essential aspect while defining a specific conservation strategy. Minimizing the selection of closely related individuals reduces the risk of inbreeding, ensuring the adaptability and long-term survival of the translocated populations. We conducted a genetic diversity survey of the target species using double digest Restriction Associated DNA sequencing (ddRAD-seq), a high-throughput genotyping method capable of identifying thousands of single-nucleotide polymorphisms (SNPs), the most frequent type of genetic variation between individuals. This approach is particularly suitable for non-model organisms for which no reference genomes are available and allows for cost-effective sequencing by processing DNA from either single or pooled individuals. With the aim of optimizing sequencing resources most of the species were sequenced after pooling DNA from eight individuals, and information on expected heterozygosity and beta diversity were obtained. For six of the project species, samples were sequenced individually; which allowed to perform expected heterozygosity and beta diversity analyses, information on observed heterozygosity, kinship, inbreeding and population structure. In total, approximately 500 samples were sequenced individually, and 800 were sequenced as 100 pools of eight individuals each and two different pipelines were created (one for individual approach and another for pooled individuals). Our results showed that overall, for the species that were sequenced following the individual approach heterozygosity was low, ranging from 10% to 4% with inbreeding values higher than zero in all the species. For most of species inbreeding coefficient was around 0.2, with the notable exception of one species (Linaria flava subsp. sardoa), in which inbreeding coefficient was higher than 0.9. The individual approach also showed high inter-population differentiation within the same species. The pattern of low genetic diversity and high isolation is compatible with the expectation for small, fragmented populations. The pooled approach revealed low to moderate expected heterozygosity, ranging from 10% to 35%, with high population differentiation, again supporting the expectation for small, fragmented populations.

Information on genetic diversity of the populations of each species will be used to inform the translocation policies foreseen in the project.

https://conferenceyoungbotanists.com/abstracts/palperbel

TALK – FISH technique to detect T. magnatum colonization in plant roots

Simone Graziosi[1], Mélanie Januario[2], Lara Deloche[2], Mirco Iotti[3], Marc-André Selosse[2], Claude Murat[4], Aurélie Deveau[4], Philippe Rech[2], Alessandra Zambonelli[1]

[1] Department of Agricultural and Food Sciences, University of Bologna, Viale G. Fanin 44, 40127, Bologna, Italy; [2] Institut de Systématique, Évolution, Biodiversité (ISYEB – UMR 7205 – CNRS, MNHN, SU, EPHE), Muséum national d'Histoire naturelle, 57 rue Cuvier, 75005 Paris, France; [3] Department of Life, Health and Environmental Science, University of L'Aquila, Via Vetoio, 67100, Coppito, L'Aquila, Italy; [4] Université de Lorraine, INRAe, IAM, Nancy, France

Fluorescence in situ hybridization (FISH) is a powerful technique for visualizing target DNA sequences or messenger RNA (mRNA) transcripts in cultured cells, tissue sections, or whole-mount preparations. The high specificity of the probes used in FISH makes it an invaluable tool for examining the taxonomic distribution of organisms within microbiomes at small spatial scales. This method has also been employed to detect bacterial and fungal endophytism in plants. Recently, FISH was utilized to confirm the endophytic behavior of the ectomycorrhizal ascomycetes Tuber aestivum (Wulfen) Spreng. and Tuber melanosporum Vittad. (black truffle) in herbaceous plants (Schneider-Maunoury et al., 2020). Tuber magnatum Picco, one of the most prized truffles globally, forms ectomycorrhizal associations with specific broadleaf trees. However, its mycorrhizae are rarely observed in natural environments, even in productive sites, and are typically generated under controlled conditions (Hall et al., 2007). In this study, we investigated the suitability of FISH combined with Confocal Laser Scanning Microscopy (CLSM) to confirm Tuber magnatum colonization in typical ectomycorrhizal host plants and herbaceous plants. Specific 18S rRNA probes labeled with fluorescent chromophores were designed and tested alongside a generic fungal eukaryotic probe on mycelium and ectomycorrhizae of T. magnatum and closely related fungal species. The FISH-CLSM technique was then applied to herbaceous plants growing at T. magnatum fruiting sites, where the presence of T. magnatum in the soil was also confirmed using PCR with T. magnatum-specific primers. The roots of 100 host plants were collected and surface sterilized, followed by DNA amplification using T. magnatum-specific primers. Tuber magnatum was detected in 12 wild plant species and in 21 plant samples. FISH detected Tuber magnatum exclusively in the roots of Carex pendula Huds. Since the FISH technique highlights only viable cells, the discrepancy between the PCR and FISH results may stem from the short-term viability of the symbiotic hyphae, compared to mycelium in pure culture. This study highlights the potential of the FISH technique to enhance our understanding of plant-fungus interactions in natural environments. 1) I. Hall, B. Gordon, A. Zambonelli (2007) 1st ed., Timber Press: Portland, OR, USA, 2007, p. 304 2) L. Schneider-Maunoury, A. Deveau, M. Moreno, F. Todesco, S. Belmondo, C. Murat, P.E. Courty, M. Jakalski, M.A. Selosse (2020) New Phytol., 225, 2542–2556

https://conferenceyoungbotanists.com/abstracts/simone.graziosi5

TALK – Antifungal activity of components from essential oils against microfungi isolated from industrial resins.

Alberto Massimi[1], Francesco Gabriele[2], Marco Leonardi[1], Cinzia Casieri[2], Mirco Iotti[1], Nicoletta Spreti[2]

[1] Dipartimento di medicina Clinica, Sanità Pubblica Scienze della Vita e dell'Ambiente; [2] Dipartimento di Scienze Fisiche e Chimiche, Università dell'Aquila

Essential oils produced by certain plants have been used since ancient times for their significant anti-inflammatory, antioxidant, biocidal, and antiparasitic properties. Many of these oils have found widespread use in industrial applications, ranging from food preservation to the production of plant protection products, as well as in the medical field. In this study, the potential biocidal activity in vitro of the most abundant components of essential oils from oregano (carvacrol), thyme (thymol), and lavender (linalool) was evaluated on four fungal species isolated from industrial resins used for the conservation of monuments. All pure cultures were molecularly identified by amplification and sequencing of their ITS regions. The four most frequent fungal species were: Cladosporium neolangeronii Bensch & Samson, Cladosporium myrtacearum K. Schub., U. Braun & R.G. Shivas, Aspergillus versicolor (Vuill.) Tirab., and Penicillium rubens (Biourge). Each strain was cultured on Petri dishes containing PDA with biocide concentrations ranging from 0% to 0.1%, and colony diameters were measured every 2-3 days. Linalool was found to be the least effective biocide, as at the highest concentration it slowed the growth of all isolates without completely inhibiting colony development. Carvacrol was the most efficient biocide, being able to inhibit the growth of all isolates even at the lowest concentration. Thymol exhibited intermediate characteristics, inhibiting growth up to concentrations of 0.05%. The conidia present in the inocula were transferred to plates without biocide to assess whether the effects of the tested substances were fungicidal or fungistatic. Both carvacrol and thymol showed biocidal effects at the highest concentration (0.1%), which was ten times lower than the maximum threshold concentration above which the biocide must be classified as extremely toxic to humans (GSH06). All tests were also replicated in liquid culture, confirming the results obtained on solid medium. In conclusion, carvacrol emerges as a promising natural biocide, capable of replacing the currently used synthetic compounds, which pose risks to health and the environment, offering a safer and eco-friendly alternative.

https://conferenceyoungbotanists.com/abstracts/albertomassimi

TALK – Landraces for valorising mountain areas: the case study of 'Articiok di Malegno' (Cynara cardunculus subsp. scolymus L. Hayek)

Alex Alberto[1], Pedrali, D.[2], Zuccolo, M.[2], Giupponi, L.[3], Giorgi, A.[3]

[1] Centre of Applied Studies for the Sustainable Management and Protection of Mountain Areas – CRC Ge.S.Di.Mont., University of Milan, Via Morino 8, 25048 Edolo (BS), Italy; [2] Centre of Applied Studies for the Sustainable Management and Protection of Mountain Areas – CRC Ge.S.Di.Mont., University of Milan, Via Morino 8, 25048 Edolo (BS), Italy;; [3] Centre of Applied Studies for the Sustainable Management and Protection of Mountain Areas – CRC Ge.S.Di.Mont., University of Milan, Via Morino 8, 25048 Edolo (BS), Italy; Department of Agricultural and Environmental Sciences - Production, Landscape and Agroenergy, University of Milan, Via Celoria 2, 20133 Milan, Italy.

Plant agrobiodiversity comprises wild relatives, landraces, and modern cultivars of agricultural and food interest. Landraces are traditional crop varieties, locally adapted, that can hold high value in terms of their agronomic and phytochemical-nutritional characteristics, as well as their ability to adapt to climatic change. In Italy, landraces are mainly located in mountain areas, thanks to the work of the inhabitants who have preserved them in time. Just for their origin, they have optimal characteristics for mountain coltivation and they are the perfect candidate for the creation the new agri-food chains in mountain. "Carciofo di Malegno" is a landrace of Cynara cardunculus subsp. scolymus cultivated in Camonica Valley (northern Italy) and it is the only alpine artichoke known to date. The cultivation of this artichoke in the municipality of Malegno is recorded in a 1904 text from the province of Brescia where its particular flavour is mentioned. The morphological characteristics of the artichoke outline demonstrated that, due to its spiky shape, "Carciofo di Malegno" differs from any other artichoke sample considered, and it appears to be similar to those belonging to the "Spinosi" group. The capitula of the "Carciofo di Malegno" showed a content of chlorogenic acid (497,2 ± 116,0 mg/100 g DW) and cynarine (7,4 ± 1,2 mg/100 g DW) comparable with that of the commercial cultivar, and luteolin was detected in a significant amount (9,4 ± 1,5 mg/100 g DW) only in the stems and in the edible parts of the capitula. In all the artichokes included in the analysis, the receptacle and the inner fleshy bracts (edible parts) had a content of these two caffeoylquinic derivatives higher than the non-edible parts of the capitula. A MaxEnt distribution model showed that in the coming decades (2040–2060s), the cultivation of this landrace could expand to the pre-Alps and Alps of Lombardy. Climate change may promote the diffusion of "Carciofo di Malegno", contributing to preservation and the enhancement of this landrace and generating sustainable income opportunities in mountain areas through exploring new food or medicinal applications. These results made it possible to valorise a local product and lay the foundations for a collaboration between the University of Milan - Unimont, the Tevini liqueur factory in Edolo and the municipality of Malegno. Starting with the leaves of the artichoke plant, considered a waste product, the Tevini liquor factory developed a hydro-alcoholic extract that was then used to produce three prototypes of spirits: a liqueur, a bitter and a gin. As part of the living lab, prototypes were assessed through a public sensory analysis held at the Unimont center. In this process, the liqueur emerged as the most favored prototype. Ultimately, the liqueur was developed and primarily sold at fairs and Christmas markets across Lombardy. This concrete outcome has brought economic benefits, fostering sustainable development in the mountainous Camonica Valley.

https://conferenceyoungbotanists.com/abstracts/alex.alberto

TALK – Epiphytic lichen biodiversity and species distribution in the area of the University Campus of Salerno (Italy).

Dario Nicola Tangredi[1], Francesca Giuliano[1], Angela Cicatelli[1], Francesco Guarino[1], Stefano Castiglione[1]

[1] University of Salerno

Lichens are symbiotic associations between fungi (mycobionts), primarily ascomycetes, and green algae or cyanobacteria (photobionts). This symbiotic relationship is one of the most successful examples of fungi obtaining carbohydrates, with nearly one-fifth of all known fungal species being obligate lichen-formers. Unlike plants, lichens lack a protective outer layer and thus absorb nutrients directly into their thalli from rainwater and the atmosphere. Epiphytic lichens are among the most important biomonitors of environmental pollution. They serve as sensitive indicators to assess the biological effects of pollutants by observing changes at community or population levels, and as accumulative monitors of persistent pollutants by analyzing their trace element content. The aim of this study was to evaluate, for the first time, the epiphytic lichen biodiversity and species distribution in the area of the University Campus of Salerno, localized in the southern Italy and covering a total surface of 1.200.000 m2. Epiphytic lichen thalli were collected in 20 square plots (33x33 m), from May 2022 to April 2024 in the established sampling units (SUs) of the University Campus. In this context, the lime trees with subacid bark were used. The different lichen species were characterized in the laboratory by means stereomicroscope, optical microscope, and chemical reagents commonly used in lichenology studies. Color, morphology and different structures of thalli were described. A high abundance of nitrophyc (e.g., Xanthoria parietina) crusted (e.g., Lecidella elaeochroma) and foliose (e.g., Punctelia subrudecta) macrolichens were identified (20). The lichen biodiversity index (LBI) ranged between 17 and 103, and an interesting trend was revealed along the SUs. From the SU located near the bus station (LBI value of 44), toward the internal area of the campus (LBI value of 68), an increasing gradient in the LBI was detected, suggesting an improvement of the air quality. However, the species of epiphytic lichens identified are recognized for their ability to tolerate major atmospheric pollutants, such as NH3 and nitrogen oxides. The LBI values recorded in the large part of the SUs can be attributable not only to a great naturalness of the site but also to a different influence of the winds, which carry pollutants along the different areas of Campus. Although the study area is in an urban context, the lichen biodiversity was very high, indicating a good degree of naturalness of this area.

https://conferenceyoungbotanists.com/abstracts/dtangredi

TALK – Urban Ethnobotany: selection process of a foreign community integrated in Milan, North of Italy.

Fabrizia Milani[1], Martina Bottoni[1], Maria Matilde Luisa Benzoni[2], Maria Vittoria Calvi[2], Piero Bruschi[3], Claudia Giuliani[1], Gelsomina Fico[1]

[1] Department of Pharmaceutical Sciences, University of Milan; [2] Department of Languages, Literatures, Cultures and Mediations, University of Milan; [3] Department of Agricultural, Environmental, Food and Forestry Science and Technology, University of Florence

While rural communities shift from natural environments to highly anthropized ones, the paradigm of ethnobotany shifts as well: humans, no more in daily contact with their original surroundings, venture in search of familiar or 'substituents' plant species in the new urban setting. If this is true when moving within the context of the same country, it is even truer when migrating from nation to nation. Undoubtedly, when diverse cultures meet in an urban scenery, remarkable phenomena of cultural exchange and contamination occur, framed within processes of reterritorialization. These intercultural phenomena are thus the main subject of study of the Urban Ethnobotany, an ever more investigated branch of ethnobotany worldwide. Though Italy has become, especially in the last decades, destination of migratory dynamics from other countries and is characterized by the presence of multiple international communities, urban ethnobotany is still largely overlooked throughout Italian territory and literature on it is still scarce. Within the framework of a three-year project titled "BE ETHNO: sharing traditions, sharing plants, sharing place, sharing future" (2024-2027, ID:2023-1454, Cariplo Foundation) we planned an ethnobotanical survey in an urban setting (Milan, Italy) with the involvement of one of the main immigrant communities. In fact, the very first phase of this project was aimed at the selection of the international community of interest, followed by bibliographic research on said community and their pluri-cultural and naturalistic landscape. According to the Annual Reports on the Presence of Migrants by the Italian Ministry of Labor and Social Policy and the Italian National Statistics Institute, in 2023 the total number of resident immigrants in Italy was 5,253,658, while the most numerous extra UE nationalities were Albania, Morocco, China, Ukraine, Bangladesh, India, Philippines, Egypt, Pakistan, Nigeria, Senegal, Sri Lanka, Moldova, Tunisia, Peru, Ecuador, Brazil, and North Macedonia. [1,2]. Lombardy is considered the region with the highest concentration of non-UE nationalities (n=1,203,138) [2]. Specifically, Milan is the third municipality in Lombardy for number of immigrants (n= 301.149; year 2023) and it especially hosts Egyptians (n=45,457), Filipinos (38,942), Chinese (37,041), and Peruvians (17,799) [3]. These preliminary data show that the Peruvian pluricultural community is one of the most prominent in Milan, as immigration of Peruvians to Italy began as early as the 1980s. Moreover, considering the presence of various generations of new Italians of Peruvian origin and the circulation of young people with higher education and entrepreneurial projects from various regions of this mega-diverse country, this community is one of the most integrated, and willing to preserve and share its traditions. Moreover, both prior personal and recent-onset work acquaintances with Peruvian mediators and scholars tilted the balance towards the selection of the Peruvian community. These connections proved vital for establishing initial contact in Milan and building links with Peruvian universities for potential academic exchanges. Finally, they were pivotal for the detection of Peruvian local Floras, useful for the analysis of the naturalistic and floristic landscape in preparation to the first interviews with Peruvian informants established in Milan. References: [1] https://immigrazione.it/docs/2024/ml-xiv-rapporto-gli-stranieri-nel-mercato-del-lavoro-in-Italia-2024.pdf [2] http://dati.istat.it/Index.aspx [3] https://sisi.comune.milano.it/

https://conferenceyoungbotanists.com/abstracts/fabrizia.milani

TALK – Conversion of grape pomace into fungal biomass: a study of Pleurotus cultivation for a sustainable agro-residue management

Federico Puliga[1], Veronica Zuffi[1], Dario Mercatante[1], Maria Teresa Rodriguez-Estrada[1], Santiago Sanchez-Cortes[2], Ornella Francioso[1], Alessandra Zambonelli[1]

[1] Department of Agricultural and Food Sciences, University of Bologna, Viale G. Fanin 40-50, 40127 Bologna, Italy.; [2] Instituto de Estructura de La Materia, IEM- CSIC, Serrano, 121, E-28006 Madrid, Spain.

Grape production, with an annual output of approximately 80.1 million tons, generates substantial agricultural waste, particularly grape pomace, a by-product rich in bioactive compounds. Moreover, its reuse is strongly recommended since storage or direct application can lead to environmental issues. This study explores the feasibility of using exhausted grape pomace, both alone and in combination with anaerobic digestate, as substrates for cultivating Pleurotus mushroom species. Grape pomace's rich composition in fiber, lipids, sugars, proteins, and phenolic compounds makes it a promising substrate. Elemental analyses revealed high carbon (46%) and nitrogen (2.5%) content, along with greater levels of macro and microelements (P, Ca, Mg, Fe) compared to conventional substrate. Fourier transform infrared spectroscopy (FTIR) identified aliphatic groups associated with fatty acids from the seeds and polysaccharide bands typical of the seedless part of grape pomace. Fatty acid evaluation confirmed partial glycerides with linoleic acid content exceeding 62%, while the phenolic composition analysis highlighted a predominance of bound phenols. These chemical characteristics led to a significant increase in production for all tested Pleurotus species, with statistical differences observed in the fresh weights of mushrooms grown with grape pomace compared to those grown without it. The mixture with digestate gave the most promising results, likely due to the balanced pH values around neutrality. Lastly, FTIR and Surface-enhanced Raman Scattering (SERS) spectra of the fruiting bodies grown on different substrates were comparable, indicating consistent quality characteristics in the mushrooms. These results provide attractive perspectives for both more sustainable grape pomace management and for the improvement of mushroom cultivation efficiency.

https://conferenceyoungbotanists.com/abstracts/federico.puliga2

POSTER – Fungal Bioresources for Mycoremediation of Glyphosate- and AMPA-Contaminated Agricultural Soils

Francesca Emili[1], Veronica Spinelli[1], Andrea Ceci[1], Valeria Crosara[1], Massimo Reverberi[1], Domenico Davolos[2], Anna Maria Persiani[1]

[1] Department of Environmental Biology, Sapienza University of Rome, Piazzale Aldo Moro 5, 00185 Rome, Italy; [2] Department of Technological Innovations and Safety of Plants, Products and Anthropic Settlements (DIT), INAIL, Research Area, Via R. Ferruzzi 38/40, 00143 Rome, Italy

Glyphosate (GP) is a widely used herbicide in agriculture, well known for its broad-spectrum effectiveness. However, its extensive use has caused significant contamination of soils and water resources. Despite concerns about its environmental and health risks, glyphosate remains authorized for use in the European Union. This situation calls for sustainable solutions to reduce GP concentration in agricultural soils. Recent research has shown that certain fungi, isolated from contaminated matrices, can degrade GP and its primary metabolite aminomethylphosphonic acid (AMPA), which exhibits a greater toxicity and persistence than GP. This study aims to explore the fungal communities in GP-contaminated agricultural soil and isolate strains with potential in mycoremediation. Here, six soil samples were collected from an agricultural field with a history of glyphosate use. DNA metabarcoding analisys of ITS region using Oxford Nanopore technology was carried out to analyze the fungal communities in soil samples. Biodiversity was assessed using the Shannon-Wiener and Pielou's Evenness indices. Selective enrichment procedure with a mixture of GP and AMPA as only phosphorus source was carried out to isolate fungal strains suitable for GP and AMPA degradation. Moreover, 22 strains of Clonostachys, which was the most adbundant isolated genus, were tested in liquid media with 10, 20, 30 mM GP and AMPA concentrations as the sole phosphorus source. Growth was monitored for 10 days, through spectrophotometric readings at 620 nm every 48 hours to select the most efficient degrading strains. DNA metabarcoding analisys revealed a high fungal diversity, with Linnemannia elongata, Mortierella globalpina, and Funneliformis mosseae abundantly present in all soil samples and few exclusive species were highlighted. The Shannon-Wiener index showed high biodiversity values, but the Pielou's Evenness index suggested that a few species were more abundant than others. Enrichment isolation revealed a high presence of entomopathogenic fungi including Clonostachys spp. and Paecilomyces spp., which were instead scarcely detected or absent in DNA metabarcoding data. These results suggested potential hormetic responses, such as increased growth and spore germination, in fungi exposed to low doses of GP and AMPA. The 22 Clonostachys strains showed variable growth responses to GP and AMPA exposure. At 10 mM GP, growth was observed but with reduced biomass development compared to AMPA exposure, while at 20 and 30 mM GP treatments spore germination was inhibited. For some Clonostachys strains, a slow growth was observed at 10 mM AMPA, while at 20 and 30 mM AMPA for 48 hours a stimulated growth was evident compared to the control, although this was less defined at the experiment endpoint. This work highlights the importance of integrating molecular and culturomics approaches to gain knowledge on fungi exposed to GP and on their abilities to degrade GP and AMPA. Further activities will focus on molecular perspective to study mechanism involved. In conclusion the insights gained in our study will benefit future efforts for mycoremediation of contaminated agricultural soils. The research was funded by the projects "INAIL-DIT, PAR 2022-2024, Ricerca Scientifica P8 O7" and "Glyphosate mycoremediation of agricultural soils: a broad spectrum of nature-based solutions" -protocol no.RM123188F7AAFA9E".

https://conferenceyoungbotanists.com/abstracts/francesca.emili

POSTER – Mycosium: sporulating knowledge. Why fungi?

Guido Silvano[1], Laura Chiesa[2], Beatrice Clementi[1], Barbara D'Albis[1], Danilo Di Francesco[3], Arianna Ferrara[4], Francesca Giattino[1], Tommaso Martellini[1], Elena Radelli[5], Edoardo Ricci[1], Alessandra Ronco[1], Clizia Sarni[1], Simone Subacchi[6], Jacopo Vujovic[7]

[1] Department of Biological, Geological and Environmental Sciences - BIGEA, Alma Mater Studiorum University of Bologna, Bologna, Italy; [2] Civil, Chemical, Environmental and Materials Engineering - DICAM, AMBIENTALE E DEI MATERIALI - DICAM, Alma Mater Studiorum University of Bologna, Bologna, Italy; [3] Centre for Agriculture Food Environment (C3A), University of Trento, Trento, Italy; [4] BIOME Lab, Department of Biological, Geological and EnvironmentalSciences, Alma Mater Studiorum University of Bologna, Bologna, Italy; [5] Pharmacy and Biotechnology - FABIT, Alma Mater Studiorum University of Bologna, Bologna, Italy; [6] WG Klatt Microcosmos Earth Center, Max Planck Institute for Terrestrial Microbiology (MPI-TM) and the Philipps University of Marburg; [7] Department of Agricultural and Food Sciences, Alma Mater Studiorum University of Bologna, Bologna, Italy

Fungi represent some of the most remarkable examples of evolutionary adaptation within the eukaryotic domain. Life on Earth would be fundamentally different without the Kingdom Fungi, which plays a pivotal role in global biogeochemistry by recycling carbon and mobilizing essential nutrients such as nitrogen and phosphorus. Moreover, fungi form intricate symbiotic relationships across all biological kingdoms, including humans, where they influence health, food systems, biotechnology, and medicine, underscoring their far-reaching impact. Despite these critical functions, fungi were only formally recognized as a distinct kingdom in the latter half of the 20th century. In the Italian academic context, mycology remains an underrepresented field, with few dedicated courses, limited research opportunities, and a scarcity of specialized academic chairs. To address these shortcomings, Mycosium was established as a project dedicated to raising awareness and fostering engagement within both the academic community and the broader public. The initiative has spearheaded a range of impactful activities, beginning with its inaugural symposium—a two-day event hosted by the University of Bologna that featured leading researchers from Italy and abroad. Building on this momentum, Mycosium has supported the introduction of a mycology course at the University of Bologna, established partnerships with cultural institutions such as MUSE, and played a central role in organizing Mico Cosmo Festival, Italy's first mycology-focused festival. These efforts have helped cultivate a dynamic network aimed at promoting fungal studies and fostering a deeper understanding of the essential roles fungi play in ecosystems and human systems. The overarching goal of Mycosium is to bridge the gaps in academic and public engagement with fungi. By exploring how fungi interact with their environments and other organisms, the initiative seeks to inspire a greater appreciation of their complexity and ecological importance. This approach also encourages broader reflections on interdependence and symbiosis, offering valuable insights into human interactions and societal structures.

https://conferenceyoungbotanists.com/abstracts/guido.silvano11

TALK – Study on the cultivation of the white truffle in abandoned fields

Letizia Conti[1], Irene Mazza[2], Claudia Perini[3], Elena Salerni[1]

[1] Department of Life Sciences, University of Siena, via P.A. Mattioli 4, 53100 Siena, Italy; [2] NBFC, National Biodiversity Future Center, Piazza Marina 61, 90133, Palermo, Italy; Department of Earth and Marine Sciences, University of Palermo, Via Archirafi 22 , 90123 Palermo, Italy; Department of Life Sciences, University of Siena, via P.A. Mattioli 4, 53100 Siena, Italy; [3] Department of Life Sciences, University of Siena, via P.A. Mattioli 4, 53100 Siena, Italy; NBFC, National Biodiversity Future Center, Piazza Marina 61, 90133, Palermo, Italy

“True tuffles” are hypogeous ectomycorrhizal ascomycetes belonging to the order Pezizales and the Tuberaceae family, naturally principally restricted to the Northern Hemisphere. Among them, the white truffle (Tuber magnatum Picco) produces fleshy fruiting bodies that are one of the most appreciated food, so much so that they are offered on the menus of the most famous restaurants in the world. The attempts to cultivate this high prized fungal species, as practiced for other few edible truffles, have often failed because many aspects of its ecology and biology remain largely unexplored and there are still various uncertainties that have to be understood and solved. Only thanks to a recent research conducted in France, positive results have been reached: i) it is possible to observe the survival in the field of T. magnatum mycorrhizas in inoculated plants, ii) it is possible to collect fruiting bodies just after 4/5 years from the planting. The interest for the cultivation of T. magnatum therefore appears remarkable, especially in the presence of abandoned fields, where characteristics of soil and environmental could be suitable for the production of the prized white truffle. In Tuscany, some areas of arable land in the plain of valleys results to be no longer adapt for agricultural activities due to new characteristics of the companies that manage the land or because not easily integrated into its cultivation systems. Truffle cultivation could therefore represent an interesting diversification of the crop system, in the face of an increase of the biodiversity of the area, for the sequestration of carbon dioxide operated by tree cultivation and for the ecological sustainability of this kind of cultivation. The main objective of this study is to evaluate the effectiveness of some agronomic planting techniques, sometimes used for the cultivation of other valuable truffle species, on the cultivation of T. magnatum in the arable land of some Tuscan farms. Experimental areas, located in environments suited to the production of white truffles, were created and usual truffle cultivation techniques were implemented in various ways. Some planting techniques that use experimental substrates, specifically prepared to encourage the rooting of the plant, the maintenance of mycorrhizae over time and to stimulate the mycorrhization process, were also evaluated. These were carried out both on seedlings previously inoculated with T. magnatum and on non-mycorrhized seedlings. Here we report the data relating to the biotic and abiotic characterization of the study areas before and one year after the planting. Moreover a real-time PCR assay for the detection and quantification of white truffle mycelium in the soil, after one year, was done.

https://conferenceyoungbotanists.com/abstracts/l.conti13

TALK – Floristic inventory of wild edible plants in the Tirli area (Northern Maremma, Italy)

Mario Pentassuglia[1], Tiziana Lombardi[1], Giovanni Bambi[1], Irene Ventura[1], Benedetta D'Ambrosio[1], Andrea Bertacchi[1], Laura Pistelli[1]

[1] Department of Agriculture, Food and Environment, University of Pisa, Via del Borghetto, 80, 56124 Pisa, Italy

Ethnobotanical studies are essential for the documentation and preservation of traditional knowledge on the use of alimurgical wild plants. This study focused on the cultural traditions and ecological systems deeply interconnected in Tirli, a small village located in the heart of Maremma territory. The region's meso-Mediterranean climate and diverse habitats provide environmental conditions that support remarkable floristic biodiversity. Field surveys conducted in 2023 and 2024 documented the floristic diversity of alimurgical plants. Data collection emphasized life-forms, chorological types and edible plant organs. Biochemical analyses conducted on selected species highlighted the content of primary metabolites (chlorophyll, carotenoids and sugars) and secondary metabolites (polyphenols and flavonoids), as well as the antioxidant activity. The floristic inventory recorded 128 taxa of Angiosperms distributed in 46 families and 106 genera. The most represented families are Asteraceae (26 taxa), Rosaceae (10 taxa) and Lamiaceae (8 taxa). The dominant life-forms include scapose Hemicryptophytes, scapose Therophytes and rosulate Hemicryptophytes. The analysis of chorological types revealed a prevalence of Euro-Mediterranean, Sub-Cosmopolitan and Steno-Mediterranean distributions, alongside the identification of one endemic species, Centaurea nigrescens Willd. subsp. pinnatifida (Fiori) Dostál. This endemic taxon, recorded for the first time in the Maremma territory during this study, enriches the floristic knowledge of the area, emphasizing the need for its ecological conservation. There is a strong association between Hemicryptophytes and Euro-Mediterranean distributions, as well as between Therophytes and wide distribution chorological type. Statistical analysis highlighted key relationships between life-forms and edible uses of specific plant organs, with scapose and rosulate Hemicryptophytes were linked to leaf use, scapose Therophytes to root use and Phanerophytes to fruit use. Asteraceae family show exceptional versatility, being associated with multiple edible parts, while Rosaceae are strongly linked to fruits. The findings highlight how the wild alimurgical flora of the Tuscan Maremma reflects an interplay between ecological adaptations and cultural practices. The most representative plants consumed by the local population were collected during their flowering period and further investigated for the determination of some bioactive compounds, such as photosynthetic pigments, primary metabolites (soluble sugars, proteins), secondary metabolites (polyphenols and flavonoids), and their respective antioxidant activity. The analyses confirmed notable variability among species. Sonchus oleraceus L. is characterized by the highest photosynthetic pigment content, followed by Cichorium intybus L. and Umbilicus rupestris (Salisb.) Dandy. Several plants exhibited a ratio chlorophyll a/chlorophyll b (range 2-3), referred to a normal growing condition. Clinopodium vulgare L. subsp. vulgare, Plantago coronopus L. and Myrtus communis L. exhibited the lowest concentration of pigments and nitrogen, but the higher polyphenols content with a significant antioxidant activity. Hypericum perforatum L. subsp. veronense (Schrank) Ces. and Laurus nobilis L. showed a notably high sugar content. This study identified the wild alimurgical flora of Tirli as a critical resource for biodiversity conservation and cultural heritage, with significant nutritional and functional value. The integration of ethnobotanical, ecological and biochemical analyses provides a robust framework for promoting the sustainable food use of wild plant species in both traditional and modern contexts.

https://conferenceyoungbotanists.com/abstracts/m.pentassuglia3

Talk – The interdisciplinarity of Urban Ethnobotany: taking the first steps within the Peruvian community living in Milan (North of Italy).

Martina Bottoni[1], Fabrizia Milani[1], Maria Vittoria Calvi[2], Piero Bruschi[3], Claudia Giuliani[1], Maria Matilde Luisa Benzoni[2], Gelsomina Fico[1]

[1] Department of Pharmaceutical Sciences, University of Milan; [2] Department of Languages, Literatures, Cultures and Mediations, University of Milan; [3] Department of Agricultural, Environmental, Food and Forestry Science and Technology, University of Florence

In the framework of a three-year project titled “BE ETHNO: sharing traditions, sharing plants, sharing place, sharing future” (2024-2027, ID:2023-1454, Cariplo Foundation) we present the first steps taken in planning the field work phase of an ethnobotanical survey in an urban setting (Milan, Italy) within the Peruvian community. The preliminary data obtained from bibliographic research on immigration patterns involving Milan, in fact, guided us in selecting this multiethnic, multilingual, and pluricultural community as subject of our investigation. First, a multidisciplinary group work was established by contacting experts of pre-Columbian civilizations, anthropologists, historians, and linguists of the Department of Languages, Literatures, Cultures, and Mediations of the University of Milan, with solid historical and socio-linguistic research experience with the Peruvian Community in Milan. This step was already pivotal to facilitate the first approach to Peruvian associations in Milan, for example by making the first encounter with the Peruvian Consul effective and beneficial. The interdisciplinary approach of work took also shape in the shared effort of adapting the ethnobotanical methodology underlying the open and semi-structured interviews at the basis of the field investigation. For example, the part of the interview dedicated to the anagraphical data of the Peruvian informants was adjusted to give space not only to the information concerning the area of origin of the informants and their families, but also specifically to the recording of phenomena of migration within the country itself, as well as the linguistic diversity associated with them. In fact, Peru has been characterized by intestine migratory movements for socio-economic and political reasons even before people left their country for others. In this framework, the population of Lima has been quite growing since the second half of 20th century. Nowadays, one third of the country population resides in the capital, which became one of the main departure points of the great Peruvian diaspora towards the USA and Europe. This undoubtedly paints a wider and more complex picture of the community now living in Milan, for their Local Ecological Knowledge is possibly the multifaceted result not only of the intertwining with Italian culture and the multiethnic landscape of Milan, but also of all these previous migratory phenomena. This adapted methodology was then tested during a trial interview with the first two Peruvian informants of our project. During this encounter, we specifically asked the respondents to help us improving the questions and our approach, thus making them actively participate to the interview not only as ‘subjects’ but also as part of the research group. Finally, in view of a future second field phase directly conducted in the country of origin and within the Citizen Science framework in which ethnobotany perfectly fits, we also made arrangements with one of them, travel organizer and guide for a sustainable and communitarian tourism, for the planning of a first exploratory and informative trip to Peru, to be made in order to better understand the megadiverse and pluricultural contexts of origin of the community, as well as their naturalistic landscapes.

https://conferenceyoungbotanists.com/abstracts/martina.bottoni

TALK – Enhancing plant photosynthetic performances by boosting plant carbonic anhydrase activity

Sara Beltrami[1], Francesca Alderotti[2], Damiano Tanini[3], Cecilia Brunetti[4], Francesco Ferrini[1], Ermes Lo Piccolo[1], Antonella Gori[1]

[1] University of Florence, Department of Agriculture, Food, Environment and Forestry (DAGRI); [2] National Research Council of Italy (CNR), Florence; [3] University of Florence, Department of Chemistry; [4] National Research Council of Italy (CNR), Institute for Sustainable Plant Protection

Photosynthesis, which provides the basis of plant productivity, holds important significance across a spectrum of agro-industrial applications. Despite genetic manipulation, alternative opportunities exist to enhance photosynthetic performances. One promising approach involves enhancing the activity of carbonic anhydrases (CAs), metalloenzymes that catalyze the reversible interconversion of carbon dioxide (CO2) and bicarbonate (HCO3−). Besides catalyzing this interconversion, CAs play a crucial role in facilitating the movement of both CO2 and HCO3− across membranes. Activation studies on animal carbonic anhydrases (CAs) highlighted that several organic compounds can modulate their activity, raising the hypothesis that treating plants with different CA-activators could increase plant photosynthetic activity. Our results showed that foliar treatments with a newly synthesized selenium-based amine (Se-AMA) improved the photosynthetic efficiency of Arabidopsis thaliana without negatively affecting plant health. Se-AMA significantly increased net photosynthesis (A) and stomatal conductance (gs) in treated plants, with the most pronounced effects observed at a concentration of 100 μM after 10 days of treatment. Higher concentrations of Se-AMA proved even more effective, boosting A and gs already after 3 days of application. A single treatment with Se-AMA at 300 μM performed in the morning enhanced plant photosynthetic performance throughout the day, confirming that the positive effect of Se-AMA on A and gs can last several hours from its application. Additionally, Se-AMA was found to increase water content in treated plants, due to the elevated transpiration rate imposed by high values of gs. These effects may be associated with the possible role of Se-AMA in regulating the activity of specific CA isoforms, which may operate together with aquaporins to facilitate water transport and stomatal regulation, thereby supporting improved physiological processes related to water absorption and resource management. Besides very preliminary, our findings highlight the potential of Se-AMA to improve plant photosynthetic performances under conditions of non-limiting water availability. Future research will focus on exploring the mechanism by examining CA activity and aquaporin expression, even under water stress conditions.

https://conferenceyoungbotanists.com/abstracts/sara.beltrami

Poster – Unlocking the potential of herbarium collections: a case study from the digitization of Silvia Zenari's specimens

Valentina Boscariol[1], Elena Canadelli[2]

[1] University of Palermo, Department of Earth and Marine Sciences, Via Archirafi 22, 90123, Palermo, Italy; University of Padova, Via 8 Febbraio 2, 35122, Padova, Italy; NBFC, Piazza Marina, 61, 90133, Palermo, Italy; [2] University of Padova, Department of Historical and Geographic Sciences and the Ancient World, Via del Vescovado 6, 35141, Padova, Italy; NBFC, Piazza Marina, 61, 90133, Palermo, Italy

Natural history collections play a key role in addressing global environmental issues, such as the conservation of biodiversity. Thanks to the vast source of information kept in the preserved collections, they have become crucial to understand how climate change and other factors are affecting biodiversity. Among these collections, herbarium specimens have been increasingly used in studying multiple aspects, ranging from taxonomy and systematics to genomics, and including ecology and evolution. These applications have been also possible due to the advancements in technological and molecular fields (e.g. use of Artificial Intelligence, High-Throughput Sequencing). In the last decades, herbarium collections have started to be digitized providing accessible metadata for exploring plant biodiversity changes over time and across spatial scales as well as making predictions about future trends. Digitization is also a fundamental step to create open access databases, promoting global studies on plant biodiversity without damaging herbarium specimens and facilitating collaboration between researchers. The italian herbarium collections are currently involved in a large-scale digitization project promoted by National Biodiversity Future Centre (NBFC), starting from the Italian Central Herbarium (HCI) in Florence. The Herbarium Patavinum (PAD), hosted in the Botanical Museum of Padova, is part of this project. It includes specimens collected by the Italian botanist Silvia Zenari who is one of the major contributors of the XX century, with a specific interest in the North-eastern Alps. In this scenario, the aim of this study is to reconstruct Zenari's biography and to characterize her collections. As a first step, we are conducting bibliographic research in the archives of the University of Padua, including the Library of the Botanical Garden, and contacting curators from institutions connected to Zenari's life and work (e.g. Museum of Natural History in Pordenone). Regarding her specimens, we collected data filtering records retrieved from GBIF as well as getting in touch with the curators of herbaria where her specimens could be preserved (e.g. HCI, MUSE, Lund Biological Museum). We expect a final count of over 20000 specimens, of which only 10% are currently indexed on GBIF. About the specimens preserved in PAD, we also plan to autonomously digitize specimens not involved in the NBFC project described above. By conducting historical research and combining data from digitization, curators and online databases we aim to have a comprehensive overview of Zenari's work. As a following step, her specimens will be used to explore distribution changes of conservation target species like endemics or policy species. Additionally, this work will help to understand the role of female scientists in the first half of XX century and to raise awareness about the historical and biological value of herbarium. To sum up, this project provides an example of valorisation of a herbarium collection using a multidisciplinary approach. Making this cultural heritage accessible is pivotal to 1) understand the past diversity and investigate current and ongoing changes 2) make available preserved collections data to scientists 3) disseminate the history of herbaria and their role.

https://conferenceyoungbotanists.com/abstracts/valentina.boscariol

TALK – Fungi's got talent: a study on fungal interactions with Gallium, Germanium, Indium and Yttrium for bio-recovery applications

Veronica Spinelli[1], Flavia Pinzari[2], Valerio Giorgio Muzzini[3], Enrica Donati[2], Valentina Iori[4], Maria Luisa Astolfi[5], Anna Maria Persiani[1], Marco Mazzonna[2], Andrea Ceci[1]

[1] Department of Environmental Biology, Sapienza University of Rome; [2] Institute for Biological Systems - National Research Council (CNR-ISB); [3] Research Institute On Terrestrial Ecosystems - National Research Council (CNR-IRET); [4] Institute of Agricultural Biology and Biotechnology - National Research Council (CNR-IBBA); [5] Department of Chemistry, Sapienza University of Rome

Strategically critical elements play important roles in modern and future technologies and are indispensable in high-tech products. Due to surging global demand, their sustainable supply is a major issue, given the environmental negative impact often associated to their extraction. Fungi in nature play crucial roles in geology and ecology, and represent valuable bioresources for sustainable recovery processes [1]. Fungi can tolerate, bioaccumulate, and transform toxic compounds and several strategic elements. Fungal-mediated bio-recovery of critical elements from electronic wastes offers an eco-friendly solution to mitigate environmental impacts, and support sustainable resource management [2]. In this study, 24 strains, isolated in previous studies and currently preserved in the culture collections of the Fungal Biodiversity Laboratory of Sapienza University of Rome and of the National Research Council, were investigated for their interactions with Gallium, Germanium, Indium and Yttrium. Tolerance screenings for these elements were performed on solid Raper Hoffman medium for 14 days at 25°C in the presence of 1.5 mM Ga as Ga2O3, 5 mM Ge as GeO2, 2.4 mM In as In2O3, 2.25 mM Y as Y2O3. Fungal tolerance was assessed by Rt:Rc (%) index, based on colony areas, and T.I. (%) index, based on dry weights [3]. The medium's pH variation and the presence of secondary biogenic minerals were also assessed. The selected fungi were then tested for siderophores production using the Chrome-Azurol-S (CAS) assay [3]. Siderophores are crucial in metal-fungi interactions and there is increasing interest in their potential for biomining. Finally, considering the relevance of laccase in bioleaching processes and the fact that these elements share chemical features with those playing primary roles in fungal biology, a screening to evaluate the production and release of laccase was carried out using the Guaiacol assay [4]. One-third of the tested strains had already released siderophores after 48 h; after 7 days, 21 strains produced siderophores, 7 of which showed high Fe-chelation activity. Laccase release was detected in only 8 strains, all basidiomycetes. Finally, all fungi could grow in all tested conditions, even though several evident effects of these elements on biomass production and morphological modification were observed. Most of the tested species resulted tolerant to Ga, Ge and In, showing indexes values higher than 70%. Interestingly, several strains showed indexes values higher than 100%, pointing out a growth stimulation due to the metal(loid) exposure. Y resulted in being more toxic, indeed only 9 species showed T.I. higher than 70%, even if most of the strains were tolerant according to Rt:Rc, suggesting an explorative mycelial growth pattern. REFERENCES 1. Gadd G.M., et al. (2012) Environ. Microbiol. Rep. 4:270–296. 2. Liang X., Gadd G.M. (2017) Microb. Biotechnol. 10:1199–1205. 3. Ceci A., et al. (2020) Appl. Sci. 10:3218. 4. Mehnert M., et al. (2017) Sol. St. Phen. 262:509–512. 5. Senthivelan T., et al. (2019) Biotechnol. Rep. 23:e00344. ACKNOWLEDGMENTS PRIN 2022 PNRR Project funded by European Union -NextGenerationEU-Project Prot. P2022ENEWL - Title "Fungal interaction with metals (FUN METALS): transformation and mechanisms for biorecovery" CUP B53D23032130001.

https://conferenceyoungbotanists.com/abstracts/veronica.spinelli

TALK – Mapping Hedera crebrescens with citizen science method

Virág Grónás[1], Péter Bodor-Pesti[2], Beáta Darabosné Maczkó[3], Mária Höhn[4]

[1] Hungarian University of Agriculture and Life Sciences; [2] Hungarian University of Agriculture and Life Sciences, Institute for Viticulture and Oenology; [3] Hungarian University of Agriculture and Life Sciences Entz Ferenc Library and Archives; [4] Hungarian University of Agriculture and Life Sciences, Institute of Agronomy, Department of Botany

Climate change has triggered major changes in the composition of natural and anthropogenic ecosystems and often resulted in the decline of natural population communities and the expansion of several, mainly alien species. The so-called lianification is also the result of the global climate change. The phenomenon refers to the uncontrolled spread of the evergreen climbers, due to mild winters, such as ivies. Hedera crebrescens Bényei-Höhn, an ivy species identified in 2017 at the Department of Botany of the former Szent István University (now Hungarian University of Agriculture and Life Sciences), Buda Campus, is one of the winners of the climate change. Due to its slight frost sensitivity, this garden species did not cause any problems earlier, but the observations over the past several years indicated that this ivy species started to spread and is even displacing native ivy (Hedera helix) and other native species from their natural habitats. Our aim was to reveal the present distribution of Hedera crebrescens and the evaluation of its invasive behaviour. We used citizen science, to collect distribution data. This method is often used in nature conservation research and to study the impact of climate change. In our university we initiated the Ivy Mapping Project which has been going on for two years with the help of volunteers. Since one of the defining traits of the species are the fruits, the main collection period is during the ripening of fruits, primarily in winter. To map species' distribution, we are collecting data from volunteers asking them to provide the locations where this ivy occurs. According to the data received so far (more than 270 H. crebrescens individuals), the species is most frequent around Budapest and in Pest County, but we received data from Komárom-Esztergom, Bács-Kiskun, Heves counties too. H. crebrescens individuals were also reported from Slovakia and Austria. Most individuals were found crawling on fences, and less were found climbing on trees. H. crebrescens was previously identified as H. hibernica. However, H. hibernica is tetraploid, but cytological studies have confirmed that H. crebrescens is a diploid species. Molecular studies also supported the distinct position of this taxon. The leaves of the two species are morphologically similar on the vegetative shoots, therefore, morphometric studies were performed aiming at distinguishing the leaves of H. crebrescens, H. hibernica, and H. helix for better identification. The leaves of the collected individuals were characterized with outline analysis. Based on the analyses, H. helix samples were well separated, but the leaves of H. crebrescens and H. hibernica could not be clearly distinguished so far. We plan to continue mapping of H. crebrescens and extending the project with the help of volunteers.

https://conferenceyoungbotanists.com/abstracts/gronas.virag

The organising committee:

Federica Betuzzi (UniGE), Geordie Biffoni (UniGE),Chiara Bonifazio (UniGE), Mattia Bosio (UniGE), Ian Briozzo (UniGE), Davide Casalino (UniGE), Mariasole Calbi (UniFI), Jacopo Calevo (Kew Gardens, UK), Gabriele Casazza (UniGE), Clara Conte (UniGE), Lucia Doni (UniGE), Maria Guerrina (UniGE), Luca Pegoraro (WSL, CH), Chiara Vallese (UniGE)

The scientific committee:

Gianmaria Bonari (Uni Siena), Florian Boucher (LECA Grenoble), Jacopo Calevo (Kew Gardens, UK), Gabriele Casazza (UniGE), Simone Di Piazza (UniGE), Steven Dodsworth (Birkbeck Uni London, UK), Karl Duffy (UniNA), Maria Guerrina (UniGE), Konstantina Koutroumpa (Bot. Garten Berlin, DE), Paola Malaspina (UniGE), Carlos Martel (Kew Gardens, UK), Laura Martinez-Suz (Kew Gardens, UK), Chiara Montagnani (UniMIBicocca), Luca Pegoraro (WSL, CH), Enrica Roccotiello (UniGE), Antonella Smeriglio (Uni Messina), Riccardo Testolin (UniBO), Salvatore Tomasello (Uni Goettingen, DE), Chiara Vallese (UniGE)

Contact:

conferenceyoungbotanists@gmail.com

Thanks to our sponsors: