

BIODIVERSITY 2025

ON BIODIVERSITY 2ND INTERNATIONAL CONFERENCE ON MEDITERRANEAN BIODIVERSITY

15TH NATIONAL CONFERENCE



BIODIVERSITY IN THE XXI CENTURY: NEW PARADIGMS FOR NEW CHALLENGES

PROGRAMME

JUNE 3-6, 2025

HOTEL GIÒ - PERUGIA CONGRESS CENTRE PERUGIA, ITALY

www.perugiabiodiversity2025.com

15th National Conference on Biodiversity 2nd International Conference on Mediterranean Biodiversity

Biodiversity in the XXI century: new paradigms for new challenges

Perugia, Italy

June 3-6, 2025

BOOK OF ABSTRACTS

Edited by:

Pietro Buzzini Benedetta Turchetti Ciro Sannino Gianmarco Mugnai

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WELCOME TO PERUGIA

Dear attendees of the 15th National Conference on Biodiversity - 2nd International Conference on Mediterranean Biodiversity,

Welcome to Perugia!

Perugia, the capital of the beautiful Umbria, is one of the most evocative destinations of the region, a city of artists such as Perugino, Pinturicchio and Raffaello, as well as the contemporary art of Burri and Beuys). Built on a hill in the valley of the Tevere river, the city, with its history and artistic and cultural heritage, is one of the most popular destinations.

Starting from its Etruscan walls and walking through the streets of Old Town, Perugia present a succession of monuments. It is also an important cultural centre, with its historic University and the oldest and most prestigious University for Foreigners in Italy.

In addition to its artistic and cultural riches, Perugia offers tasty itineraries to try food and wine, with all the flavour of simple regional cuisine. Perugia also offers many opportunities for fun, with pubs and discos, or by visiting it on the occasion of its major events, such as the renowned international festival Eurochocolate, which transforms Perugia in October in the most coveted destination for lovers of the food of the gods. Equally noteworthy is the Umbria Jazz Festival in July, which offers ten days of shows and jazz, ranking among the most important jazz events in Europe.

Besides, the beauty of the surrounding towns (Assisi, Todi) and nature (Trasimeno lake, Marmore falls) and the rich cultural heritage of the region will provide an excellent opportunity for scientific presentations and discussions as well as for the informal encounters.

FROM THE ORGANIZING COMMITTEE

Dear Friends and Colleagues,

welcome to the 15th National Conference on Biodiversity - 2nd International Conference on Mediterranean Biodiversity, Perugia, Italy, organized by the Department of Agricultural, Food and Environmental Sciences of the University of Perugia, in cooperation with the Accademia delle Scienze della Biodiversità Mediterranea (ASBM).

Current human activities are leading to a significant loss of biodiversity of both natural and agricultural ecosystems. The new millennium has led to new opportunities for the conservation and the sustainable use of biodiversity, but at the same time has meant about the emergence of new threats. The rapid progress of scientific knowledge (including new and more advanced study methodologies), the impact of climate change, the increasing consumption of land, the spread of invasive alien species and the emergence of new pathogens have profoundly changed the overall picture (including the human perception) of the strategic value of biodiversity, stimulating the research and development of new and more effective solutions for its sustainable use.

The assessment of biological diversity is a key indicator for monitoring the health of terrestrial ecosystems, often subjected to a growing human impact, including the effects of global warming. The correct functioning of the biosphere is based on the presence of multiple biological networks that are resilient to changes, ensuring the continuity of animal, plant and microbial life. The extinction of one or more species can lead to unexpected impacts, sometimes threatening the loss of entire ecosystems. Climate change, loss of biodiversity and degradation of ecosystems are interconnected phenomena, with devastating consequences for the economic, environmental and social stability of the planet.

Globally, plants constitute over 80% of the human diet: 30,000 plant species are considered edible, 7,000 are cultivated for food, but only 30 are used for food purposes on a large scale. Among them, rice, wheat, corn, millet and sorghum ensure 60% of global food resources. Among animals, of the 30 domesticated species, only 14 ensure 90% of food of animal origin. About microorganisms, it has been estimated that less than 1% of total microbial biodiversity has been described and studied so far.

The 15th National Conference on Biodiversity will disseminate the latest basic and applied scientific knowledge on the study, conservation and sustainable use of animal, plant and microbial biodiversity. The topic of the Conference, "Biodiversity in the 21st century: new paradigms for new challenges", was chosen to provide answers to the new challenges imposed by the growing impact of human activities and climate change on animal, plant and microbial biodiversity in natural and agricultural ecosystems, suggesting possible solutions and defining innovative intervention models, both aimed at in-situ and ex-situ conservation, as well as sustainable enhancement, also in light of the principles of circular economy, in line with the EU strategies envisaged within the European Green Deal.

The 15th National Conference on Biodiversity is also associated with the 2nd International Conference on Mediterranean Biodiversity. The Mediterranean basin represents not only an area important for its history, cultures and traditions, but also a complex of natural and agricultural ecosystems that are hotspots of plant, animal and microbial biodiversity still understudied.

INVITED LECTURES

Biodiversity monitoring and knowledge in the implementation of the nature restoration regulation – NRR

June 3, 2025, 16:00

CARLO BLASI

Sapienza University of Rome, Italy

Professor Emeritus of Sapienza University of Rome He is currently Director of the scientific council of the Interuniversity Center for Biodiversity, Ecosystem Services and Sustainability" (CIRBISES); president of the Foundation for Italian Flora (from 2008); member of the National Observatory for Biodiversity; He was also president of the Italian Botanical Society (SBI); president of the Italian Society of Vegetation Science (SISV); president of the Fédération internationale de phytosociologie (FIP); president of the Italian Federation of Natural and Environmental Sciences (FISNA) Furthermore on behalf of the Ministry of the Environment (MASE) he is member of the National Commission for Natural Capital (since 2016); member of the Control Room of Measure M2C4 I 3.1 (Protection and enhancement of urban and extraurban greenery) of the NRRP dedicated to urban, peri-urban and extra-urban forestry (2021); His most recent interests include the ecological classification of the territory, the dynamics of vegetation and the evaluation of the state of conservation, with research aimed at producing cartographic and descriptive syntheses at national and regional scale, such as the Vegetation of Italy (with the Map of the Vegetation Series of Italy), the Vegetation Prodrome of Italy, the Map of the Eco-Regions of Italy and the Flora of Italy. He is currently interested in restoration ecology applied in particular to the urban system and the definition of the national ecological network. He is the author of over 440 publications, most of which are in international journals and 40 book chapters. He is also the author of several volumes on flora, vegetation and plant landscape, is a member of the editorial board of numerous international journals and was Editor-in-chief of the international journal Plant Biosystems.

INVITED LECTURES

Nature based solutions for ecosystem restoration: the experience of the National Biodiversity Future Centre

June 3, 2025, 16:45

CARLO CALFAPIETRA

Institute of Research on Terrestrial Ecosystems (IRET), CNR, Italy

Director of the Institute of Research on Terrestrial Ecosystems (IRET) of CNR. PhD in Forest Ecology at University of Padova and Marie Curie fellow at University of Madison- Wisconsin (USA). His main interests are the biosphere-atmosphere interactions and the effects of global change and air pollutants on these with a particular focus on the biogenic VOC emission both in urban and rural environments. He is expert for the EU Commission for Green infrastructure and Nature Based Solutions (NbS). He has published more than 100 research papers on international journals/books on these topics (H-index: 58) and has coordinated past or ongoing international and national projects including a PRIN project and a COST Action on Urban forests, two Infrastructural PON projects, vice coordinator of a H2020 project on NBS. He is the Italian Focal point of the European Research Infrastructure ICOS and Coordinator of the Italian Hub of the NbS. He is in the Coordination team and CNR Responsible of the National Centre of Biodiversity of the PNRR. He is regularly invited as key-note speaker in a number of international events. (www.carlocalfapietra.com).

INVITED LECTURES

10 years after the Nagoya Protocol: the road ahead June 3, 2025, 17:30 pm

VALENTINA VENEROSO

Udine Bar Association, Italy

Valentina Veneroso is an Italian lawyer, with a Post Graduate Certificate in Environmental Law. She gives advice and assistance in the field of environmental law and bio law. Over the last 10 years, she has gained in-depth knowledge and experience in the field of biodiversity law and "access and benefit sharing" (ABS") and has been active in capacitating users of genetic resources (e.g. academic research, collections, private companies and Associations) on ABS legal framework. From 2013 to 2015 she collaborated with the Ministry of the Environment by providing assistance and advice to the relevant Directorate in the activities aimed at the ratification and implementation of the Nagoya Protocol at national level and at European level in the writing of the EU ABS Regulation (n. 511/2014) and derived acts, participating as an expert in the related work in the EU Commission. During the European semester of the Italian presidency of the EU Council (1 July – 31 December 2014), she was appointed as a member of the Biodiversity Italian team of the EU Presidency and consultant to the WPIEI-Biodiversity Italian core team for the ABS issues. In 2014, as a member of the Italian Delegation, she attended the Nagoya Protocol COP-MOP1, with the role appointed ABS expert. She is the author of articles and publications on biodiversity law and ABS, as well as a speaker in courses and conferences on the subject at Italian research institutions and universities.

PROGRAMME

Tuesday, June 3

Auditorium of S. Francesco al Prato Church

Welcome Introduction

10:00 - 15:00 Registration

15:00 - 16:00 Welcome Introduction - Major of Perugia, Rector of the University of Perugia, Director of the Department of Agricultural, Food and Environmental Science, University of Perugia, Chair of the ASBM, Chair of the Organizing Committee

Auditorium of S. Francesco al Prato Church

Opening Session – Chairs: P. Buzzini (University of Perugia), L. De Bellis (University of Salento)

16:00 - 16:45 Carlo Blasi

Biodiversity monitoring and knowledge in the implementation of the nature restoration regulation - NRR

16:45 - 17:30 Carlo Calfapietra

Nature based solutions for ecosystem restoration: the experience of the National Biodiversity Future Centre

17:30 - 18:15 Valentina Veneroso

10 years after the Nagoya Protocol: the road ahead

Auditorium of S. Francesco al Prato Church

Welcome Party 18:15 - 22:00

Wednesday, June 4

Hotel Giò - Perugia Congress Centre - Auditorium

Plenary session: Impact of climate change on biodiversity – Chairs: A.C. Elia (University of Perugia), L. De Bellis (University of Salento)
8:30 - 8:50 Claudia Coleine
Global-scale human pathogenic fungi under climate change
8:50 - 9:10 Marta Azzolin
Bottlenose dolphins (*Tursiops truncatus*, Montagu 1821) in the Adriatic Sea: an analysis of their habitat shifts over the last two periods of the habitats directive
9:10 - 9:30 Greta Giovagnoli
Microbiomes in cold soils: novel strategies for conserving biodiversity and promoting sustainable development
9:30 - 9:50 Barbara Caldaroni
Fifty years of changes in phytoplankton diversity in a closed lake. Cyanobacteria like it salty?
9:50 - 10:10 Maria Landolfi
Plant-microbial interactions: tracing a 2 million-year-old alliance with ancient DNA

Hotel Giò - Perugia Congress Centre

Coffee/Tea Break

10:10 - 10:40 Coffee/Tea Break

Hotel Giò - Perugia Congress Centre - Auditorium

Parallel session: The challenges of crop biodiversity in 21st Century – Chairs: E. Albertini (University of Perugia), S. Salvi (University of Bologna)

10:40 - 10:52 Aaron Anderson

Exploring the process of polyploidization through structural genomic changes in neotetraploid Alfalfa

10:52 - 11:04 Chiara Delvento

Haplotype-resolved assembly and resequencing of wild and cultivated genomes shed light on the almond evolutionary history and the genetic basis of self-compatibility

11:04 - 11:16 Eleonora Grassi

Taxonomical and functional biodiversity of nematodes to assess the eco-friendly potential of alternative approaches in crop protection

11:16 - 11:28 Giacomo Bongiorno

A Pan-Genome of the diplosporous grass *Eragrostis curvula* to investigate genetic diversification among genotypes with different ploidy levels and reproductive modes

11:28 - 11:40 Marzia Guerriero

Establishment of a comprehensive germplasm collection of chate melon informed with wholegenome sequence and phenotypic data

11:40 - 11:52 Paola Semenzato

LIFE Olivares Vivos+: A scalable model for reconnecting olive farming with biodiversity conservation and supporting the Common Agricultural Policy (CAP)

11:52 - 12:04 Pasquale Venerito

Varietal characterization and valorization of traditional fruit germplasm in Puglia

12:04 - 12:16 Francesco Arcieri

Resistance mechanisms to *Orobanche crenata* in pea (*Pisum sativum* L.): beyond strigolactones **12:16 - 12:30 Marco Maccaferri**

The challenge of developing the tetraploid wheat pangenome and leveraging it to improve wheat resilience to climate change

Hotel Giò - Perugia Congress Centre - Room A

Parallel Session: Innovation in vine and wine microbiology – Chairs: G. Cardinali (University of Perugia), P. Romano (Universitas Mercatorum, Rome)

10:40 - 10:50 Vittorio Capozzi

Italian Geographical Indications, wine science, microbial diversity and autochthonous resources

10:50 -11:00 Laura Moretti

Yeasts in the vineyard: a promising tool for biocontrol action

11:00 - 11:10 Angela Capece

Role of apiaries located in the vineyard on biodiversity of culturable yeast population associated with grape must

11:10 - 11:20 Tiziana Nardi

The grape microbiome throughout post-harvest withering and its correlations with berry metabolites

11:20 - 11:30 Vasileios Englezos

Investigating the role of temperature in shaping the microbiota and its functionality during a wine spontaneous alcoholic fermentation

11:30 - 11:40 Nicola Francesca

Use of novel non-conventional yeasts *Candida oleophila* and *Starmerella lactis-condensi* for profiling the fruity and floral aroma of Catarratto wines: focus on microbial interaction and metabolome

11:40 - 11:50 Alessio Pio Rossetti

Effect of Starmerella bacillaris strains on Montepulciano d'Abruzzo wine color

11:50 - 12:00 Gianluigi Cardinali

Microbial wine protection and exploitation in view of the new Italian plan for the biodiversity of agricultural interest

12:00-12:30 Discussion

Hotel Giò - Perugia Congress Centre – Room B

Parallel session: Fungal diversity and bioprospecting (part 1) – Chairs: S. Tosi (University of Pavia), G. Venturella (University of Palermo)

10:40 - 11:02 Lucia Muggia

The diversity of the lichen mycobiota

11:02 - 11:24 Pamela Anelli

Characterization of secondary starters occurring on traditional Apulian cheese: a chance to improve and control the aging process

11:24 - 11:46 Alessia Romano

Graphite for graphene: digging into the diversity of degrading fungi from graphite-containing soils and rocks of NW-Italy

11:46 - 12:08 Lobna Hajji-Hedfi

Mycoconservation in arid and Mediterranean North Africa: biodiversity, bioprospecting, threats, and SDG synergies in Tunisia and Egypt

12:08 - 12:30 Simone Buratti

Two different realities come together: how woody decay fungi can lead to safe hydrogen use

Hotel Giò - Perugia Congress Centre - Room C

Parallel session: New frontiers in the studies of animal biodiversity – Chairs: E. Lasagna (University of Perugia), M. Albenzio (University of Foggia) 10:40 - 10:58 Francesca Bertolini

Genomic diversity and signatures of selection in Italian heavy pig breeds: insights into the genetic foundation of dry-cured ham production

10:58 - 11:16 Daniele Colombi

Genetic diversity and selection signatures in three Italian local beef cattle breeds

11:16 - 11:34 Lucia Sepe

Chemical characterization of goat meat obtained from native breeds in inland areas of the Basilicata Region – Italy

11:34 - 11:52 Fabio Formenti

IoT Technologies for the sustainability of Suino Nero Cinghiato farming: innovation and biodiversity

11:52 - 12:10 Vittorio Sarchese

Complete genomic sequencing of Canine Distemper Virus (CDV) with nanopore technology in wild animals in northern Italy

12:10 - 12:30 Laura Garzoli

Bats as bioindicators of environmental levels of trace elements and legacy organic contaminants through non-invasive approaches

Hotel Giò - Perugia Congress Centre

Lunch Break 12:30 - 14:00 Lunch Break

Hotel Giò - Perugia Congress Centre - Auditorium

Plenary session: Biodiversity, invasive species, and multitrophic interactions – Chairs: E. Conti (University of Perugia), P. Pollegioni (CNR-IRET, Porano)

14:00 - 14:22 Paola Pollegioni

Understanding the invasion mechanisms of the alien tree species *Ailanthus altissima* (Mill:) Swingle across Italy: the role of Arbuscular Mycorrhizal Fungi

14:22 - 14:44 Claudio Cucini

Exploring Popillia japonica through molecular lenses

14:44 - 15:06 Elena Chierici

Manipulating the foraging behaviour of the egg parasitoid *Trissolcus japonicus*: possible non-target effects on local biodiversity

15:06 - 15:28 Francesca Boero

Monitoring of insect invasive alien species *Scyphophorus acupunctatus* and *Xylosandrus* spp: (Coleoptera: Curculionoidea) in Western Liguria (Northern Italy)

15:28 - 15:50 Irene Tatini

Invasive species monitoring and community engagement: a multilevel approach within the RICONOSCERE Project

Hotel Giò - Perugia Congress Centre

Coffee/Tea Break

15:50 - 16:20 Coffee/Tea Break

Hotel Giò - Perugia Congress Centre - Auditorium

Parallel session: SUS-MIRRI.IT Strengthening the MIRRI Italian research infrastructure for sustainable bioscience and bioeconomy – Chairs: B. Turchetti (University of Perugia), G. Perrone (CNR-ISPA, Bari)

16:20 - 16:42 Maria Grazia Caruso

Assessment of relationships with indolamines in a collection of tomato culturable endophytic bacteria

16:42 - 17:04 Luciana De Vero

New insights into the long-term preservation of microbial communities associated with Apulian table olives

17:04 - 17:26 Annamaria Bevivino

Enhancing the ENEA Microbial Culture Collection: a valuable resource for advancing biotechnology and bioeconomy development

17:26 - 17:48 Sandro Gepiro Contaldo

Empowering Microbial Research: SUS-MIRRI.IT Collaborative working environment platform **17:48 - 18:10 Marino Moretti**

The Future Sustainability of the Research Infrastructure MIRRI-IT: an overview on objectives to pursue, KPIs to reach, and strategies to adopt

Hotel Giò - Perugia Congress Centre - Room A

Parallel session: Insect genetic and functional biodiversity – Chairs: M.A. Bologna (University of Rome3), F. Frati (University of Siena)

16:20 - 16:35 Ilaria Latella

Biodiversity of diurnal and nocturnal Lepidoptera in different environments of South Italy 16:35 – 16:50 Martina Falagiarda

How diversity of stink bugs and their parasitoids is affected by habitats and host plants 16:50 – 17:05 Antonio Cugliuzzo

16:50 - 17:05 Antonio Gugliuzzo

Increasing plant diversity into Mediterranean tomato greenhouses: benefits for natural enemies and effects on key pest management

17:05 - 17:20 Roberto Catania

Towards integrated pest and pollinator management: the role of functional biodiversity

17:20 – 17:35 Alessandra Riccieri

Patterns of endemism of Italian insects: different biogeographic histories uncovered by phylogenetic and phylogeographic approaches

17:35 - 17:50 Emiliano Mancini

Conservation of saproxylic beetles in the genomics era

17:50 - 18:10 Davide Badano

Pit-traps and pitfalls: reconstructing the evolutionary history of neuropteroid insects

Hotel Giò - Perugia Congress Centre - Room B

Parallel session: Fungal diversity and bioprospecting (part 2) – Chairs: S. Tosi (University of Pavia), G. Venturella (University of Palermo)

16:20 - 16:38 Giuseppe Venturella

Bioprospecting of medicinal mushrooms: a bet for the future

16:38 - 16:56 Francesco Bergese

Exploring the plastisphere: a culturomic approach to uncover the floating microplastic-related fungal biodiversity in the Mediterranean Sea

16:56 - 17:14 Mara Rondolini

Unraveling the soil fungal diversity of a white truffle-producing floodplain forest

17:14 - 17:32 Segula Masaphy

Diversity of *Morchella* species: effect of ecosystem changes on proliferation of two ecotypes of *Morchella* spp. in Israel

17:32 - 17:50 Francesco Di Serio

Viroid-like RNAs infecting fungi: an unforeseen source of biodiversity and of potential innovative biotechnological tools

17:50 - 18:10 Carolina Elena Girometta

Diversity of corticoid fungi in the relict Abies alba population of Monte Nero (North Apennines)

Hotel Giò - Perugia Congress Centre - Room C

Parallel session: Animal biodiversity hotspots and conservation strategies for endangered species – Chairs: F.M. Sarti (University of Perugia), A. Sevi (University of Foggia)

16:20 - 16:35 Caterina Spiezio

Breeding success of the critically endangered red-headed vulture (*Sarcogyps calvus*): an international partnership to save the species from the extinction

16:35 - 16:50 Lorenzo Attili

Genetic variability and differentiation of an endangered Mediterranean falcon (*Falco biarmicus feldeggii*) through a multi-marker approach: a support for conservation efforts

16:50 - 17:05 Francesca Maria Sarti

MuVal – The future of tradition: an immersive journey through Valnerina

17:05 - 17:20 Morena Carlentini

Characterization of heterozygosity-rich regions in Sicilian horse breeds

17:20 - 17:35 Marco Bertoli

Ecology of the lasca *Protochondrostoma genei* (Bonaparte 1939) in the Chiarò di Cialla Creek (Northeast Italy): new insights from a biodiversity hotspot affected by human impacts and alien species

17:35 - 17:50 Francesco Perini

Genetic characterization and conservation strategies for Mediterranean trout (*Salmo ghigii*) in Italian freshwater ecosystems

17:50 - 18:10 Serena Tumino

Genomic insights into runs of homozygosity and heterozygosity of Sicilian cattle breeds

Hotel Giò - Perugia Congress Centre

Poster Session 18:10 - 19:30 Poster session

Thursday, June 5

Hotel Giò - Perugia Congress Centre – Auditorium

Plenary session: Biodiversity in anthropized environments: issues and prospects – Chairs: M. Rebora (University of Perugia), P. Mattarelli (University of Bologna)

8:30 - 8:43 Gianni Gilioli

Discovering unexpected pollinators suitability in urban environment

8:43 - 8:56 Anna Poli

Enrichment procedures for the selection and isolation of promising polycyclic aromatic hydrocarbons (PAHs) - degrading fungal strains: towards a Nature Based Solution (NBS) soil restoration

8:56 - 9:09 Beatrice Falcinelli

The effect of biodiversity on phenolic content and antioxidant activity of sprouts from fruit-tree species

9:09 - 9:22 Giulio Barone

An updated Plant Landscape Map of the Oreto river basin (Palermo, NW Sicily)

9:22 - 9:35 Ilaria Fracasso

Impact of ski slope management on soil properties and biodiversity in mountain grasslands

9:35 - 9:48 Laura Scirè Calabrisotto

Novel aerobic 1,2-DCA degrading consortia from a contaminated aquifer for enhanced bioremediation purposes

9:48 - 10:01 Antonella Trisorio

A strategic tool for agrobiodiversity: the national portal of genetic resources for food and agriculture

10:01 - 10:15 Raffaella Pergamo

The role of organic districts in nature and biodiversity protection and climate change mitigation. The example of the biodistricts in the Lazio Region

Hotel Giò - Perugia Congress Centre

Coffee/Tea Break

10:15 - 10:45 Coffee/Tea Break

Hotel Giò - Perugia Congress Centre – Auditorium

Parallel session: Biodiversity in cropping systems – Chairs: C. Moretti (University of Perugia), A. Ferrante (Sant'Anna School of Advanced Studies, Pisa)

10:45 - 11:06 Ilaria Bruno

From diversity to multifunctionality: Integrating marginal area and cover crops for enhanced agroecosystem performance

11:06 - 11:27 Luigi De Bellis

Physiology and endophytic communities of *Xylella*-resistant and susceptible olive tree cultivars **11:27 - 11:48 Alessandro Frontini**

Structural and metabolic changes in *Xylella fastidiosa* resistant and susceptible olives **11:48 - 12:09 Beppe Benedetto Consentino**

Solanum aethiopicum gr. gilo accessions and their potential use as eggplant rootstock **12:09 - 12:30 Francesco Vitali**

Multilevel assessment of soil biodiversity after application of biostimulant based on arbuscular mycorrhizal fungi in three cropping systems

Hotel Giò - Perugia Congress Centre - Room A

Parallel session: Insect biodiversity in the modern era - Chairs: R. Romani (University of Perugia), G. Burgio (University of Bologna)

10:45 - 11:02 Matteo Montagna

Insect taxonomic and functional diversity: opportunities from genetic approaches

11:02 - 11:19 Daniele Sommaggio

Hoverfly (Diptera, Syrphidae) biodiversity in Italian National Parks

11:19 - 11:36 Adriana Poccia

Using biosolutions in fruit orchards against the invasive *Halyomorpha halys* to reduce pest control impact on biodiversity

11:36 - 11:53 Stefano Vanin

Funerary archaeoentomology: a discipline to investigate biodiversity, local extinction and new arrivals

11:53 - 12:10 Giuseppina Carta

The use of archaeoentomology and cartography to investigate the landscape transformation in the modern era

12:10 - 12:30 Barbara Manachini

Small creatures, big impact: unveiling the power of nematode diversity in the Mediterranean ecoregion

Hotel Giò - Perugia Congress Centre - Room B

Parallel session: Microbial biodiversity in foods: evolving insights and uncharted horizons – Chairs: M. Gullo (University of Modena and Reggio Emilia), V. Capozzi (CNR-ISPA, Foggia)

10:45 - 11:06 Maria De Angelis

Phenotypic and genomic assessment of sugar assimilation in the pomegranate yeast *Hanseniaspora valbyensis*

11:06 - 11:27 Davide Gottardi

From by-product to innovation: exploiting biodiversity of *Yarrowia lipolytica* strains to valorize cheese whey and develop adjunct cultures for improved cheese ripening and quality

11:27 - 11:48 Chiara Nasuti

Development of a new brewing strain with improved aroma through hybridization and UV mutagenesis

11:48 - 12:09 Michela Pellegrini

Microbial resources for sustainable meat productions in the green deal era

12:09 - 12:30 Giovanni De Francesco

Yeast biodiversity in brewing: a comprehensive screening of 30 strains of *Saccharomyces cerevisiae* isolated from different ecological niches

Hotel Giò - Perugia Congress Centre

Lunch Break

12:30 - 14:00 Lunch Break

Hotel Giò - Perugia Congress Centre – Auditorium

Parallel session: Plant biodiversity: environmental preservation to face global change – Chairs: L. Reale (University of Perugia), A. Canini (University of Rome Tor Vergata)

14:00 - 14:22 Giuseppe Bonanno

Climate changes, habitat transformation and germination behavior. A complex story from three Mediterranean plants of conservation interest: *Muscari gussonei, Petagnaea gussonei* and *Poterium spinosum*

14:22 - 14:44 Laura Bassolino

Shading lights on *Silybum* genus biodiversity: chemodiversity, genetic and genomic characterization of a wide germplasm collection

14:44 - 15:06 Waed Tarraf

The potential of the terpene profile of Mediterranean fir species in the chemotaxonomic study and the conservation prospects

15:06 - 15:28 Daniela Gigante

Conservation status of Annex I habitats in Italy: first overview from the Fifth National Report under Article 17 of the Habitats Directive

15:28 - 15:50 Camilla Wellstein

Plant biodiversity and conservation of endemic species of the Dolomites and Southeastern Alps

Hotel Giò - Perugia Congress Centre - Room A

Parallel session: Round table - Biodiversity and PNRR infrastructures: what future beyond projects? – Chairs: P. Buzzini (University of Perugia), A. Bevivino (ENEA, Rome)

14:00 - 15:50

Discussion with F. Frati (NATIONAL BIODIVERSITY FUTURE CENTER), F. Pennacchio (AGRITECH CENTER) and A. Moretti (SUS-MIRRI.IT)

Hotel Giò - Perugia Congress Centre - Room B

Parallel session: Agro-environmental microbiology: emerging perspectives and new frontiers – Chairs: C. Sannino (University of Perugia), L. Borruso (Free University of Bozen)

14:00 - 14:16 Silvia Gattucci

Occurrence and distribution of yeast communities related to honeybees system: an ecological overview

14:16 - 14:32 Sara Del Duca

Enhancing soil bacterial community profiling: PMA treatment and long-read sequencing across biogeographic regions and land uses

14:32 - 14:48 Debora Casagrande Pierantoni

Plant Growth-Promoting Yeasts (PGPYs) as a sustainable solution to mitigate salt-induced stress on zucchini plant growth

14:48 - 15:04 Oussama Bouaicha

Cascade effect of microplastic aerial deposition affects tomato growth, root metabolome and exudome, and rhizosphere microbiome

15:04 - 15:20 Michela Paglialunga

Characterisation of *Pseudomonas syringae* pv. *syringae* Italian strains causing severe wilting in eggplants

15:20 - 15:35 Simone Cutajar

The environmental context of honey bee gut microbiota: insights from the endemic Maltese subspecies, *Apis mellifera ruttneri*

15:35 - 15:50 Daniele Alberoni

Microbial drivers of nectar flows: the case study of sunflower

Hotel Giò - Perugia Congress Centre

Coffee/Tea Break 15:50 - 16:20 Coffee/Tea Break

Hotel Giò - Perugia Congress Centre - Room A

ASBM General Assembly 16:20 - 18:00

Hotel Giò - Perugia Congress Centre

Poster Session 2 16:20 - 19:00 Poster session

Hotel Giotto - Assisi Gala Dinner (optional) 19:30 - 00:00

Friday, June 6

Hotel Giò - Perugia Congress Centre – Auditorium

Plenary session: Challenges and opportunities for the implementation of the EU Nature Restoration Law – Chairs: L. Rocchi (University of Perugia), C. Catalano (CNR-IRET), L. Servadei (CREA-PB)

9:00 - 9:30 Chiara Catalano, Luigi Servadei

The challenges and opportunities of the EU Nature Restoration Law and the role of research. The national project for the development of a catalogue and planning support tool for Nature-Based Solutions

9:30 - 10:00 Luisa Paolotti

The role of integrated LIFE programmes in restoring ecosystems: a case study from the "Integrated management and actions for a green and Innovative nature" Project

10:00 - 10:30 Matteo Pallottini

The LIFE IMAGINE UMBRIA project for the conservation of insect species of community importance in Umbria

10:30 - 11:00 Franziska Zimmermann

Tipping points of biodiversity and sustainability of South Tyrol traditional pasture systems (BIOPAS)

Hotel Giò - Perugia Congress Centre

Coffee/Tea Break

11:00 - 11:30 Coffee/Tea Break

Hotel Giò - Perugia Congress Centre – Auditorium

Farewell considerations and introduction of the next meetings 11:30 – 12:00 Awards Chair of the ASPM Chair of the Organizing Committee

Chair of the ASBM, Chair of the Organizing Committee

Hotel Giò - Perugia Congress Centre – Auditorium 12:00 End of the Conference and Departure

ORAL LECTURES ABSTRACTS

Opening Session

Biodiversity monitoring and knowledge in the implementation of the nature restoration regulation – NRR

Carlo Blasi

carlo.blasi@uniroma1.it

The Farm to Fork Strategy is at the heart of the Green Deal, which aims to make food systems fair, healthy and respectful of the natural environment. For the first time at European level, the strategy for a sustainable national agricultural system and the biodiversity strategy is directed to protecting and enhancing nature have several objectives in common. In some points of the Farm to Fork strategy the need to protect the Natura 2000 Network and the Habitats Directive in general is highlighted in addition to biodiversity.

In fact, the agricultural system intends to support the vision of restoration ecology by joining the Nature Restoration Regulation, which considers, among other things, bringing nature back to 10% of the agricultural system by 2030. The territorial models obtained from the knowledge of the flora, vegetation and ongoing dynamics analyzed with the phytosociological method contribute to making the agricultural system increasingly resilient. They provide indeed the necessary elements to define both the state of conservation of habitats and ecosystems and the most suitable serial stages to recover the resilience of natural ecosystems. With the right and expected integration of skills, rural systems typical of internal areas can provide ecosystem services and enhance sustainable activities also in terms of tourism and food production, suitable for mitigating the effects of the ongoing climate crisis.

Opening Session

Nature based solutions for ecosystem restoration: the experience of the National Biodiversity Future Centre

Carlo Calfapietra

carlo.calfapietra@cnr.it

The role of Nature-based Solutions (NBS) in restoring urban ecosystems has now been widely recognized since the EU has made NBS one of the critical pillars in its political and executive agenda in 2015. Nature Restoration Law and Green Deal targets of Climate Neutrality and reduction of biodiversity loss provide now an unprecedented chance.

At the same time in Italy a unique initiative has started in 2022, thanks to the PNRR funds, The National Biodiversity Future Centre (NBFC) which is involving more than 2000 researchers and is focusing on a variety of topics of the Terrestrial, Marine and Urban Biodiversity.

While Monitoring, Conservation and Valorization represent three important keywords of this initiative, Restoration assumes a priority topic thanks to the recent international mandate related to the new policies. For this reason a new Report on Restoration is being released by the NBFC providing an important contribution to the effort that each member state is carrying out. It is particularly relevant to identify gaps and protocols to validate scientifically innovative and practical solutions for successful and effective NBS applications also quantifying the benefits of the NBS implementations in European cities.

Opening Session

10 years after the Nagoya Protocol: the road ahead

Valentina Veneroso

avv.veneroso@gmail.com

On October 12, 2024, the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization ("ABS") celebrated its 10th anniversary since entering into force. The Nagoya Protocol, an additional treaty to the Convention on Biological Diversity (CBD), was adopted in 2010 to combat biopiracy and reduce inequalities between countries providing genetic resources (typically developing nations) and those utilizing them (generally industrialized nations). Over the past decade, more than 130 national ABS laws have been adopted worldwide, turning the acquisition and exchange of genetic resources into a complex and challenging process. These regulations directly impact anyone conducting research on animal, plant, or microbial biodiversity.

In addition, in 2022, the Kunming-Montreal Global Biodiversity Framework (GBF) recognized Access and Benefit Sharing as one of its four overarching goals for 2050. The GBF calls for a substantial increase, by this deadline, in the amounts of the benefits shared. For the first time, the framework also addresses the need to share benefits derived from the use of digital sequence information (DSI) on genetic resources. To this end, a multilateral benefit-sharing mechanism for open-access DSI was approved and the 'Cali Fund for the Fair and Equitable Sharing of Benefits from the Use of Digital Sequence Information on Genetic Resources' was officially launched on February 25, 2025, during the resumed 16th Conference of Parties (COP16) to the CBD in Rome. This fund will collect contributions from industries relying on DSI from plants, animals, and microorganisms, including sectors such as pharmaceuticals, cosmetics, agriculture, and biotechnology.

The presentation will explore the lessons learned in the 10 years since the Nagoya Protocol came into force, as well as the current and future challenges for ABS in the context of biodiversity and scientific research.

Global-scale human pathogenic fungi under climate change

<u>Claudia Coleine</u>¹, Federico Biagioli¹, Tadeo Saez-Sandino², Eleonora Egidi², Antonis Rokas³, Leho Tedersoo⁴, Manuel Delgado-Baquerizo⁵

¹University of Tuscia, Italy, ²Western Sydney University, Australia, ³Vanderbilt University, USA, ⁴University of Tartu, Estonia, ⁵CSIC-IRNAS, Spain

coleine@unitus.it

Soils are the largest reservoir of human fungal pathogens, yet their global biogeographical distribution and environmental drivers remain poorly understood. Using high-resolution PacBio sequencing on 3,200 soil samples from 108 countries, we performed the first global-scale assessment of soil-borne human pathogenic fungi. Our results reveal that warmer and more mesic ecosystems harbor a higher relative abundance of key pathogens, including *Fusarium solani, Candida tropicalis,* and *Cunninghamella echinulata.* We observed species-specific climatic preferences, with thermotolerant taxa more prevalent in arid zones, while others favored cooler and wetter climates. Predictive models under future climate scenarios forecast a substantial redistribution of pathogenic fungi by 2050, with expansions expected in tropical and coastal regions. This global atlas of fungal pathogen diversity and projected shifts under climate change provides a critical foundation for risk assessment and the development of long-term surveillance and mitigation strategies.

Keywords: Fungal pathogens, Climate Change, Global Future Projections, Soils

Bottlenose dolphins (*Tursiops truncatus*, Montagu 1821) in the Adriatic Sea: an analysis of their habitat shifts over the last two periods of the habitats directive

<u>Marta Azzolin^{1,2,3},</u> Matteo Costantino^{1,3}, Livio Favaro^{1,3}, Marco Gamba^{1,3}, Cristina Giacoma^{1,3}, Andrea Giovannini², Sonia Silvestri⁴, Maria Aurora Iorfino⁴, Antonella Arcangeli⁵

¹University of Torino, Italy, ²Gaia Research Institute, Torino, Italy, ³Centro Interuniversitario per la Ricerca sui Cetacei (CIRCE), University of Siena, Italy, ⁴University of Bologna, Italy, ⁵ISPRA, National Institute for Environmental Protection and Research, Roma, Italy

marta.azzolin@gmail.com

Studying the distribution of suitable habitats for bottlenose dolphins (Tursiops truncatus, Montagu, 1821) in the Adriatic Sea is essential for management reasons. Any change might signal shifts in prey availability or water quality, represent an early sign of climate-related modifications, or increased human pressure. Bottlenose dolphins' presence data collected from ferries by the FLT-Med network, before and within the framework of the LIFE Conceptu Maris project, were analysed employing the software Maxent to develop Species Distribution Models (SDM) for the last two reporting periods of the Habitat Directive, 2013-2018 and 2019-2024. Ten environmental variables (bathymetry, seabed slope, distances from the coast, the 200meter platform and canyons, currents, sea surface temperature, salinity, chlorophyll concentration, and primary productivity) were used as models' explanatory factors. Respectively, 38 and 103 sightings were employed to develop the SDMs for the two periods. The Sightings Per Unit of Effort is 0.0023 sight/km for 2013-2018 and 0.0041 sight/km for 2019-2024, indicating an increased presence of bottlenose dolphins in the study area in the second period, which is statistically significant (Mann-Whitney Test, N=241; U=5909; p=0.0177). The 2013-2018 SDM (AUC, Area Under the Curve, = 0.85) shows suitable habitats extending throughout the central and southern Adriatic. In contrast, 2019-2024 (AUC = 0.92) SDM shows a more restricted distribution, primarily along coastal areas. The analysis of the dynamic variables of the two periods shows that the shift in suitable habitats likely follows variable's changes over time. In fact, in the 2019-2024 period, there is a general increase of temperature and salinity in the northern and central Adriatic, while the chlorophyll concentration is reduced and concentrated along the Italian coasts. It would be worth investigating if anthropogenic threats other than maritime traffic may also have affected the distribution of suitable habitats.

Keywords: Bottlenose dolphin, Species Distribution Model, Climate change

Microbiomes in cold soils: novel strategies for conserving biodiversity and promoting sustainable development

<u>Greta Giovagnoli</u>¹, Pietro Buzzini¹, Ciro Sannino¹, Gianmarco Mugnai², Benedetta Turchetti¹

¹University of Perugia, Italy, ²University of Padova, Italy

greta.giovagnoli@dottorandi.unipg.it

Cold soils found in low-temperature regions host distinctive microbiomes that are vital for ecosystem functions and hold notable biotechnological potential. With the effects of global warming, these habitats are experiencing ongoing changes and have emerged as climate change hotspots. They support psychrophilic biological diversity that has adapted to cold environments but is particularly sensitive to rising temperatures. It is crucial to preserve these microbial communities for a deeper understanding of their ecological significance, while also facilitating environmental knowledge and biotechnological innovations. This study sought to assess the effectiveness of various "standard" preservation techniques over a period of 180 days, tracking shifts in microbial composition and functionality to evaluate the microbiome's stability and resilience. In order to determine the best conservation strategies, multiple analyses were performed, which included: (i) examining community structure and quantifying microbial populations, (ii) characterizing taxonomic diversity by considering both total and transcriptionally active populations, and (iii) analysing the metabolic activity and functional profiles of the microbial communities. By linking preservation techniques to microbial stability and functional performance, we identified the most effective conservation method. These results help establish best practices for ex-situ soil microbiomes preservation, ensuring the reliability and reproducibility of microbiome studies across various temporal and spatial conditions, while also promoting long-term environmental biodiversity conservation.

Part of this work was granted by the European Commission - NextGenerationEU, Project SUS-MIRRI.IT "Strengthening the MIRRI Italian Research Infrastructure for Sustainable Bioscience and Bioeconomy", code n. IR0000005.

Keywords: Microbiome, Preservation, Biodiversity, Bacteria, Fungi

Fifty years of changes in phytoplankton diversity in a closed lake. Cyanobacteria like it salty?

Alessandro Ludovisi, <u>Barbara Caldaroni</u>, Mariantonietta Brancale, Chiara Todini, Antonia Concetta Elia

University of Perugia, Italy

barbara.caldaroni@dottorandi.unipg.it

Long-term ecological research (LTER) plays a crucial role in tracing and predicting ecosystem trends in response to environmental changes and anthropogenic disturbances. Lake Trasimeno is an LTER site which has been the subject of naturalistic and ecological investigations since the beginning of the last century. The availability of historical data and the strict dependence of the water balance of the lake on meteo-climate conditions make Lake Trasimeno a special site for evaluating climate-driven effects.

Herein, we present the results of an analysis of monthly data series of phytoplankton collected over the last 50 years in Lake Trasimeno.

Overall, the results revealed significant long-term changes in phytoplankton, including species composition, community structure, seasonal succession, and diversity. A general shift of dominance towards Cyanobacteria was recorded, which resulted in a marked reduction in the number of represented algal classes, orders, and equitability.

A statistical analysis identified salinity and water column stability as the main potential driving forces behind the observed changes along the course of the seasonal succession, while temperature and water depth seem to play an uncertain role.

Keywords: Climate change, Algae, Salinity, Lake Trasimeno

Plant-microbial interactions: tracing a 2 million-year-old alliance with ancient DNA

<u>Maria Landolfi</u>¹, Nikolay Oskolkov², Federica Villa³, Tanja Mimmo¹, Eran Elhaik², Luigimaria Borruso¹

¹Free University of Bozen, Italy, ²Lund University, Sweden, ³University of Milan, Italy

maria.landolfi96@gmail.com

Microbial communities, mainly bacteria and fungi in the rhizosphere, play a crucial role in plant health. Nitrogen-fixing microorganisms are of particular importance, as their ancient associations with plants likely contributed to the colonization of terrestrial environments approximately 450 million years ago. While fossil records support these long-standing interactions, direct molecular evidence from ancient DNA (aDNA) remains limited. Here, we reanalyzed the Kjær et al. (2022) dataset, where a variety of tree and shrub species were found associated with the early Pleistocene in the Kap København Formation permafrost (North Greenland). Metagenomic sequencing data from forty-one soil samples across four distinct sites, with depths ranging from 10 to 60 meters, were re-analyzed to detect microbial aDNA. Our analysis focused on uncovering potential plant-microbe associations in 2-million-year-old DNA derived from the original dataset. We identified 318 statistically significant cooccurrences between bacteria and various plant genera. Most of these co-occurrences involved bacteria from the Rhizobiales and Burkholderiales orders, known for their plant growthpromoting and nitrogen-fixing abilities. Additionally, we observed that certain plant-microbe co-occurrences were conserved across sites, while others were site-specific, suggesting that rhizosphere microbial communities dynamically adapt to environmental changes. These results reinforce the ancient origins and dynamic nature of plant-microbe interactions in the rhizosphere, highlighting their resilience and adaptability to climatic and environmental shifts.

Keywords: Ancient DNA, Rhizosphere, Plant-microbe associations, Permafrost

Session: The challenges of crop biodiversity in 21st Century

Exploring the process of polyploidization through structural genomic changes in neotetraploid Alfalfa

<u>Aaron Anderson</u>¹, Danilo Fabrizio Santoro¹, Matthew Davis², Nooshin Alavi¹, Giulia Ambrosi¹, Grey Monroe², Emidio Albertini¹, Charles Brummer², Daniele Rosellini¹

¹University of Perugia, Italy, ²University of California, Davis, USA

aaron.anderson@dottorandi.unipg.it

Many agronomically important crop species are polyploids. The process of polyploidization can cause a genetic bottleneck of sorts where genes and alleles present in diploid progenitors are not present in an established polyploid population. Therefore, some of the biodiversity for these species can only be found in diploid populations. The *Medicago sativa* complex encompasses several diploid and tetraploid species and subspecies which are able to interbreed resulting in cultivated alfalfa, an autotetraploid (2n=4x=32). Many studies on the mechanisms of polyploidization have focused on inbred allopolyploid species, so we believe focusing on an outcrossing autopolyploids species will provide unique insights. This work seeks to understand the process of polyploidization to bridge the gap between diploid and tetraploid germplasm to ease the introduction of more biodiversity into breeding programs. By comparing a unique population of neotetraploids that arose from bilateral sexual polyploidization by crossing two diploid meiotic mutants to their diploid full siblings, we sought to better understand the structural genomic changes between diploids and their polyploid siblings. Using long read consensus sequencing from the Pac Bio Revio system, we have constructed telomere to telomere genomes of 3 neotetraploids, 3 diploid full siblings, and the 2 diploid parents to determine regions of interest for genes and structural changes that allow for the formation of viable polyploids. This natural polyploidization pathway can circumvent the formation of adverse gene mutations through chemical polyploidization and may allow for prebreeding gains in diploid wild relatives to be more effectively introduced into polyploid cultivated varieties while addressing a lack of research on obligate outcrossing autopolyploid evolution.

Keywords: Neotetraploid, Polyploidization, Structural Genomics, Alfalfa, Breeding

Session: The challenges of crop biodiversity in 21st Century

Haplotype-resolved assembly and resequencing of wild and cultivated genomes shed light on the almond evolutionary history and the genetic basis of self-compatibility

<u>Chiara Delvento</u>¹, Gaetano Giudice¹, Pasquale Luca Curci², Fabio Palumbo³, Marco Santo Cannarella¹, Gaetano Pazienza¹, Marzia Guerriero¹, Francesco Arcieri¹, Luigi Forte¹, Concetta Lotti⁴, Luigi Ricciardi¹, Stefano Pavan¹

¹University of Bari Aldo Moro, Italy, ²Institute of Biosciences and Bioresources, CNR, Italy, ³University of Padova, Italy, ⁴University of Foggia, Italy

chiara.delvento@uniba.it

Almond (*Prunus amygdalus* Batsch) is a major nut crop worldwide and one of the oldest domesticated trees; however, its evolutionary history and phenotypic diversification still require thorough investigation. Moreover, there is limited genomic, genetic and phenotypic information on wild almond relatives, which hinders studies on almond domestication, and restricts the use of the extensive wild almond gene pool in breeding. Herein, we present haplotype-resolved assemblies of the almond cv. Tuono, dominating global breeding programs as a source of self-compatibility, and the self-compatible wild almond species *Prunus webbii*, together with a genetic variation map obtained by *P. amygdalus* and *P. webbii* whole-genome resequencing. Population genomic analyses indicated that *P. webbii* did not contribute to the evolution of self-compatible *P. amygdalus* cultivars, in contrast with a previous assumption. Rather, haplotype profiling revealed that the self-compatibility alleles of Tuono and P. webbii arose from parallel evolution, as they originated from independent losses of the stylar RNAse gene involved in the Prunus self-incompatibility system. The analysis of nutritional components in genetically homogeneous samples of P. amygdalus and P. webbii revealed significant differences in volatile compounds and amygdalin content. Genome-wide scan for selective sweeps resulted in the detection of several loci and genes putatively associated with P. amygdalus domestication and breeding. Overall, our study highlights the potential of haplotyperesolved genomic information for the genetic analysis of highly heterozygous species and provides information of broad interest for plant biologists and breeders.

Keywords: Almond, Wild relative, Genome assembly, Selective sweeps, Nutritional components

Session: The challenges of crop biodiversity in 21st Century

Taxonomical and functional biodiversity of nematodes to assess the eco-friendly potential of alternative approaches in crop protection

<u>Eleonora Grassi</u>¹, Linda Catani¹, Loretta Guidi¹, Priscilla Farina², Camilla Tani², Barbara Conti², Anna Annibaldi³, Federico Girolametti³, Roberta Ascrizzi², Guido Flamini², Luana Da Costa Monteiro⁴, Federica Semprucci¹

¹University of Urbino Carlo Bo, Italy, ²University of Pisa, Italy, ³Università Politecnica delle Marche, Italy, ⁴University of Ghent, Belgium

eleonora.grassi@uniurb.it

The preservation of biodiversity is essential to ensure the resilience of agroecosystems, which are increasingly threatened by anthropogenic pressures and climate change. Nematodes, among the most abundant and functionally diverse soil invertebrates, are ideal indicators for assessing soil ecological quality. In line with the Farm to Fork strategy, essential oils (EOs) are emerging as promising alternatives to synthetic pesticides, as their high volatility and biodegradability suggest a low environmental risk. However, their actual effects on non-target soil fauna remain largely unknown. To address this gap, a field study was conducted to evaluate the effects of EOs on the taxonomic and functional structure of nematode communities. Specifically, the experiment was carried out on chickpea crops and aimed to assess the potential disturbance caused by basil EO on free-living nematodes. The seed coating was obtained using chitosan (CHI), a natural, non-toxic, and edible polymer derived from the deacetylation of chitin. CHI is used in combination with EOs to reduce their volatility and to form a protective coating on seeds. A Before-After-Control-Impact design was adopted to distinguish biodiversity changes due to temporal dynamics from those caused by treatments. Overall, 44 genera were identified, and Tylenchidae, Dorylaimidae, Cephalobidae, and Hoplolaimidae were the most abundant families. The results revealed that basil EO + CHI seed coatings had no significant negative impact on nematode taxonomic diversity or functional indices. The taxonomic community structure, considered one of the most sensitive detection metrics, showed that the observed effects were mainly driven by temporal variations, likely reflecting the natural progression of the crop system rather than the EO treatment itself. These findings are particularly promising, as they suggest that basil EO-based coatings can preserve soil biodiversity, ecosystem functioning, and natural capital.

Keywords: Biodiversity, Free-living nematodes, Functional diversity, Ecological quality assessment, Sustainable alternatives

Session: The challenges of crop biodiversity in 21st Century

A Pan-Genome of the diplosporous grass *Eragrostis curvula* to investigate genetic diversification among genotypes with different ploidy levels and reproductive modes

<u>Giacomo Bongiorno</u>¹, José Carballo², Cristian Andres Gallo², Viviana Echenique², Emidio Albertini¹

¹University of Perugia, Italy, ²Universidad Nacional del Sur (UNS-CONICET), Argentina

giacomo.bongiorno@unipg.it

As large-scale genomic studies have progressed, it has become clear that a single reference genome cannot capture the genetic diversity present at the species level. The pan-genome approach offers an efficient system to detect missing genetic information from a single reference genome, identify large-scale structural variants, and better understand how different evolutionary trajectories drive changes in reproductive strategies. *Eragrostis curvula* (Weeping lovegrass) exemplifies these processes, as it includes genotypes with diverse ploidy levels (2x to 8x) and reproductive modes ranging from sexuality to apomixis. In this study, we constructed a pan-genome of *E. curvula* to detect genomic variation, establish phylogenetic relationships, and analyze the effects of ploidy on genome evolution and reproductive mode. To achieve this, we used the genome assembly of cv. Victoria and genomic data obtained through Illumina sequencing from 10 genetically diverse accessions. The pan-genome was constructed using an iterative mapping-and-assembly approach. First, reads from each accession were mapped to the reference genome. Unmapped reads were then assembled de novo to identify novel genomic fragments and annotate new genes. These newly assembled sequences were integrated into the reference genome. The process was repeated iteratively with each accession, resulting in a final pan-genome comprising both the reference genome and newly assembled sequences. This approach proved to be efficient for constructing a pan-genome using an already published reference genome and short-read sequences from genetically distant *E. curvula* genotypes. Ultimately, the genomic resources and insights generated in this work provide a comprehensive basis for understanding the phylogenetic relationships among genotypes and offer new perspectives on the correlation between their path of genetic diversification culminating in a shift in ploidy and transitions between sexual and apomictic reproduction.

Keywords: Pangenomes, Genetic diversity, Apomixis
Establishment of a comprehensive germplasm collection of chate melon informed with whole-genome sequence and phenotypic data

<u>Marzia Guerriero</u>¹, Francesco Arcieri¹, Chiara Delvento¹, Gaetano Giudice¹, Marco Santo Cannarella¹, Luigi Ricciardi¹, Concetta Lotti², Stefano Pavan¹

¹University of Bari Aldo Moro, Italy, ²University of Foggia, Italy

marzia.guerriero@uniba.it

The species *Cucumis melo* L. includes several minor crops, such as the chate melon (*C. melo* subsp. melo var. chate), found in Apulia (Southern Italy) as a relic of its former wider cultivation, spanning from the time of Ancient Egypt to the Middle Ages. Recently, the consumption of chate melon has been gaining popularity both inside and outside the regional boundaries as a substitute for cucumber. Here, we describe the collection and characterization of fifteen openpollinated, farmer-maintained chate melon populations, known by the folk names "meloncella", "spuredda" and " cucummaru", which are representative of the germplasm cultivated in Salento (Southern Apulia). Whole-genome resequencing of population DNA pools was performed to investigate genetic diversity within and between populations. A high level of variation was found in terms of heterozygosity. Notably, the lowest heterozygosity was associated with the population known as meloncella striata, characterized by deep grooves on the pepo and more widely distributed in commerce, indicating a greater selective pressure exerted by farmers. A total of 1,352 alleles were found to be fixed privately in the populations under study, including 170 private alleles fixed in the meloncella striata population, which are valuable for its traceability. Replicated field trials enabled the selection of superior populations based on key agronomic and commercial traits, including fruit number per plant, fruit shape, yield per plant, and earliness. Overall, this study secures the chate melon gene pool from further genetic erosion. Additionally, genomic and phenotypic data reported here offer a basis for utilizing the chate melon gene in breeding and for introducing this crop into mainstream agrifood systems.

Keywords: *Cucumis melo* L., Chate melon, Whole-genome resequencing, Genetic diversity, Phenotypic diversity

LIFE Olivares Vivos+: A scalable model for reconnecting olive farming with biodiversity conservation and supporting the Common Agricultural Policy (CAP)

<u>Paola Semenzato</u>¹, Luigi Servadei², Pedro J. Rey³, Rubén Tarifa4, Francisco Valera⁴, Georgios Koubouris⁵, José Herrera⁶, Davide Ridente¹, Carlos Ruiz⁷, José Eugenio Gutiérrez⁷

¹Dimension Research, Ecology and Environment (D.R.E.Am. Italia), Italy, ²CREA-Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria, Italy, ³Universidad de Jaén, Spain, ⁴Estación Experimental de Zonas Áridas, EEZA-CSIC, Spain, ⁵Institute of Olive Tree, Subtropical Crops & Viticulture Hellenic Agricultural Organization ELGO DIMITRA Leoforos Karamanli, Greece, ⁶University of Cádiz, Spain, ⁷Sociedad Española de Ornitología, Spain

semenzato@dream-italia.it

Introduction-The LIFE20NAT/ES/001487 Olivares Vivos+ (OV) aims to reconnect olive cultivation with biodiversity conservation, addressing the decline in biodiversity and soil health. It seeks to identify evidence-based good practices for agronomically, and socio-economically sustainable farming that contributes to halting biodiversity loss, improving environmental governance and to support the transition towards a CAP increasingly oriented to providing public goods.

Methods-The agri-environmental scheme was tested in olive farms across Spain, Italy, Portugal, and Greece and focused on sustainable herbaceous cover management, restoration of non-productive areas, and installation of fauna-supporting structures. Biodiversity monitoring assessed species richness, abundance, and ecological functions (pollination, pest control).

Results-Olive groves are key refuges for Mediterranean biodiversity. First tested in Spain, OV model increased species richness by 7% and abundance by 18% over three years. The greatest gains occurred on farms with poorer initial conditions. Key drivers were landscape complexity and well-managed ground covers. Ants showed high pest control efficiency, while insectivorous birds were limited by lack of nearby vegetation. Solitary bees proved reliable sustainability indicators, with even small floral patches enhancing ecosystem services. These results support CAP2023/27 goals and contribute the design of agro-climatic-environmental measures in both the CAP and the Vision for Agriculture and Food 2040 EC COM(2025)75.

Discussion-OV model proves that biodiversity restoration and profitability are compatible. It works across farm sizes and encourages adoption through policy-linked ecosystem services. Although training gaps remain, many farmers are willing to transition when properly supported. OV offers a robust foundation for eco-schemes aligned with CAP biodiversity goals, positioning olive farming as a driver of nature-positive agriculture in the EU.

Keywords: LIFE Olivares Vivos+, Olive cultivation, Biodiversity conservation, CAP, Sustainable farming

Varietal characterization and valorization of traditional fruit germplasm in Puglia

<u>Pasquale Venerito</u>¹, Andrea Turco¹, Francesco Loperfido², Sabrina Pupillo², Aronne Galeotti², Giuseppe Maggi², Carmine Summo³, Donato Mondelli⁴, Donato Perrelli¹, Pierfederico La Notte⁵

¹CRSFA Basile Caramia, Italy, ²ITS ACADEMY AGRIPUGLIA, Italy, ³University of Bari Aldo Moro, Italy, ⁴CIHEAM, Istituto Agronomico Mediterraneo di Bari, Italy, ⁵CNR-IPSP Bari, Italy

pasqualevenerito@crsfa.it

A significant boost to the recovery, conservation and characterization of old fruit germplasm has been achieved in Puglia since 2012 with the implementation of integrated projects for biodiversity financed by the Puglia Region with the Rural Development Program. With the aforementioned projects it was possible to strengthen the laboratories functional to the conservation, characterization, evaluation of the health status and sanitation of the recovered germplasm. Through the new integrated projects for Biodiversity ReGEFRUP 2.1, Stonefruits and Pome Fruits, and REGEFRUP 2.2 Minor and Citrus Fruits, financed by the PSR Regione Puglia 2014/2022 on a selection of fruit varieties worthy of valorization, preliminarily chosen on the basis of the tradition of different products in the area and the preliminary results of the previous pomological and genetic characterizations, agronomic, productive, chemical and technological characterization actions were carried out on different accessions at risk of genetic erosion for their valorization. For this purpose, agro-food transformation tests were also conducted on different fruit varieties to verify their technological aptitude, in particular for the production of dried fruits, concentrates, juices, jams, fermented drinks, extracts. Both fresh and processed products were also subjected to organoleptic analyses in order to draw up the sensory profile of the fruit or product. The main objective of the work was to significantly support the protection and valorization of the biodiversity of the regional native fruit species, with a view to supporting agricultural companies in the production, transformation and distribution of specific local varieties, with a view to developing new supply chains.

Keywords: Technological characterization, Traditional fruit germplasm, Recovery of fruit germplasm, Agronomic characterization, Valorization of germplasm

Resistance mechanisms to *Orobanche crenata* in pea (*Pisum sativum* L.): beyond strigolactones

<u>Francesco Arcieri</u>¹, Gaetano Giudice¹, Imran Haider¹, Chiara Delvento¹, Marzia Guerriero¹, Mario Schilder², Angelica Giancaspro³, Harrow Bouwmeester², Concetta Lotti³, Luigi Ricciardi¹, Stefano Pavan¹

¹University of Bari, Italy, ²University of Amsterdam, Italy, ³University of Foggia, Italy

francesco.arcieri@uniba.it

Strigolactones (SLs) are a group of carotenoid-derived compounds occurring in plant root exudates, known to stimulate the germination of parasitic weeds belonging to the large family of Orobanchaceae, such as broomrapes and witchweeds. In several economically important crops, resistance to Orobanchaceae is associated with reduced SL biosynthesis and/or altered blend of individual SL molecules. In pea (Pisum sativum L.), we previously selected the line ROR12, associated with low SL levels and nearly complete field resistance to the parasitic weed Orobanche crenata Forsk. (Oc). Here, we performed field trials to select pea genotypes with contrasting response to Oc, starting from: 1) a population of recombinant inbred lines (RILs) originating from the cross between ROR12 and the susceptible cultivar Sprinter; 2) a germplasm population. Notably, liquid chromatography tandem mass spectrometry (LC-MS/MS) analysis of root exudates indicated that, in both populations, genotypes showing lower parasitization rates also display significantly lower (although detectable) levels of the pea SLs orobanchol, orobanchyl acetate and fabacyl acetate, suggesting that SLs play an effective role in field resistance against Oc. Unexpectedly, a third field trial carried out with the pea wild-type cultivar Térèse and its mutants rms5 and rms1, impaired for key SL biosynthetic genes, indicated that complete lack of SLs only confers partial resistance to Oc. Overall, our results indicate that ROR12 resistance might be partially due to mechanisms that are independent from SL biosynthesis. In addition, considering negative pleiotropic effects associated with severe SL deficiency, such as extensive branching and dwarfism exhibited by the rms mutants, we envisage that the exploitation of post-germination and post-attachment defense mechanisms to Oc might be valuable for pea breeding.

Keywords: Strigolactones (SLs), Orobanche crenata (Oc), Pea, Field resistance

The challenge of developing the tetraploid wheat pangenome and leveraging it to improve wheat resilience to climate change

<u>Marco Maccaferri</u>¹, Cristian Forestan¹, Matteo Bozzoli¹, Elisabetta Mazzucotelli², Jennifer Ens³, Harmeet Chawla⁴, Kevin Fengler⁵, Victor Llaca⁵, Primetta Faccioli², Mario Giorgioni², Sandra Stefanelli¹, Anna Maria Mastrangelo⁶, Matthew Hayden⁷, Agata Gadaleta⁸, Karim Ammar⁹, Rajeev Varshney¹⁰, Brande Wulff¹¹,Simon Krattinger¹¹, Brian Steffenson¹², Justin Faris¹³, Steven Xu¹⁴, Taner Sen¹⁴, Eduard Akhunov¹⁵, Dario Copetti¹⁶, Nicola Pecchioni¹⁷, Pasquale De Vita¹⁷, Nathalie Chantret¹⁸, Vincent Ranwez¹⁸, Sean Walkowiack¹⁹, Aldo Ceriotti²⁰, Raul Pirona²⁰, Gabriella Sonnante²¹, Stefania Masci²²,Francesco Sestili²², Michele Morgante²³, Filippo Maria Bassi²⁴, Michael Baum²⁴, Gina Zastrow-Eyes²⁵, Curtis Pozniak²⁶, Luigi Cattivelli², Silvio Salvi¹, Roberto Tuberosa¹

¹University of Bologna, Italy, ²CREA Research Centre for Genomics and Bioinformatics, Italy, ³University of Saskatchewan, Canada, ⁴University of Manitoba, Canada, ⁵Corteva Agriscience, Johnston, USA, ⁶CREA Research Centre for Cereal and Industrial Crops, Italy, ⁷AgriBio, Centre for AgriBiosciences, Agriculture Victoria, Bundoora, Australia, ⁸Università di Bari, Italy, ⁹International Maize and Wheat Improvement Centre (CIMMYT), Kenya, ¹⁰Murdoch University, Perth, Australia, ¹¹King Abdullah University of Science and Technology, Saudi Arabia, ¹²University of Minnesota, USA, ¹³United States Department of Agriculture, Agricultural Research Service, Edward T. Schafer Agricultural Research Center, Fargo, USA, ¹⁴Western Regional Research Center, USDA-ARS, Albany, USA, ¹⁵Kansas State University, Manhattan, USA, ¹⁶University of Arizona, Tucson, USA, ¹⁷CREA Research Centre for Cereal and Industrial Crops, Italy, ¹⁸University of Montpellier, France, ¹⁹Canadian Grain Commission, Grain Research Laboratory, Winnipeg, Canada, ²⁰National Research Council-Institute of Agricultural Biology and Biotechnology, ²³University of Udine, Italy, ²⁴International Center for Agricultural Research in the Dry Areas (ICARDA), Rabat, Morocco, ²⁵Corteva Agriscience, Johnston, IA, USA, ²⁶University of Saskatchewan, Saskatoon, USA

marco.maccaferri@unibo.it

Whitin the Genus Triticum, the tetraploid wheat (carrying the BBAA and GGAA genomes) group includes up to 11 highly diverse species and subspecies that underwent two independent and consecutive events of domestication and subsequent evolution. Tetraploid genetic diversity was shaped by exposure to diverse environments, pathogens and human selection, thus providing valuable alleles for resilience to abiotic and biotic stresses. To retrieve this valuable adaptive diversity, the durum wheat community developed a long-term collaborative project. A comprehensive, highly diverse Global Durum Genomic Resource (https://wheat.pw.usda.gov/GG3/global_durum_genomic_resources) was retrieved from genebanks and breeders, purified, and genotyped with a common genotyping platform. At the same time, the Svevo Platinum reference sequence was used as a framework. Haplotype-based analysis led to unfolding the genomic and demographic structure. A Tetraploid wheat Core Collection (TCC; 432 accessions), effectively capturing most of the diversity in tetraploids, was assembled and the tetraploid wheat pangenome was developed, including 40 accessions PACBIO25X sequenced. The GDGR is currently under distribution and phenotypic evaluation for: (i) phenology, (ii) resistance to diseases, (ii) root architecture, (iii) grain Yield components and grain quality. GWAS allowed to discover loci relevant for wheat breeding and haplotype-tagging KASP markers were developed. Main results will be presented and discussed.

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Italian Geographical Indications, wine science, microbial diversity and autochthonous resources

<u>Vittorio Capozzi</u>¹, Ester Presutto², Lucia Bonassisa², Giuseppe Spano², Maria Lucia Valeria de Chiara¹, Mariagiovanna Fragasso²

¹Institute of Sciences of Food Production, CNR, Foggia, Italy, ²University of Foggia, Italy

vittorio.capozzi@cnr.it

Geographical Indications (GIs) in oenology represent a strategic sector for the European agrifood sector. In this context, Italian GIs are a relevant sector and a good model of innovation trends in the sector, aimed at protecting tradition and improving the quality and safety of production. An overview of the relevant scientific literature is proposed to highlight the research and development directions in this field. A particular focus is dedicated to microbial diversity as a reservoir of bio-resources useful for positively modulating the global quality of wines with GIs status. Specifically, an examination of the isolations of autochthonous yeasts and bacteria that have been isolated from Italian wines is reported. The importance of microbial collections in the management, enhancement and conservation of the microbiodiversity associated with oenological production is highlighted.

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Keywords: Wine, Innovation, Saccharomyces, non-Saccharomyces, Malolactic bacteria

Yeasts in the vineyard: a promising tool for biocontrol action

<u>Laura Moretti</u>, Silvia Gattucci, Laura Canonico, Alice Agarbati, Francesca Comitini, Maurizio Ciani

Università politecnica delle Marche, Italy

laura.moretti@pm.univpm.it

In vineyard many fungal infections can affect the grapes, roots, trunk, canes, leaves and berries. Generally, chemical antifungals have been used, but in recent decades the European Union has been taking measures to reduce the use of chemical compounds in vineyards. For this reason, the research focused to identify and characterize new microorganisms as natural biocontrol agents. The aims of the present study were characterizing a wide range of yeasts, isolated from different environmental and food sources, for their antimicrobial activity against *Botrytis* cinerea, *Aspergillus carbonarius, Penicillium expansum, Penicillium digitatum* and *Cladosporium* spp. A preliminary screening evaluated the metabolites and volatile organic compounds produced by yeasts for their antimicrobial activity. A selected strain of *M. pulcherrima* was then evaluated in vineyard. Fifteen days before the harvest, the strain was sprayed on both red and white grape. At harvest time grape colonization and biocontrol action the grapes were evaluated. Results showed significant colonization of the *M. pulcherrima* strain and significant mold control. These findings highlight the potential of yeast-based biocontrol strategies as sustainable and effective tools for vineyard management.

Keywords: Biocontrol, Molds, Vineyards, Yeasts, Metschnikowia

Role of apiaries located in the vineyard on biodiversity of culturable yeast population associated with grape must

Angela Capece¹, Gabriella Siesto¹, Rocchina Pietrafesa¹, Patrizia Romano²

¹Università degli Studi della Basilicata, Italy, ²Universitas Mercatorum, Italy

angela.capece@unibas.it

The studies evaluating the agents carrying the yeasts on the grapes demonstrated that animal vectors, such as insects and birds, play a key role in yeast spreading in the environment. Furthermore, social insects (such as wasps and bees), can host the yeasts in their gut, contributing to their survival and biodiversity. This study, performed for two consecutive years, investigated the influence of the presence of apiaries in the vineyard on culturable yeast community of both grape/wine and honey bees collected in these apiaries. The yeast population isolated from spontaneously fermented grapes randomly collected in two vineyards with apiaries on the borders were compared to those isolated from spontaneously fermented grapes collected from a vineyard without apiary. At the same time, yeast community was analyzed on bees collected in each apiary placed in the vineyards, in comparison to yeasts isolated from an apiary located far from the vineyards. The isolated yeasts were identified by restriction analysis of amplified ITS region, followed by sequencing. Results showed that the presence of apiaries increased the occurrence of oenologically relevant yeasts on grapes; furthermore, during the second vintage, S. cerevisiae strains were found also among the yeasts isolated from bees. These findings corroborate the role of bees as both yeast vectors and reservoirs for *S. cerevisiae* during unfavorable seasons. The approach proposed in this study was aimed to contrast the loss of biodiversity in the agroecosystems, such as vineyards. The new yeasts isolated in this study represent an important bioresource which will be further characterized to select new strains for production of distinctive wines or for other biotechnological applications.

Keywords: Culturable yeast community, Honey bees, Yeast dispersion, Biotechnological application

The grape microbiome throughout post-harvest withering and its correlations with berry metabolites

<u>Tiziana Nardi</u>¹, Luca Nerva¹, Walter Chitarra¹, Giovanni Mian¹, Alessandro Romano¹, Raul Romor¹, Lorenzo Lovat1, Diego Tomasi²

¹CREA - Council for Agricultural Research and Economics - Research Centre for Viticulture and Enology, Conegliano, Italy, ²Consorzio Tutela Conegliano Valdobbiadene Prosecco Superiore, Pieve di Soligo, Italy

tiziana.nardi@crea.gov.it

Grape withering is a post-harvest process for producing reinforced and sweet wines. The microbiome associated with withering grapes is closely linked to the process and its resulting wines. This study investigated the mycobiome and bacteriome of grape carposphere throughout withering, aiming to: (a) detail bacterial and fungal community evolution during grape withering using NGS metabarcoding, (b) compare two dehydration methods (non-controlled and controlled environments), and (c) correlate microbial communities with grape metabolites, including volatile organic compounds (VOCs).

Samples were collected from Valpolicella, Italy, where Amarone wine is produced. Drying was performed in traditional well-aired rooms (non-controlled, NC) or warehouses with set airflow and humidity (controlled, C). NGS metabarcoding (ITS and 16S) depicted fungal and bacterial species at four time points, and VOCs were measured using GC-MS and UHPLC-QTOF.

Microorganism evolution during withering was variable, with slight differences between the two systems. Overall, 144 bacterial genera (32 classes) and 176 fungal genera (19 classes) were found. Betaproteobacteria was the main bacterial class throughout the process, followed by Sphingobacteria. Dothideomycetes was the dominant fungal class, with *Aureobasidium* and *Alternaria* as major genera. *Botrytis*, which can damage grapes, grew during withering, showing significant diversity between NC and C.

Microbial taxa correlated with grape metabolites: for instance, aliphatic alcohols linked with four fungi genera, monoterpenes with 3, D-viniferin correlated with 16 bacterial genera, and trans-resveratrol with 11.

Understanding the microbial ecology of the grape carposphere can significantly inform winemaking practices. NGS metabarcoding has proven to be an effective tool for studying the microbiome of withering grapes, revealing changes in microbial communities due to different drying systems and drawing their correlation with grape metabolites.

Keywords: Grape carposphere microbiome, Post-harvest withering, Volatile Organic Compounds

Investigating the role of temperature in shaping the microbiota and its functionality during a wine spontaneous alcoholic fermentation

<u>Vasileios Englezos</u>, Paola Di Gianvito, Francesca Crisetti, Simone Giacosa, Lorenzo Ferrero, Luca Cocolin, Kalliopi Rantsiou

University of Torino, Italy

vasileios.englezos@unito.it

Winemaking is a complex process in which fermentation temperature plays a crucial role, influencing the rate of the process, the microbial population dynamics as well as wine quality. In this study, shotgun metagenomic sequencing was combined with chemical analyses to investigate the impact of temperature on the microbiome, its functional profile, and on wine quality. Spontaneous fermentations of Vitis vinifera L. cv. Nebbiolo grapes were conducted in laboratory scale at 28 °C and 18 °C, joined with a maceration process from the grape solid parts. At different time points, the chemical properties of the wine and its metagenome were analysed. No significant differences were observed in microbial composition based on alpha diversity, while temperature clearly shaped bacterial community beta diversity. The relative abundances of certain species differed significantly between the two temperatures. *Tatumella ptyseos* and Komagataeibacter saccharivorans dominated high-temperature fermentations, while fermentations at 18°C exhibited high variability over time, with *Gluconobacter* spp. prevailing at days 2 and 4, and *Bradyrhizobium* spp. becoming dominant at the end of fermentation. Regarding fungal communities, Saccharomyces cerevisiae established dominance earlier in high-temperature trials, leading to lower biodiversity. The evolution of chemicals over time differed between the two temperatures and reflected significant differences in the metabolism of both bacterial and fungal communities, as evidenced by the analysis of Kyoto Encyclopedia of Genes and Genomes (KEGG) Orthology functional categories and Carbohydrate-Active Enzymes (CAZymes). The higher temperature led to a significant modification of the sugar consumption rate. An accelerated grape skin softening in the 28°C trials promoted tannin and anthocyanin extraction, but the latter content underwent a pronounced degradation, achieving way less pigments concentration (-40%) at the end of the monitored period.

Keywords: Wine fermentation, Temperature, Microbiome evolution, Wine color

Use of novel non-conventional yeasts *Candida oleophila* and *Starmerella lactis-condensi* for profiling the fruity and floral aroma of Catarratto wines: focus on microbial interaction and metabolome

<u>Nicola Francesca</u>¹, Vincenzo Naselli¹, Antonino Pirrone¹, Enrico Viola¹, Azzurra Vella¹, Valentina Craparo¹, Antonella Maggio¹, Antonella Porrello¹, Luca Settanni¹, Paola Vagnoli¹, Anne Julien-Ortiz¹, Stephanie Weidmann-Desroche², Giancarlo Moschetti¹, Antonio Alfonzo¹

¹University of Palermo, Italy, ²Institut Universitaire de la Vigne et du Vin Jules Guyot, France

nicola.francesca@unipa.it

Volatile organic compounds (VOCs) are fundamental to wine quality. Although it is known that significant influences are carried out by the microbial component in the volatile fraction of wine, little is known about the effects of microbial interactions in the production of aromas. Therefore, the aim of this work was to promote microbial interactions using *Candida oleophila* (C. oleophila) and Starmerella lactis-condensi (St. lactis-condensi) to bio-stimulate the production of VOCs in Catarratto wines. The combination of St. lactis-condensi and C. oleophila with Saccharomyces cerevisiae (S. cerevisiae) induced significant increases in ethyl esters and acetates in the theses compared to the control tests fermented in pure culture. The co-presence of Oenococcus oeni (O. oeni) in the microbial consortia together with the non-Saccharomyces stimulated the microbial interactions and thus the effects. The use of St. lactis-condensi in the O. oeni - S. cerevisiae consortia significantly lowered the ester hydrolysis reactions while preserving their quantity. In contrast, the introduction of C. oleophila in O. oeni - S. cerevisiae consortia stimulated the biosynthesis of ethyl esters by increasing them by about 110% compared to the control. It is conceivable that this behavior can be traced back to the ability of *C. oleophila* to improve the biotechnological performance of the entire microbial consortia. Indeed, untargeted metabolomic investigations detected in C. oleophila the ability to biosynthesise vitamins and their precursors such as vitamin B6 and B5 respectively. For the first time studying the impact of two novel non-conventional yeast on wine quality, both volatilome and exo-metabolome is reported. The use of C. oleophila and St. lactis-condensi constitutes a potential biotechnological resource to cope with the wine quality decay stimulated by the current climate change scenarios in terms of fresh fruity and floral aroma.

Keywords: non-conventional yeast, *Candida oleophila, Starmerella lactis-condensi*, Metabolome, Carattatto wine

Effect of Starmerella bacillaris strains on Montepulciano d'Abruzzo wine color

<u>Alessio Pio Rossetti</u>, Giorgia Perpetuini, Giuseppe Arfelli, Rosanna Tofalo

University of Teramo, Italy

aprossetti@unite.it

Yeasts can influence wine color through several mechanisms e.g. direct adsorption of pigments on yeasts' cell wall, and producing metabolites such as pyruvic acid and acetaldehyde that have been found to react with different phenolic compounds. In this study, the influence of 10 *Starmerella bacillaris* strains inoculated as either planktonic or biofilm-detached cells on the chromatic properties of Montepulciano d'Abruzzo wine was evaluated. Wines obtained with biofilm-detached cells exhibited higher glycerol content and cell counts, and lower ethanol levels compared to those inoculated with planktonic cells. These wines were also characterized by higher concentrations of pyruvic acid, polyphenols, and anthocyanins than the others. These differences in anthocyanins and polyphenols notably influenced wine color, with wines obtained with biofilm-detached fermentations displaying lower b* (yellowness) and h* (hue) values, and higher a* (redness) values, indicative of a stronger red color, along with reduced clarity (lower L* values). Moreover, a regression model predicting wine color was developed. Future studies will expand on these findings by examining the effects of other non-*Saccharomyces* yeasts grown in various aggregation states on wine color.

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Keywords: Wine color, *Starmerella bacillaris*, Montepulciano d'Abruzzo

Microbial wine protection and exploitation in view of the new Italian plan for the biodiversity of agricultural interest

<u>Gianluigi Cardinali</u>

University of Perugia, Italy

gianluigi.cardinali@unipg.it

The upcoming National Plan for the Biodiversity of Agricultural Interest poses several challenges at the ruling, scientific, technological and economic level for the preservation and the exploitation of the microbial diversity bound to the agricultural and food chain. Several aspects must be considered to guarantee an efficient conservation of the microbial diversity, respectful of the rural conditions and of the farmers to guarantee an effective long-term sustainability of the measures undertaken.

This specific work calls for a real "convergence" approach considering microbial biology, ecology, conservation technology and strategies, as much as rural conditions and respect of the current rulings.

Conservation strategies are basically those *ex situ*, i.e. in collections and *in situ*, i.e. in specific areas with strong restrictions for the agricultural activities to avoid perturbation of the environment and therefore of the biodiversity. Already in 2012, the "Guidelines for the conservation and the exploitation of the biodiversity of agricultural interest" (https://www.reterurale.it/flex/cm/pages/ServeBLOB.php/L/IT/IDPagina/9580), in the part relative to microorganisms suggested the inclusion of the in farm and in factory conservation, where the former attains to the genetic resources used in agriculture and mostly bound to the soil, whereas the latter is specific for food transformation activities. Both strategies aim at maintaining the microbial diversity of interest without affecting the economic activity, as it could happen in some ex situ stringent conditions. All strategies require a deep understanding of several scientific and technical issues that are necessary to individuate, conserve, register and exploit Microbial Genetic Resources of agricultural interest, that will be presented and discussed in the presentation.

Keywords: Biodiversity, Agricultural interest, in factory, in farm, in situ and ex situ

The diversity of the lichen mycobiota

Lucia Muggia¹, Laura Selbmann², Martin Grube³

¹University of Trieste, Italy, ²University of Tuscia, Italy ³University of Graz, Austria

lmuggia@units.it

Lichen thalli are multi-kingdom symbioses in which fungi, algae and bacteria interact to form communities of variable composition, often shaped by the environmental conditions under which the lichen thalli develop. Particularly under extreme environmental conditions, lichens are one of the most successful groups of organisms, where they serve as unique niches for microbial diversification. The lichen-associated microfungi, i.e. the lichen mycobiota, have been investigated at different geographic scales, including cosmopolitan lichen species as well as endemic lichens from Antarctica, using both a culture-dependent approach and environmental DNA metabarcoding. We show that the lichen mycobiota are predominantly composed of Ascomycota belonging to the classes Chaetothyriomycetes and Dothideomycetes, while some key representative taxa were recognized as basidiomycetous yeasts. The variation of the mycobiota is extremely high, and a stable species-specific core mycobiota is not detected with the methods we applied. Most taxa were present in a low fraction of the samples, indicating that the mycobiota are thus composed of heterogeneous fungi, of which some taxa are detectable only by culture-dependent approaches. Among these, eight new species have been recognized at a worldwide scale, which seem to select lichens as their preferred niche. Indeed, the major representatives of the lichen mycobiota are fungi that do not show any specificity toward a particular lichen host species, rather toward the lichen thallus in general, as a structure in which spores, yeast cells and mycelia fragments thrive or rest.

Keywords: Extremophiles, Fungi, Lichens, Metabarcoding, Symbiosis

Characterization of secondary starters occurring on traditional Apulian cheese: a chance to improve and control the aging process

<u>Pamela Anelli</u>, Giuseppe Cozzi, Daria Carella, Annalisa De Girolamo, Vincenzo Lippolis, Salvatore Cervellieri, Antonio Moretti, Antonia Susca

Institute of Sciences of Food Production, CNR, Bari, Italy

pamela.anelli@cnr.it

Filamentous fungi contribute significantly to the organoleptic characteristics of mature cheese when used as secondary starters during the aging process, because their metabolic activities can positively influence aroma, texture, colour, and appearance. However, uncontrolled fungal colonisations may include species capable of producing mycotoxins, secondary metabolites that pose risks to human and animal health. To mitigate these hazards and enhance cheese quality, the deliberate addition of selected secondary starters can be an effective strategy in leading the aging process.

In this study aiming to select appropriate strains, we evaluated the pro-technological activities of nineteen Penicillium spp. strains, isolated from the surface of Apulian cheese aged in cave and refrigerated cell. The fungal strains were DNA-based identified and further characterized in vitro, through polyphasic approach. Metabolic activities, such as proteolysis and lipolysis, responsible for flavour development, and the capacity to grow on a cheese-like synthetic substrate were evaluated. A subset of strains was further assessed for the volatile organic compounds (VOCs) emission, providing insights into related potential role in the sensory profile of aged cheese and in the identification of markers for traceability.

Additionally, the interaction between *Penicillium* spp. strains and *Aspergillus westerdijkiae*, an unwanted ochratoxin A-producing species often associated with natural-aged cheese, was evaluated in vitro. Among the selected strains, *Penicillium biforme* ITEM 19069 emerged as good candidate as potential secondary starter, due to its compatibility with the cheese-like environment, its high proteolytic and lipolytic activities, as well as a characteristic VOCs emission, and ability to affect the growth of *A. westerdijkiae*.

Keywords: Food safety, Cheese ripening, Selected cultures, Fungal biodiversity

Graphite for graphene: digging into the diversity of degrading fungi from graphitecontaining soils and rocks of NW-Italy

<u>Alessia Romano¹</u>, Gaia Bartolomeo², Claudio Gennaro Ametrano³, Maura Tomatis¹, Iris Bertani⁴, Cristina Bez⁴, Vittorio Venturi⁴, Eleonora Bonifacio¹, Sara Negri¹, Mariangela Girlanda¹, Sergio Enrico Favero Longo¹, Lucia Muggia²

¹University of Torino, Italy, ²University of Trieste, Italy, ³University of Graz, Austria, ⁴International Centre for Genetic Engineering and Biotechnology, AREA Science Park

alessia.romano@unito.it

Graphene is a carbon-based nanomaterial with extraordinary physical, mechanical, and electronic properties and, for this reason, it is used in numerous applications, from optoelectronics and energy storage to medicine. Although graphene-based materials bring several advantages, they will eventually accumulate into the environment, but their fate in terrestrial ecosystems is unclear. Graphene is strictly derived from graphite and usually commercialised in different forms such as few-layer graphene (FLG). Therefore, graphite mining sites may be potential hotspots of graphene degraders. In this work, graphite-containing samples of soil and rocks were collected from three sites in Piedmont (Roure, San Germano Chisone, Villasecca; TO, Italy), along with control (not graphite-containing) samples. From the over one thousand fungi isolated, six species (Penicillium citreosulfuratum, P. virgatum, Penicillago nodositata, Exophiala bergeri, Aaosphaeria arxii and Didymella exigua) were selected which were not retrieved from the control samples and were found in at least two sites. One strain per species was incubated in 0.1% Malt Extract Broth or water with FLG powder at a concentration of 50 mg/mL. The mycelia of all strains were observed to aggregate FLG, to a greater extent than an isolate (Trichoderma sp.) from control soil. Raman spectroscopy showed FLG alteration (lattice disordering under irradiation associated with vacancy containing regions) after one month of incubation with five out of the six strains, *P. citreosulfuratum* being the most active. These preliminary findings suggest that FLG is prone to natural soil biodegradative processes.

Keywords: Biodegradation, Soil fungi, Environmental fate

Mycoconservation in arid and mediterranean North Africa: biodiversity, bioprospecting, threats, and SDG synergies in Tunisia and Egypt

Lobna Hajji-Hedfi^{1,2}, Ahmed Abdel-Azeem^{3,4,5}

¹Regional Centre of Agricultural Research of Sidi Bouzid, CRRA, Tunisia, ²Carthage University, Tunisia, ³Faculty of Science, Suez Canal University, Egypt, ⁴Research Institute of University of the Bucharest (ICUB), Romania, ⁵University of the Free State, Bloemfontein, Republic of South Africa

elhajjilobna@yahoo.fr

North Africa, encompassing six nations (Algeria, Egypt, Libya, Morocco, Sudan, and Tunisia), spans ~ 6 million km² and supports over 275 million inhabitants. Fungi are invisible ecosystem engineers, living as hyphae and mycelium. Globally, fungal mycelium in soil's top 10 cm exceeds 450 quadrillion km2 id est about half our galaxy width. Yet fungal conservation remains overlooked in North Africa; only Algeria and Egypt acknowledge fungi in CBD reports. Tunisia's diversity includes 400-500 macrofungi, thousands of fungal microfungi, vital mycorrhizal/endophytic species, and 200+ lichenized fungi. Egypt has recorded 2,502 fungal species. Climate change threatens fungal biodiversity, disrupting ecosystem services tied to SDGs. Rising temperatures harm mycorrhizal networks (SDG 2), while pathogenic fungi spread (SDG 3). Saprobic fungi aid carbon sequestration (SDG 13) and bioremediation (SDG 15), but desertification risks extinction (SDG 15.5). This study highlights fungal diversity in Tunisia and Egypt, exposing gaps in research, conservation, awareness, and policy. It advocates sustainable use, legal protections, bioprospecting oversight, and protected-area management. Prioritizing fungal resilience in climate strategies can advance SDGs while safeguarding this overlooked kingdom.

Keywords: Climate resilience, Endemism, Ethnomycology, Policy frameworks, Soil restoration

Two different realities come together: how woody decay fungi can lead to safe hydrogen use

<u>Simone Buratti</u>, Sara Paraboschi, Carolina Elena Girometta, Alessandro Girella, Marzia Guerrini, Chiara Milanese, Elena Savino

University of Pavia, Italy

simone.buratti@unipv.it

Wood decay fungi (WDF) have great morphological, trophic, and adaptive diversity that results in broad application prospects. WDF are studied in many fields, but their use to prepare H2 storage materials is a novelty never tried before. H2 transport normally occurs through procedures requiring high safety measures, thus representing an issue. H2 transport on solid and stable compounds, such as by adsorption on carbon-based materials, has been proposed as a safe and affordable solution. Biochar (BC) is a solid carbon powder produced by pyrolysis of biomasses and is attracting attention as gas storage medium. To improve the preparation yields and the storage efficiency, plant materials can be pre-treated with chemical and physical methods, but also with biological ones.

The aim of this study was to investigate how a biological pre-treatment of vegetable wastes by chosen WDF strains could optimize the pyrolysis process of vegetable biomasses and enhances their H2 storage performance.

Different vegetable wastes were collected in Lombardy region (Italy) and used as a growth substrate for WDF strains belonging to the fungal culture collection of Pavia University (MicUNIPV). The pre-treated materials were subjected to pyrolysis to obtain BC and then chemically activated by KOH treatment to increase porosity.

The fungal action was monitored via FT-IR technique, evidencing changes in the IR spectra with respect to the starting biomass and with particular concern to the main constituting polymers, i.e. lignin, cellulose and hemicellulose. Fungal pre-treatment obtained several effects: 1) increasing the BC production yield compared to control (up to 40% in rice bran); 2) increasing H2 storage capacity (up to 4.2 wt%); 3) higher H2 sorption rates (<1 min for adsorption and around 1.5 min for desorption).

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Bioprospecting of medicinal mushrooms: a bet for the future

Giuseppe Venturella, Ilenia Cicero

University of Palermo, Italy

giuseppe.venturella@unipa.it

Many species of Basidiomycetes, and to a lesser extent Ascomycetes, fall into the category of socalled "medicinal mushrooms", or those fungi that are used for prevention, alleviation, or healing of diseases and/or for nutritional purposes. Due to the presence of high content of biologically active compounds they are used as (a) dietary food, (b) dietary supplement products, (c) a new class of drugs called "Mushroom Pharmaceuticals"; (d) natural biocontrol agents in plant protection; and (e) cosmeceuticals. Eco-sustainable reuse of agricultural wastes allows to obtain growth substrate for producing edible and medicinal mushrooms. Besides, the food industry has been incorporating natural components into traditional products to improve and prevent diet-related diseases. There has been a growing interest in adding mushroom powders and extracts because their content of bioactive molecules. Fortifying cereal-based foods with fungal mycelia or sporophores enhances the availability of vitamins, minerals, fibers, beta-glucans, and antioxidants in baked goods. In addition to illustrating the above uses, an assessment of the medicinal mushroom market is provided. This market has been growing in recent years due to consumer demand for natural health remedies and the potential health benefits of mushrooms.

Keywords: Medicinal mushrooms, Bioprospecting, Human Health

Exploring the plastisphere: a culturomic approach to uncover the floating microplasticrelated fungal biodiversity in the Mediterranean Sea

<u>Giuseppe Bergese</u>¹, Matteo Florio Furno¹, Carlo Pretti², Valeria Prigione¹, Giovanna Cristina Varese¹

¹University of Torino, Italy ²Interuniversity Consortium of Marine Biology and Applied Ecology "G. Bacci" (CIBM), Italy

francesco.bergese@unito.it

Microplastics (MPs) are widespread in natural environments and represent a sign of the human impact. In marine environment they introduce allochthonous microorganisms and chemicals creating a new ecological niche (plastisphere), where fungi and other microorganisms form a biofilm. Investigating floating MPs is essential for understanding the composition of the fungal community and its ecological role. Since marine fungal biodiversity is still largely unexplored, a culturomics approach is pivotal to discover and preserve taxa with potential biotechnological applications.

To collect MPs, Manta nets were towed along 6 transects located between the Livorno harbour and the protected area "Secche della Meloria" (Tuscany, Italy). Surface water samples were also collected to compare the culturable mycobiota between the two matrices. MPs were sonicated or directly plated, using three culture media (CMA, MEA and SNA) supplemented with sea salts and incubated at 15°C. Fungi were identified through a polyphasic approach combining morphological observation and molecular analyses.

Overall, the nearly 400 strains isolated were ascribable to about 100 taxa, 55 were exclusively found on MPs, while 22 were retrieved in the surface water; only 20% of the taxa was shared. The two fungal communities were clearly distinct. Most of the taxa were ascribable to the phylum Ascomycota (87%), whereas Basidiomycota (11%) were more represented in the MPs mycobiota than in the surface water, where only two Basidiomycota spp. were retrieved.

Many taxa were rare/or unexpected in the marine environment, and their preservation will increase the ex-situ biodiversity of the Mycotheca Universitatis Taurinensis. Preliminary observations suggest the presence of a putative new *Penicillium* species. In the near future, strains isolated from MPs will be characterized for their potential degradation capabilities toward different xenobiotics.

Keywords: Plastisphere, Marine fungi, Culturomics, Microplastics, Mediterranean Sea

Unraveling the soil fungal diversity of a white truffle-producing floodplain forest

<u>Mara Rondolini</u>¹, Gilberto Bragato², Barbara Sladonia³, Gian Maria Niccolò Benucci⁴, Lara Reale¹, Domizia Donnini¹

¹University of Perugia, Italy, ²CREA - Research Centre for the Soil-Plant System, Gorizia, Italy, ³Institute of Agriculture and Tourism, Porec, Croatia, ⁴Great Lakes Bioenergy Research Center, Michigan State University, USA

mara.rondolini@dottorandi.unipg.it

Floodplain forests are unique ecosystems that harbor exceptional biodiversity. In the Mediterranean region, the Motovun forest in Istria (Croatia) represents one of the last remaining examples of this habitat. Among its ecological rarities is the prized white truffle (Tuber magnatum Pico), a hypogeous mushroom famous for its unique flavor and significant economic value. Due to its limited natural distribution and the challenges of cultivation, the white truffle remains one of the most expensive fungi in the world. In Istria, it has become a symbol of the region's natural heritage, playing a crucial role in the local economy through direct harvesting and associated industries such as gastronomy and tourism. This study explores the biotic and abiotic factors that characterize the Motovun forest, aiming to define the environmental characteristics of a truffle alluvial forest. Understanding these interactions is essential for evaluating potential conservation practices that safeguard truffle resources and overall forest biodiversity. In addition to assessing vegetation and soil physico-chemical properties, we employed amplicon sequencing to analyze soil fungal biodiversity. Our findings emphasize the ecological conditions that promote white truffle growth, while also identifying significant threats related to land management practices, such as alterations in the river's course, which can greatly impact its survival. The characterization of soil fungal communities allowed the identification of dominant taxa (Mortierellomycota, Basidiomycota and Ascomycota), and further analysis of the trophic classes revealed that ectomycorrhizal fungi are highly present with an important presence of *Sebacina*, *Membranomyces*, and *Naucoria*. These insights enhance our understanding of the complex ecological network surrounding the white truffle environment, offering valuable knowledge that could aid in the sustainable management and conservation of this unique alluvial forest ecosystem.

Keywords: White truffles, Soil, Amplicon sequencing, Fungi, Floodplain forest

Diversity of *Morchella* species: effect of ecosystem changes on proliferation of two ecotypes of *Morchella* spp. in Israel

Segula Masaphy

MIGAL Research Institute and Tel Hai College, Kiryat Shmona, Israel

segula@migal.org.il

An increasing understanding of the impact of environmental factors on mushroom temporal and spatial proliferation in nature is important for conservation and control of mushroom populations, especially but not exclusively, with regard to edible mushrooms. Both local climate changes and site-related environmental changes such as disruptive activities, may affect mushroom proliferation. Morels (*Morchella* spp., Pezizales) are important edible mushrooms known for their delicate taste and aroma, as well as their medicinal properties. Range of *Morchella* species exhibit are found in the Mediterranean zone, including in Israel. Morels usually appear for only a short duration in a season and in wide range of habitats. The proliferation pattern of two distinguished *Morchella* species, exhibiting mycorrhizal and freeliving saprotrophic modes, was monitored in Israel together with climatic and soil condition data. Results: air climatic changes were found to affect the temporal fruiting pattern of morels as well as the mushroom phenotypic and chemical composition properties such as color and phenolic content. Moreover, both population types were affected by disruptive activities such as fires and site forest management activities.

Keywords: Morchella species, Morel, Trophic mode, Environmental conditions, Phenotypes

Viroid-like RNAs infecting fungi: an unforeseen source of biodiversity and of potential innovative biotechnological tools

<u>Francesco Di Serio</u>¹, Marco Forgia¹, Michela Chiumenti¹, Cristina Formiglia¹, Nadia Serale¹, Paolo Mussano¹, Yi Guo¹, Stefania Daghino¹, Vittorio Balmas², Beatriz Navarro¹, Massimo Turina¹

¹Istituto per la Protezione Sostenibile delle Piante, CNR, Italy, ²University of Sassari, Italy

francesco.diserio@cnr.it

Viroids are circular non-coding RNAs infecting plants. Some of them contain ribozymes, which are catalytic elements self-cleaving the multimeric RNA replicative intermediates. Only about 50 viroids were known till a few years ago, when, by screening publicly available metatranscriptomes for circular and ribozyme-bearing RNAs, tens of thousands of new viroidlike RNA elements, here referred as ribozycirculome, were discovered in several ecological niches. The largest elements coincided with ambiviruses, which were found in isolates of orchid endomycorrhizal fungal collections and in *Cryphonectria parasitica*. The genome of ambiviruses is composed of 5 kb encoding a putative viral RNA-dependent RNA polymerase and a highly conserved protein of unknown function, thus being a first example of a hybrid between RNA viruses and viroid-like elements. We showed that the ambivirus infecting Cryphonectria parasitica interfere with the fungus pathogenicity. Other circular RNA elements carrying ribozymes in each polarity strand were some mitoviruses (around 3kb in size), circular elements encoding delta-like antigens (circa 1.5-2 kb), and thousands of smaller (< 1kb) viroidlike RNAs. The circularity of genomic and anti-genomic RNAs and their self-cleaving capability mediated by the embedded ribozymes was shown for ambiviruses as well as for several nonprotein coding viroid-like RNAs from fungi, including the plant pathogen Rhizoctonia solani and Trichoderma spirale. Infectivity and replication of viroid-like RNAs into Trichoderma species were confirmed by a reverse genetics method and by horizontal transfer via anastomosis. Interestingly, viroid-like RNAs reduce the antagonistic potential of Trichoderma species against Rizoctonia solani, providing further evidence of interference with the host behaviour. We, therefore, propose that the ribozyciruculome is a new layer of biodiversity in the fungal mycobiota and a source for identifying potential new biocontrol agents.

Keywords: Infectious circular RNAs, Ribozymes, Mycovirus, Mycobiota

Diversity of corticoid fungi in the relict *Abies alba* population of Monte Nero (North Apennines)

Carolina Elena Girometta¹, Luca Piovanelli¹, Simone Buratti¹, Annarosa Bernicchia

¹University of Pavia, Italy

carolinaelena.girometta@unipv.it

The relict *Abies alba* Mill. population in Mt. Nero (Ferriere-Bedonia municipalities, SIC IT4010003) is placed on ophiolites in an Alpic temperate-oceanic, hyper-humid orotemperate phytoclimate. It is a never managed, native relict in the Apennine Subprovince disjuncted from the main Alpic corpus and includes few hundred individuals up to 350 years old.

Aim of the work was to survey the diversity of corticioid fungi growing on *Abies alba* in this population.

Field surveys were conducted in October-November especially in 2022, 2023 and 2024. Living fir individuals were surveyed as well as fallen decaying trunks. Samples were identified based on both macro and micromorphology.

Less than 10 cumulative lignicolous species were recorded from the *Abies alba* population in Mt. Nero including the corticioids: *Cyphella digitalis* (Alb. & Schwein.) Fr., *Hymenochaete cruenta* (Pers.) Donk, *Aleurodiscus amorphus* (Pers.) Rabenh., *Radulomyces confluens* (Fr.) M.P. Christ., *Gloiothele citrina* (Pers.) Ginns & G.W. Freeman. The latter was found in decaying trunks in the South side only. *C. digitalis* recorded 1.82 id/ha Northward, 1.59 id/ha Southward and co-occurred with other species on the same branch as follows: with *H. cruenta* in 4/19 samples; *A. amorphus* 2/19; *A. amorphus* + *H. cruenta* 1/19. The outgroup localities in Trentino (Noana and Lavarone) yielded *C. digitalis* by 0.1 id/ha and 0.052 id/ha respectively, each one including *A. amorphus* too on the same branch.

The poor lignicolous fungal spectrum lacks significant decayers and includes strictly saproxylic species only; 3/5 corticioids are considered monophagous (*C. digitalis, H. cruenta*) or almost monophagous (*A. amorphus*) on *A. alba*. Before these surveys, *C. digitalis* had been recorded only once in Italy in 1901, whereas *H. cruenta* is really scattered and perhaps overlooked. This study confirms the value of the relict *A. alba* population in Mt. Nero for fungal conservation.

Keywords: Corticioid fungi, Abies alba, Cyphella digitalis, Relict, Mt. Nero

Genomic diversity and signatures of selection in Italian heavy pig breeds: insights into the genetic foundation of dry-cured ham production

<u>Francesca Bertolini</u>¹, Giuseppina Schiavo¹, Samuele Bovo¹, Anisa Ribani¹, Stefania Dall'Olio¹, Paolo Zambonelli¹, Maurizio Gallo², Luca Fontanesi¹

¹University of Bologna, Italy, ²Associazione Nazionale Allevatori Suini, Roma, Italy

francesca.bertolini3@unibo.it

The Italian pig farming industry focuses on producing high-quality dry-cured hams through crossbreeding Italian Duroc, Italian Landrace, and Italian Large White pigs, which have been subjected to distinct selection pressures over the past four decades. This study explores the genomic landscape of these breeds using high-density SNP data from over 9,000 pigs genotyped for over 60,000 markers. We applied four different selection scan methods, two within breeds (runs of homozygosity and integrated haplotype score) and two across breeds (Fixation index and cross-population extended haplotype homozygosity) to identify genomic regions under selection, relevant genes within these regions and biological pathways. Our results reveal that Italian Duroc exhibits greater genetic differentiation (pairwise FST = 0.20) from Italian Landrace and Italian Large White, which are more closely related (pairwise FST = 0.13). This likely reflects distinct origins and breeding goals. Despite clear differentiation, few selection signatures reached fixation, likely due to the polygenic nature of selected traits. Enrichment analyses revealed genes and pathways linked to growth and fat deposition, suggesting a common selection direction across breeds but involving distinct biological mechanisms. These genes may play a crucial role in defining breed-specific characteristics and influencing traits in crossbred pigs. Overall, this study enhances our understanding of how selective breeding has shaped the genome of Italian heavy pig breeds and provides valuable insights for optimizing selection strategies to support the dry-cured ham industry.

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Keywords: Pig breeds, Single Nucleotide Polymorphisms, Fst, Runs of Homozygosity

Genetic diversity and selection signatures in three Italian local beef cattle breeds

Daniele Colombi¹, Francesco Perini¹, Fiorella Sbarra², Andrea Quaglia², Emiliano Lasagna¹

¹University of Perugia, Italy, ²National Association of Italian Beef Cattle Breeders (ANABIC), Italy

daniele.colombi@dottorandi.unipg.it

Marchigiana (MAR), Chianina (CHI), and Romagnola (ROM) are three autochthonous Italian beef cattle breeds which are selected for meat production. These breeds have a very ancient history, CHI breed is reported to exist in Italy for 22 centuries, while ROM originated after barbaric invasions in the IV century AD. MAR breed originated by crossbreeding of CHI, ROM, and local Marche cattle at the beginning of the last century. Nonetheless, their genetic background is still mostly unknown. To fill this gap, we analysed the genetic diversity of these breeds using 980 MAR, 1000 CHI, and 967 ROM young bulls from performance test at ANABIC genetic station and genotyped with a 33K SNP-chip array. Principal components, structure, neighbour-joining tree, and minor allele frequency correlations were computed with PLINK, ADMIXTURE, ape and pcadapt packages on R, and suggest that CHI and ROM are the most differentiated breeds, while MAR falls in between of the two. We finally observed selection signatures by iHS and XP-EHH methods in these breeds using rehh package on R, within nonoverlapping windows of 100kbp. Among all, several regions resulted for both statistics: more specifically on BTA1 and BTA13 in MAR, harbouring respectively DPP2 and DPP4 and CDH6 genes. Regarding CHI, multiple regions resulted under selective pressure on BTA2, and on BTA5 harbouring EMP1, GSG1, FAM234B, HEBP1 genes. Two windows in BTA6 and BTA23 resulted finally for ROM, harbouring respectively ABCG2, PKD2, SPP1, and ILRUN, SNRPC, SNORA70 genes. The same window on BTA6 also resulted under selective pressure for MAR and CHI, according to XP-EHH. Indeed, a bigger region of 3.2Mbp on BTA6, harbouring several genes associated with muscularity and growth ability, was observed selected, also for XP-EHH, for the derived alleles in ROM, while selection for the ancestral ones is observed for MAR and CHI. These results deepen our knowledge on these breeds history and could be considered for selection strategies.

Keywords: Autochthonous breeds, Genomics, Adaptation, iHS, XP-EHH

Chemical characterization of goat meat obtained from native breeds in inland areas of the Basilicata Region – Italy

<u>Lucia Sepe</u>¹, Federica Capano², Carmen Cabato², Mrika Di Paolo², Marica Egidio², Sophia Alesio², Loriana Casalino³, Matteo Santinello², Roberta Matera², Raffaele Marrone²

¹CREA Animal Production and Aquaculture, Bella-Muro, Italy, ²University of Napoli Federico II, Italy, ³Universitas Mercatorum, Roma, Italy

lucia.sepe@crea.gov.it

Lesser-known goat breeds are recognized to exhibit high nutritional quality in their meat. Although these breeds are economically less sustainable for farmers, their meat quality is relevant but not well-documented. The COLAUTOC 2.0 project (PSR 2014-2020, Basilicata Region, CUP C63D24000140002) investigates the quality of kid meat raised in Basilicata region. Ten kids from each breed (Garganica, GR; Derivata di Siria, DS; Capra di Potenza, CP) aged 55±2 days, were selected. The left half-carcasses were chosen, and the Longissimus dorsi (LD) and Quadriceps femoris (QF) muscles were sampled. The pH of the carcasses was measured at 30 minutes and 24 hours after slaughter, showing an acidification of the meat at the second measurement. Samples underwent wet aging for 7 days at 4°C and were analyzed at 0, 3, and 7 days of aging for chemical and sensory properties. The average dressing percentages for GR, DS, and CP were 59%, 49%, and 51%, respectively. Results showed that cut selection influenced weight loss (higher in the LD) regardless of breeds. Among the breeds, meat of DS showed a lower brightness, while the redness was higher in QF at the end of the aging period, regardless of the breed. The trend of the aw, for all breeds, appears constant over time for both LD and QF. No differences in nutritional quality (protein and fat) were observed. The QF of CP showed a higher amount of secondary oxidation products over time compared to the other breeds. Shear strength tests revealed an increasing trend in the shear strength of QF over time in GR and CP, while DS showed the opposite trend. Regarding sensory properties, analysis using the electronic nose showed that both cuts were more sensitive to sulfur compounds for all breeds. Preliminary results underscore that studying local breeds is essential for preserving biodiversity and supporting sustainable farming practice.

Keywords: Kid's meat, Wet aging, Local breed, Nutritional quality, Electronic nose

IoT Technologies for the sustainability of Suino Nero Cinghiato farming: innovation and biodiversity

Fabio Formenti¹, Valeria Rossi¹, Claudia Furiani¹, Francesca Maria Sarti²

¹Goodmen.it s.r.l., Perugia, Italy, ²University of Perugia, Italy

fabio.formenti@goodmen.it

The enhancement of native breeds is crucial for biodiversity conservation and the sustainability of agri-food production systems. This project focuses on the free-range breeding of the Suino Nero Cinghiato, a reconstituted breed closely tied to its territory, requiring innovative and sustainable conservation methods.

Our initiatives involve farms specializing in extensive breeding of the Suino Nero Cinghiato and an IT company developing Internet of Things (IoT) technologies. The goal is to optimize freerange management through smart devices that enable real-time monitoring of environmental and physiological parameters. Technologies such as the Smart Feeding Breed scale and the FollowPig System enhance animal welfare and address challenges in extensive farming.

The FollowPig system aids breeders in genetic selection and provides traceability for end consumers throughout the supply chain. The integrated Smart Feeding Breed system monitors weight variations by tracking feed consumption per animal at the feeder. This data is invaluable for farm management, enabling yield monitoring and analysis of environmental impacts on nutrition and growth, as well as health monitoring and early disease detection. The collected data can be processed with R, Python, SAS, and Tableau, facilitating strategic scientific research. R&D in IoT technologies for free-range farming is essential for improving operational efficiency and reducing environmental impact, while ensuring high-quality products. The synergy between innovation and biodiversity fosters a sustainable farming model, preserving native breeds and contributing to ecosystem conservation, thereby minimizing challenges and enhancing genetic and cultural heritage with significant economic and environmental benefits.

Keywords: Biodiversity, Suino Nero Cinghiato, IoT (Internet of Things), Sustainability, Production Management

Complete genomic sequencing of Canine Distemper Virus (CDV) with nanopore technology in wild animals in northern Italy

<u>Vittorio Sarchese</u>¹, Federica Di Profio¹, Serena Robetto², Riccardo Orusa², Vito Martella³, Barbara Di Martino¹

¹University of Teramo, Italy, ²Istituto Zooprofilattico Sperimentale Piemonte, Liguria e Valle d'Aosta, Italy, ³University of Bari Aldo Moro, Italy

vsarchese@unite.it

Canine distemper virus (CDV) is an RNA virus that belongs to the Paramyxoviridae family in the Morbillivirus genus. CDV is a significant viral pathogen capable of triggering epizootic events, resulting in a negative impact on wild animal populations. Over the last two decades, CDV caused local epizootics among wild carnivores in Europe. Herein, we report the results of a surveillance study aimed at detecting CDV RNA among various wild animal species and performing complete genomic sequencing. Between 2023 and 2024, as part of a PRIN project 2022 "Investigating Hepatotropic Viruses in carnivores and humans in a One Health perspective (HVOH)", duodenal samples were collected from a total of 108 wild animals found dead, including 10 wolves (Canis lupus), 80 foxes (Vulpes vulpes), 6 stone martens (Martes foina), 10 Eurasian badgers (Meles meles), 1 squirrel (Sciurus vulgaris), and 1 otter (Lutra lutra). Sampling was conducted under a National passive surveillance programme by the National Reference Centre for Wild Animal Diseases (CeRMAS-IZS PLV) in North-Western Italy. Molecular screening was carried out using primers targeting a highly conserved region of the nucleocapsid (N) gene. Two positive samples underwent a sequence-independent enrichment protocol and were sequenced using the MinION Mk1C platform (ONT, Oxford, UK). Viral RNA was detected in 11 animals (10.2%, 11/108). In detail, CDV RNA was identified in samples collected from ten foxes (12.5%, 10/80) and one marten (16.7%, 1/6). The complete genome sequences of two fox strains were generated. Upon sequence analysis, strains exhibited the highest identity to Europe lineage CDV strains recently identified in martens and otters in Hungary. We provided novel CDV genomic sequence data and demonstrated the reliability of ONT sequencing in genomic epidemiological studies, which may facilitate rapid response actions during future epizootic situations that can threaten animal biodiversity in a One Health perspective.

Keywords: CDV, Animal biodiversity, Surveillance, Nanopore, Sequencing

Bats as bioindicators of environmental levels of trace elements and legacy organic contaminants through non-invasive approaches

<u>Laura Garzoli</u>¹, Fabrizio Gili¹, Emanuele Ferrari¹, Angela Boggero¹, Cristina Corti², Paolo Debernardi³, Francesca Lapadula², Elena Patriarca³, Davide A.L. Vignati⁴, Damiano Monticelli², Roberta Bettinetti²

¹Water Research Institute CNR-IRSA, Italy, ²University of Insubria, Italy, ³Stazione Teriologica Piemontese, Italy, ⁴Université de Lorraine, CNRS, LIEC, France

laura.garzoli@cnr.it

Bioindicators play a crucial role in revealing the environmental effects of human activities. Occupying high trophic levels, insectivorous bats are sensitive to accumulation of pollutants such as trace elements and persistent organic contaminants. Maternity colonies are at particular risk, as reproductive females consume large amounts of prey to meet their increased energy needs. At the same time, they are especially valuable for studying the impact of contaminants and can serve as proxies for evaluating environmental pollution. Finally, due to their roost fidelity, maternity colonies are optimal bioindicators for short- and long-term monitoring.

In the framework of the PRIN "BAT-SIGNALS", we developed a non-invasive biomonitoring protocol to evaluate the exposure of bat colonies to environmental contaminants. We sampled maternity colonies of different species (*Myotis blythii*, *M. capaccinii*, *M. myotis*, *M. emarginatus*, *Rhinolophus ferrumequinum*, and *R. hipposideros*) in NW Italy in 2024.

We collected guano under all colonies prior and after parturition, and faeces and hair samples from a limited number of captured individuals. We characterized bat diet by guano metagenomics and quantified different kind of pollutants: legacy organic contaminants (DDT and PCBs) and trace elements (As, Ni, Pb, Cd, Hg, Se, and Hg), comparing concentration ratios in guano and hair. Finally, we investigated the presence of possible oxidative stress biomarkers in bat hair, using proteomics. We explored relationships among several environmental factors (urbanisation level, crop type, pesticide use, environmental conditions, bat diet) and biological responses (contaminant levels in bat guano and hair, stress biomarkers), with the ultimate aim of proposing bats as bioindicators of environmental contamination, while also promoting their conservation by highlighting emerging threats posed by trace elements and pesticides.

Keywords: Bats, Legacy contaminants, Trace elements, Mercury, Proteomics

Understanding the invasion mechanisms of the alien tree species *Ailanthus altissima* (Mill.) Swingle across Italy: the role of Arbuscular Mycorrhizal Fungi

<u>Paola Pollegioni</u>, Marco Ciolfi, Carlotta Volterrani, Luciano Spaccino, Francesca Chiocchini, Marco Lauteri

CNR-IRET, Porano, Italy

paola.pollegioni@cnr.it

Ailanthus altissima (Mill.) is a fast-growing species native to Asia, introduced to Europe for ornamental purposes in the late 18th century. It is classified as one of the most invasive woody plants in Europe and is listed as a species of EU concern. With strong pioneering traits, A. altissima grows successfully across a range of ecosystems, from urban landscapes to forests, and is widely distributed throughout temperate regions. Its rapid spread is facilitated by winddispersed seeds, extensive root suckers, and adaptability to various soil and water conditions, particularly in disturbed areas such as roadsides. This species threatens biodiversity by altering native tree diversity, community composition, and ecosystem functions. Effective management is crucial to mitigate its impact and limit further expansion. Recent studies highlighted the facultative ability of A. altissima to establish and modulate various forms of endomycorrhizal associations, which confer significant ecological plasticity. This, consequently, would promote the evolution of an increased competitive ability (EICA) in A. altissima. While the beneficial effects of arbuscular mycorrhizae on the early development of A. altissima seedlings have already been demonstrated, these mutualistic relationships warrant further exploration. This study integrates high-throughput amplicon sequencing of the fungal internal transcribed spacer (ITS) region with stable isotope analysis of soil samples to examine soil fungal communities across an A. altissima density gradient (Absence, Front, Infested) in three pilot sites (Urban Park, Rural, Natural) in central Italy. Our results revealed the lowest AMF diversity in the Urban Park compared to the Natural and Rural sites. Although significant differences in Glomeromycota composition were found across sites, two of the most abundant genera, Glomus and Septoglomus, progressively increased with A. altissima density in both the Natural and Urban Park sites.

Keywords: Invasive species, *Ailanthus altissima*, Microbiome, Increased competitive ability, AMF

Exploring Popillia japonica through molecular lenses

<u>Claudio Cucini</u>, Rebecca Funari, Antonio Carapelli, Francesco Frati, Francesco Nardi

University of Siena, Italy

claudio.cucini2@unisi.it

Invasive species pose an increasing global threat due to their ability to rapidly spread and adapt to novel environments. The ecological and economic impacts of these species emphasize the urgent need to understand the mechanisms driving their invasion processes and success. *Popillia japonica* is a notable invasive pest, feeding on hundreds of economically valuable plant species. Since the last century, it has expanded beyond its native range in Japan, colonizing large areas of North America and Europe. Due to the significant threat it poses to agriculture and biodiversity, *P. japonica* has been designated as a quarantine pest while the EU has funded different research lines aimed at developing innovative strategies to combat this invasive species.

To improve the reference genome, we de novo sequenced and assembled *P. japonica* using ONT and Illumina libraries, annotating it with RNA-seq data from various life stages. We analyzed duplication levels of key gene families (CYPs, IRs, GRs, ORs). Population genomics involved resequencing individuals across the beetle's range, variant calling, and SNP dataset analysis to trace invasion routes. Lastly, RNA-seq was used to study gene expression responses to three treatments - *Bacillus thuringiensis*, LLINs, and *Metarhizium robertsii* - at two time points. Genome analysis revealed significant expansion of CYP genes, linked to detoxification, and ORs, associated with olfactory perception. Population genomics confirmed *P. japonica*'s invasion route from Japan to the US, followed by two independent introductions into the Azores and Italy, respectively. RNA-seq showed that the response to deltamethrin focusses on detoxification and Ca²⁺ modulation, whereas response to *M. robertsii* and *B. thuringiensis* is systemic and entails a complex immune response.

These molecular insights enhance our understanding of *P. japonica* biology, providing a foundation for developing targeted control strategies.

Keywords: Invasive species, Japanese beetle, Population genomics, Gene expression, Genomics

Manipulating the foraging behaviour of the egg parasitoid *Trissolcus japonicus*: possible non-target effects on local biodiversity

<u>Elena Chierici</u>¹, Gabriele Rondoni¹, Lucrezia Giovannini², Giuseppino Sabbatini Peverieri², Pio Federico Roversi², Eric Conti¹

¹University of Perugia, Italy, ²CREA, Research Centre for Plant Protection and Certification, Firenze, Italy

elenachierici9@gmail.com

Classical biological control is a promising strategy for sustainable pest management, offering pest suppression while reducing the ecological impact of chemical pesticides. However, the introduction of exotic natural enemies may pose risks to biodiversity, particularly through unintended effects on native species closely related to the target. The egg parasitoid Trissolcus japonicus (Ashmead) (Hymenoptera: Scelionidae), an effective biocontrol agent against the invasive brown marmorated stink bug Halyomorpha halys Stål (Hemiptera: Pentatomidae), has been approved for release in Italy as part of a classical biocontrol programme. The foraging behaviour of parasitoid females is mediated by host-associated cues, such as herbivore-induced plant volatiles and adult host odours. Behavioural attraction may be influenced by the host used for rearing the parasitoid and by parasitoid conditioning during its adult life. Fundamental host range tests demonstrated that *T. japonicus* can develop on native non-target stink bug species. Using the tri-trophic system Vicia faba - stink bugs - T. japonicus, we assessed how the rearing host and exposure to host-related volatiles influence parasitoid foraging. Trissolcus japonicus females responded positively to *H. halys* oviposition-induced volatiles only when reared on this target host. Parasitoids reared on alternative hosts did not respond to either plant or host cues. Notably, female conditioning through exposure to *H. halys*-associated cues enabled recognition of volatiles associated to an intense stink bug feeding activity. These findings highlight the importance of parasitoid conditioning in modulating host specificity, with key implications for biocontrol efficacy and biodiversity conservation.

Keywords: Hemiptera, Invasive species, Learning, Scelionidae

Monitoring of insect invasive alien species *Scyphophorus acupunctatus* and *Xylosandrus* spp. (Coleoptera: Curculionoidea) in Western Liguria (Northern Italy)

<u>Francesca Boero</u>¹, Elena Zappa², Mauro Mariotti¹, Stefano Vanin¹

¹University of Genoa, Italy, ²Hanbury Botanic Gardens, University of Genoa, Italy

francesca.boero@edu.unige.it

Invasive alien species are one of the main causes of biodiversity loss and species extinction. Arthropods invasions are one of the most pervasive, impacting human health, food, clean water, and sustainable economies. This work focuses on the study of insect invasive alien species, *Scyphophorus acupunctatus* and *Xylosandrus* spp. (Coleoptera: Curculionoidea). The first one, known as the black agave weevil, is native to America and is a polyphagous species that feeds on species of Asparagaceae, causing important damage to ornamental plants. The bark beetles of the genus *Xylosandrus*, of tropical origin, are highly polyphagous species infesting woody, arboreal and shrubby plants, impacting both ornamental and native plants. Hanbury Botanical Gardens (Ventimiglia, Italy) has suffered extensive damage to historic plant collections by the arrival of these new phytophagous insects. Therefore, a monitoring of the species is being carried out since 2024.

Scyphophorus acupunctatus monitoring is carried out during all the years using pitfall traps, baited with the species aggregation pheromones, and a visual control of the weevils on the plants. Monitoring of *Xylosandrus* spp. is carried out using a multifunnel trap, triggered with ethanol, α -pinene, α -copaene, and quercivorous.

A total of 1177 adults of *S. acupunctatus* were captured throughout the whole year but peaking in spring and autumn. The bark beetles monitoring has detected the presence of *X. compactus*, *X. crassiusculus* and *X. germanus* peaking in May. In addition, the exotic species *Dactylotrypes longicollis* (n=124), *Coccotripes dactyliperda* (n=7) and *Hypotenemus eruditus* (n=329) were trapped.

The monitoring data suggest a good adaptability of the exotic species to the mediterranean environment and their increase in the Hanbury Botanic Gardens, currently hosting already a large number of exotic arthropods, making the management and the conservation of botanical collections difficult.

Keywords: Invasive alien species, Coleoptera, Pest, Monitoring

Invasive species monitoring and community engagement: a multilevel approach within the RICONOSCERE Project

<u>Irene Tatini¹</u>, Tianshi Li¹, Gabriele Cananzi², Sara Verni³, Jacopo Franzoni¹, Antonio Giacò¹, Giacomo Bruni⁴, Giovanni Astuti¹, Daniele Antichi¹, Giulio Petroni¹, Massimiliano Petrolo⁴, Valentina Serra¹

¹University of Siena, Italy, ²University of Florence, Italy, ³Scuola Superiore Sant'Anna, Pisa, Italy, ⁴Ecoistituto delle Cerbaie, Italy

irene.tatini@phd.unipi.it

The increasing spread of invasive alien species (IAS) across Italy poses significant threats to native biodiversity and ecosystem functioning, and calls for updated conservation policies. Addressing these challenges requires both rigorous ecological monitoring and the integration of local knowledge. Since November 2024, researchers from the University of Pisa, Scuola Superiore Sant'Anna, and the University of Florence have been collaborating with the Ecoistituto delle Cerbaie on the RICONOSCERE Project, a citizen science initiative active in the Special Area of Conservation "Cerbaie" (IT5170003). The collaborators have implemented a multitaxa monitoring framework combining traditional field protocols and environmental DNA (eDNA) analysis, with a focus on aquatic habitats and cryptic or neglected taxa. This integrative approach enables non-invasive detection of native and allochthonous species, contributing to the development of an updated species checklist for the study area. In parallel with data collection, the project offers a series of educational activities. Some are specifically designed to address IAS-related issues, aiming to foster ecological awareness and informed dialogue, with particular attention to communicating the concept of alien species without emphasizing stigmatization. Although preliminary, results from evaluation and self-assessment forms collected during the educational activities and field sessions suggest an improvement in participants' understanding of concepts related to IAS and their interactions with native species. In this preliminary phase, the RICONOSCERE Project reaffirms the potential of participatory approaches, combined with molecular tools, to enhance IAS surveillance while simultaneously empowering local communities in long-term biodiversity monitoring.

Keywords: Citizen science, Biodiversity monitoring, Neglected taxa, Naturalist, Metabarcoding

Session: SUS-MIRRI.IT Strengthening the MIRRI Italian research infrastructure for sustainable bioscience and bioeconomy

Assessment of relationships with indolamines in a collection of tomato culturable endophytic bacteria

Maria Grazia Caruso, Maria Ventimiglia, Cristiana Sbrana

CNR Institute of Agricultural Biology and Biotechnology, Pisa, Italy

mariagrazia.caruso@ibba.cnr.it

Endophytes can benefit plants by promoting growth and nutrition and by inducing tolerance to biotic and abiotic stresses, thus they are often described as the "second functional genome" of host plants. The composition of endophytic communities is shaped by both plant genotype and environmental factors, and it may differentially impact plant phytochemical profiles. Recent evidence suggests that bacterial endophytes produce indolamines in vitro and that they may affect the expression of melatonin-related biosynthetic genes in plants exposed to abiotic stress.

Lycopersicum esculentum MicroTom plants known to differentially accumulate serotonin and tryptamine depending on genotypes, tissues and plant growth stages, were used to isolate endophytic bacteria. Culturable endophytic bacterial strains isolated from roots, stem, leaves and fruits of tomato plant were maintained in the CNR-MLIP culture collection, identified by 16S rDNA sequencing and characterized for their sensitivity in vitro to indolamines.

The analysis of strains growth responses in the presence of different doses of serotonin and tryptamine revealed that tryptamine did not significantly affect bacterial growth, whereas high concentrations of serotonin inhibited growth. Interestingly, a potential growth-promoting effect of low serotonin levels was detected in several strains. Investigation on indolamine production by the isolated strains may provide further data on the complex and multifunctional roles of endophytes in plant indolamines physiology.

This study received funding from the European Union - Next-GenerationEU - National Recovery and Resilience Plan (NRRP) - Mission 4 Component 2, Investment n. 1.1, call PRIN 2022 D.D. 104 02-02-2022 - (TAM & SER) CUP N. B53D23018160006 and by European Commission "Next-GenerationEU, Project "Strengthening the MIRRI Italian Research Infrastructure for Sustainable Bioscience and Bioeconomy", code n. IR0000005.

Keywords: Culture collections, Plant endophytic bacterial communities, Melatonin biosynthesis, Indolamine production
New insights into the long-term preservation of microbial communities associated with Apulian table olives

<u>Luciana De Vero</u>¹, Katia Gialluisi¹, Nicola De Simone², Giuseppe Petruzzino¹, Giancarlo Perrone¹, Antonio Moretti¹, Vittorio Capozzi², Massimo Ferrara¹

¹Institute of Sciences of Food Production (ISPA), CNR, Bari, Italy, ²Institute of Sciences of Food Production, CNR, Foggia, Italy

luciana.devero@ispa.cnr.it

Microbial biodiversity associated with fermented foods is a crucial resource for promoting human health and boosting innovation in the food industry. Scientific research and biotechnological valorization of specific microbial consortia require the preservation of their viability and functionality, which are the traits guaranteed by Microbial Culture Collections. However, assessing the best practices to promote the maintenance and revitalization of complex microbial communities is still challenging. Here, we present the strategies designed for the long-term preservation of microbiomes associated with table olives, a relevant example of plant-based fermented food worldwide, a key product in the Mediterranean diet, and among the main heritage foods in the Apulian region. The fermentation of these matrices is driven by a complex community involving mainly lactic acid bacteria and yeasts. To assess the best condition for their preservation, naturally fermented olives cv. Leccino, a typical Apulian cultivar, were sampled. Two cryopreservation protocols were developed by using 15% glycerol or DMSO as cryoprotectants and a storage temperature of -135 °C. The microbial consortium was studied before and during a 1-year storage period using a culture-dependent approach, RNA-based metabarcoding analysis, and metabolic profiling evaluation by Biolog Ecoplate®. The results showed that after 1 year of cryopreservation, the viability of the microbial consortium slightly decreased, regardless of the cryoprotectant used, and no significant changes in the metabolic profile were observed. Moreover, the metabarcoding analysis showed no significant differences in relative abundances after the storage period. Thus, we confirmed the effectiveness of the developed cryopreservation protocols, proper preservation of the microbial consortium, and its functionality during a long-term storage period.

This research is related to a specific task within the EU project SUS-MIRRI.IT (N. IR0000005).

Keywords: Glycerol, DSMO, Cryopreservation, Metabarcoding analysis, Metabolic profiling

Enhancing the ENEA Microbial Culture Collection: a valuable resource for advancing biotechnology and bioeconomy development

<u>Annamaria Bevivino</u>¹, Federico Sbarra², Eleonora Colantoni¹, Filippo Sevi¹, Valeria Poscente¹, Beatrice Curci³, Andrea Visca¹, Silvia Tabacchioni¹, Patrizia Paganin¹, Chiara Alisi¹, Flavia Tasso¹, Luciana Di Gregorio¹, Manuela Costanzo¹, Chiara Lico¹, Alfredo Ambrico⁴, Linda Bianco⁵, Daniela Cuna⁶, Patrizia Casella⁷, Antonio Molino⁷, ENEA team SUS-MIRRI.IT Project⁸

¹Department for Sustainability, ENEA, Italian National Agency for New Technologies, Energy and Sustainable Economic Development, Casaccia Research Center, Rome, Italy, ²University of Torino, Italy, ³University of Rome, La Sapienza, Italy, ⁴Department for Sustainability, Italian National Agency for New Technologies, Energy and Sustainable Economic Development, Trisaia Research Center, Rotondella, Italy, ⁵Department of Energy Technologies and Renewable Sources, Italian National Agency for New Technologies, Energy and Sustainable Economic Development, Trisaia Research Center, Portici, Italy, ⁶Department for Sustainability, Italian National Agency for New Technologies, Energy and Sustainable Economic Development, Brindisi Research Center, Brindisi, Italy, ⁷Department for Sustainability, Italian National Agency for New Technologies, Energy and Sustainable Economic Development, Portici Research Center, Portici, Italy, ⁸ENEA team SUS-MIRRI.IT Project, Italian National Agency for New Technologies, Energy and Sustainable Economic Development, Italy

annamaria.bevivino@enea.it

The ENEA microbial collection (EMCC) is a significant resource comprising over 1,400 strains, including bacteria, fungi, yeasts, two microalgae, and a plant virus. Over the past year, as part of the PNRR SUS-MIRRI.IT project, the EMCC has expanded in both biological resources and service quality.

Operative procedures were implemented for sampling, characterization, safe storage, and cultivation. Recent isolates were obtained from environmental sources, identified via MALDI-TOF and/or 16S rRNA gene analysis, and evaluated for plant growth-promoting (PGP) traits.

Among the 281 isolates from strawberry rhizosphere soil, 8 N-fixing strains were identified, belonging to *Agrobacterium, Enterobacter* and *Raoultella* genera; 109 strains produced siderophores, and 42 exhibited antifungal activity, mainly from *Achromobacter, Acinetobacter, Agrobacterium, Bacillus, Enterobacter, Ochrobactrum, Peribacillus, Priestia, Roultella, Serratia* and *Stenotrophomonas*. Of 92 isolates from strawberry washing water and homogenates, 58 strains from 24 genera were successfully identified by MALDI-TOF, including *Bacillus, Listeria, Pseudomonas,* and *Curtobacterium.* From 49 isolates collected from a Sardinian abandoned mine (27 genera), ten with strong PGP traits were selected for phytoremediation trials to support *Helichrysum* growth. Over 300 isolates from kiwivine, grapevine, and strawberry rhizosphere soils were cryopreserved at -80 °C for future analysis.

These developments will enrich the EMCC collection and foster the design of microbial consortia for sustainable agriculture and biotechnological applications. Ongoing efforts focus on expanding the collection with strains exhibiting biodegradation and bioremediation potential, including cellulose, biopolymer, and microplastic degraders, as well as bacteria from contaminated sites for soil restoration and ecosystem recovery.

Funded from the SUS-MIRRI.IT Project, Project code IR0000005.

Keywords: Microbial culture collection, Biotechnology, Bioeconomy, Sustainable agriculture, Phytoremediation, Biomarkers, Food quality and safety

Empowering Microbial Research: SUS-MIRRI.IT collaborative working environment platform

<u>Sandro Gepiro Contaldo</u>¹, Lorenzo Bosio¹, Francesco Venice¹, Daniela Volpatto¹, Michele Metta1, Simone Donetti¹, Luigi Di Caro¹, Giovanna Cristina Varese¹, Antonio d'Acierno², Marco Beccuti¹

¹University of Torino, Italy, ²Institute of Food Sciences, CNR-ISA, Avellino, Italy

sandrogepiro.contaldo@unito.it

The Italian Node of the Microbial Resource Research Infrastructure (MIRRI-IT), coordinated by the Joint Research Unit MIRRI-IT, plays a main role in advancing microbial research in Italy. To meet the growing needs for collaboration, data sharing, and access to services, the Italian Collaborative Working Environment (ItCWE) was developed. ItCWE aims to support the Italian microbial research community by integrating tools and services that enhance accessibility, interoperability, and scientific cooperation.

ItCWE integrates several services:

(i) The Catalogue service provides access to the Culture Collections (~39k strains), offering a user-friendly interface for browsing microbial strains and associated metadata, with advanced features such as the automatic generation of SQL queries from natural language;

(ii) The Data Analysis service for supporting reproducible microbiological data analysis (e.g., de novo assembly and metagenomic) on HPC infrastructure through a user-friendly web interface;

(iii) Supporting services include infrastructure-level features such as backup and monitoring tools and a JSON Schema-based system for validating and structuring microbial metadata, as well as a data correction module to improve data quality.

The ItCWE platform provides a centralized and accessible environment for microbial researchers. It currently supports the exploration of biological resources, the execution of computational analyses, expert consulting, and access to training materials. The integration of versioning, validation, and observability mechanisms ensures data quality, system reliability, and ease of use.

ItCWE represents a significant step forward in supporting microbial research in Italy and Europe. Its flexible and modular architecture allows for future expansion and adaptation to emerging research needs, positioning ItCWE as a model for national and international research support infrastructures.

Keywords: Database, Microbiology, Workflow, Dataverse, HPC

The Future Sustainability of the Research Infrastructure MIRRI-IT: an overview on objectives to pursue, KPIs to reach, and strategies to adopt

<u>Marino Moretti</u>, Edoardo Borlatto, Edoardo Crocco, Iolanda Perugini, Valeria Prigione, Giovanna Cristina Varese

University of Torino, Italy

marino.moretti@unito.it

Long-term sustainability poses great challenges to the administration of Research Infrastructures (RIs). RIs are typically operational for several decades, and, therefore, they require continuous and stable support in terms of financial funding and resource management, in order to fully develop their potential in Research and Innovation and sustain top-level economic growth at national and European levels.

Some of the objectives for the effective long-term governance of a RI are: enabling and maintain scientific excellence, delivery of high education and training for the up-skilling of the human capital, enhancing collaborations in EU, facilitating economic activities through industrial partnerships and international cooperations, optimising data management and use, outreach to the public, provision of scientific advice, and managing revenues.

MIRRI-IT is the Italian RI for the conservation, characterization, distribution and valorization of microbial biodiversity and resources. To verify the long-term sustainability of such infrastructure, the strategic guidelines of the Sustainability Plan will be outlined highlighting the key actions to undertake for each objective, such as the stakeholder engagement, and the ad hoc KPIs which will be measured to assess the outputs and achievements of the RI like the usage of MIRRI-IT cutting-edge facilities or the numbers of collaborations with academia, industries, territorial bodies, and policy makers. Overall, the achievement and maintaining of scientific excellence and the attainment of key objectives that demonstrate the positive impact and benefits of the RI for the society are, indeed, associated with an increased capacity to attract funding, thereby contributing to the long-term economic and financial sustainability.

Keywords: Microbial biobanks, Sustainable bioscience, Sustainability plan, Funding strategy, Technological transfer

Biodiversity of diurnal and nocturnal Lepidoptera in different environments of South Italy

Ilaria Latella¹, Antonio Modafferi¹, Stefano Scalercio², Orlando Campolo¹

¹University of Reggio Calabria, Italy ²Council for Agricultural Research and Economics, Research Centre for Forestry and Wood, Cosenza, Italy

ilaria.latella@unirc.it

The global decline in butterfly populations, attributed to different environmental perturbations (climate changes, agricultural intensification, and habitat loss), has a detrimental effect on biodiversity and ecosystem resilience. Due their close association with plants and their sensitivity to environmental changes, diurnal Lepidoptera are often used as bioindicators to evaluate the effects of different perturbation.

In this study, a monitoring program was carried out in the Aspromonte massif (Calabria, Italy) aimed to assess the impact of different anthropogenic pressures on the qualitative and quantitative community composition of these pollinators. Diurnal Lepidoptera were monitored on a bi-monthly basis from May to September along a total of ten 500 meters long transects located in a range of different contexts, including intensive and extensive grazing areas, cultivated fields, burned areas, and natural environments. The study also included a monthly monitoring of moths to assess the role of forest composition on the population's structure. Monitoring was carried out using UV LED light traps placed in areas of ecological or conservation interest (beech, fir, or mixed forests).

During the three years of observation, 63 species of diurnal Lepidoptera were recorded while a total of 141 moth species were sampled with the UV LED light traps. The abundance of different taxa as well as the diversity of sampled species of both diurnal and nocturnal Lepidoptera were affected by the year of sampling and the surveyed habitats.

Results highlighted the negative effects of habitat degradation, including overgrazing and wildfires, on pollinator communities. Even organic farming, despite being less invasive than conventional one, contributed to biodiversity loss, likely due to habitat simplification. Areas with minimal human disturbance showed the highest butterfly richness and diversity, emphasizing the need for conservation strategies to mitigate anthropogenic pressures.

Keywords: Moths, Butterflies, Perturbations, Bioindicators

How diversity of stink bugs and their parasitoids is affected by habitats and host plants

Martina Falagiarda¹, Francesco Tortorici¹, Sara Bortolini², Manfred Wolf², Luciana Tavella¹

¹University of Torino, Italy, ²Research Centre Laimburg, Italy

martina.falagiarda@laimburg.it

Stink bugs (Hemiptera: Pentatomidae) pose significant challenges to crop management due to their broad host range. This study explored biodiversity patterns of stink bugs and their egg parasitoids across different habitats and altitudes in South Tyrol, Italy.

Monthly surveys were conducted over two years (2022-2023) across 27 sites including apple orchards, urban areas, and forests, in three altitude ranges (200-500 m, 501-800 m, above 801 m a.s.l.). Moreover, we examined the association between the three most abundant stink bug species (*Halyomorpha halys, Palomena prasina*, and *Pentatoma rufipes*) and plant families.

Results revealed that forests and urban environments hosted the highest stink bug abundance, with 21 and 20 species present, respectively. The invasive *H. halys* was dominant in urban areas, while forests showed higher prevalence of native species. Altitude significantly influenced species composition, with greater stink bug diversity recorded in the altitude range 500-800 m. Egg parasitoid species diversity was higher above 801 m and in urban environments.

Among plant families, Sapindaceae and particularly Acer species supported the highest number of stink bug and parasitoid species, representing the most biodiverse host. *Halyomorpha halys* displayed a broad host range but showed strong associations with Sapindaceae and Oleaceae.

A total of 12 parasitoid species were identified, with native parasitoids exhibiting higher parasitism rates on native bug species. The exotic parasitoid *Trissolcus japonicus* was mainly associated with *H. halys* in urban areas. Parasitism rates differed significantly among species and plant families, with *H. halys* and *P. prasina* experiencing high parasitism during reproductive peaks.

These findings suggest that maintaining habitat heterogeneity and plant diversity can create ecological reservoirs that support natural biological control mechanisms, potentially mitigating stink bug populations through enhanced parasitoid diversity.

Keywords: Hemiptera, Egg parasitoids, Species diversity, Habitat heterogeneity, Biological control

Increasing plant diversity into Mediterranean tomato greenhouses: benefits for natural enemies and effects on key pest management

<u>Antonio Gugliuzzo</u>¹, Emanuele Porcu², Giovanni Pollara¹, Michele Ricupero¹, Gaetano Siscaro¹, Lucia Zappalà¹, Antonio Biondi¹

¹University of Catania, Italy, ²University of Reggio Calabria, Italy

antonio.gugliuzzo@unict.it

Functional biodiversity finds increasing application contexts in plant protection. Many success stories occurred on perennial crops in open field, while its application in greenhouse crops, including tomato, has been less explored. Current integrated management approaches targeting key tomato pests (i.e., whiteflies, moths, etc.) in Southern Europe include augmentative releases and/or conservative strategies of different biological control agents. Among them, the zoophytophagous mirid *Nesidiocoris tenuis* (Reuter) (Hemiptera: Miridae) is one of the most effective in reducing pest densities. Nevertheless, N. tenuis is also capable to develop and reproduce by feeding on plants, and in shortage of prey it can damage tomato growing tissues. In such a context, habitat management strategies aimed at increasing the functional diversity of alternative plants and natural enemies could also mitigate the negative impact of *N. tenuis* on tomato. Here, we explored the potential of two alternative plants, i.e., sesame (Sesamum indicum L.) and verbena (Verbena x hybrida Voss), when grown near tomato plants, to influence the population trends of natural enemies in commercial greenhouses. We monitored the population density of *N. tenuis*, other pests and natural enemies, and counted the number of mirid feeding-induced necrotic rings throughout the entire crop cycle. Results showed that both alternative plants increased natural enemy density and diversity (e.g., Aphidius spp., Diglyphus isaea, Orius spp., etc.) and supported the early establishment of N. tenuis, while mitigating its damage to tomato plants. However, contrasting results were observed for other natural enemies (i.e., Necremnus tutae, parasitoid of Tuta absoluta). The results suggest that alternative plants can ensure the early establishment of mirid predators and increase natural enemy populations by promoting their biological control activity, with the potential as a novel pest management tool in tomato greenhouses.

Keywords: Functional diversity, Habitat management, IPM, Natural enemies, *Tuta absoluta*.

Towards integrated pest and pollinator management: the role of functional biodiversity

Roberto Catania¹, Marta Bonforte¹, Gaetano Mazzeo¹, Michele Recupero¹, Maria Augusta Pereira Lima², Lucia Zappalà¹

¹University of Catania, Italy, ²University of Viçosa, Brazil

roberto.catania@phd.unict.it

Pollination by bees (Hymenoptera: Apoidea) is a key ecosystem service for human welfare and environmental health. Although crop pollination can be provided by managed pollinators, such as *Apis mellifera* or *Bombus terrestris*, a greater abundance and diversity of wild pollinators can improve crop yields and quality. However, both managed and wild bees in agricultural landscapes are threatened by anthropogenic factors, including the habitat fragmentation and overuse of agrochemicals. Bees can be exposed to agrochemicals by different routes and, besides lethal effects, the sublethal exposures can cause alterations at morphological, physiological and behavioural level. Within this context, modern and sustainable agriculture relies on Integrated Pest and Pollinator Management (IPPM) to harmonize pest control with pollinator conservation, optimizing environmental and economic benefits. This research aimed to assess i) how habitat management practices (e.g. enhancing floral diversity), which underlie the IPPM pyramid, can increase wild bee diversity and activity, and ii) the effects of agrochemicals, which are at the apex of the same pyramid, in specific agricultural settings. The effects of habitat management practices are still ongoing, but preliminary results of trails in open field and protected conditions are discussed. Agrochemicals showed lethal and sublethal effects on several bee species. Specifically, commonly used agrochemicals reduced the survival of ground-nesting bees of the genus Andrena and altered the locomotion of managed bees. Insecticides used to protect greenhouse tomato plants reduced the survival, caused changes in feeding behavior and midgut alterations in *B. terrestris*. By contrast, essential oil-based insecticides were found selective towards the stingless bee Melipona mondury. The results of these studies will be useful for optimizing IPPM practices and pollinator conservation by fostering agroecosystem resilience.

Keywords: Agroecology, Companion plants, Ecotoxicology, Habitat management, Pollinators

Patterns of endemism of Italian insects: different biogeographic histories uncovered by phylogenetic and phylogeographic approaches

<u>Alessandra Riccieri</u>¹, Joaquín Ortego², Marina Trillo², Fabrizio Freda¹, Bruno Massa³, Paolo Fontana⁴, Francesco Forte¹, Lorenzo Minelli¹, Lucrezia Spagoni⁵, Marco A. Bologna¹

¹University of Rome Tre, Italy, ²Department of Ecology and Evolution, Estación Biológica de Doñana, EBD-CSIC, Seville, Spain ³University of Palermo, Italy, ⁴Fondazione Edmund Mach (FEM), San Michele all'Adige, Trento, Italy, ⁵Department of Integrative Marine Ecology, Stazione Zoologica Anton Dohrn, Calabria Marine Centre, Italy

alessandra.riccieri@uniroma3.it

Italy has a complex history due to the geological and climatic events of the Eocene and the Pleistocene, its position at the centre of the Mediterranean, and its variety of ecosystems. This explains the high number of animal species (>60,000) and endemic taxa (>15%), most of which are insects (38,000 spp., 15% endemic), and the diversified biogeographic patterns characterizing its biota. Such diversity has been scarcely investigated with a phylogeographic approach, in particular regarding endemic insect species. We explored phylogenetic and phylogeographic patterns in several Italian endemic taxa among Coleoptera (Meloidae, Oedemeridae), Dermaptera (Forficulidae), and Orthoptera (Acrididae) to elucidate their relationship with other congeneric, and to delineate their biogeographic history and population structure. Most of our results confirmed the uniqueness of the Italian genetic lineages ascribed to endemic species, and in some cases new ones were delineated (e.g. the new endemic Meloe *digiuliorum*; the two lineages, Sicilian and Maghrebian, within *Mylabris impressa*, and the two lineages, Greek and Italian, of both *My. quadripunctata* and *Lydus trimaculatus*). Different and intriguing biogeographic patterns were revealed even among closely related taxa, corroborating the correlation between the complex history of the Italian region and the evolutionary history of its biota (e.g. the three endemic species of Eurymeloe showed three different patterns of biogeographic affinities; the endemic genus *Italopodisma* hides a complex history of isolation and admixture among populations). Our results have also implications in conservation: most of the taxa investigated have a restricted range, sometimes confined to habitats threatened by climate change (e.g. Forficula apennina, F. galvagni, F. orsinii, M. *digiuliorum*), some are included in the IUCN red lists (e.g. *Italopodisma*, *Italohippus*), while others show a surprisingly low genetic variability (e.g. *Mylabris obsoleta*).

Keywords: Biogeography, Coleoptera, Orthoptera, Dermaptera, Conservation

Conservation of saproxylic beetles in the genomics era

Emiliano Mancini

University of Rome, La Sapienza, Italy

emiliano.mancini@uniroma1.it

Genome-wide data have become essential for assessing the conservation status of endangered populations and identifying key genes involved in local adaptation, particularly for species confined to fragmented habitats.

Saproxylic insects - associated with dead or decaying wood - are especially vulnerable to habitat fragmentation, as they rely on dying trees and old-growth forests during part of their life cycle. These forest ecosystems are themselves increasingly threatened across Europe.

Among saproxylic insects, beetles play a pivotal role in forest ecosystems, contributing substantially to nutrient cycling and overall ecosystem functioning. Notably, *Rosalia alpina* (Coleoptera: Cerambycidae) and *Osmoderma eremita* (Coleoptera: Cetoniidae) are both listed on the IUCN Red List and included in Annexes II and IV of the EU Habitats Directive. While *R. alpina* in Italy comprises several evolutionary significant units (ESUs) that are yet to be clearly defined, two endemic relatives of *O. eremita* - *O. cristinae* in Sicily and *O. italicum* in Southern Italy - have been described.

As part of the initiatives of the National Biodiversity Future Center (NBFC), the phylogeographic structure of *R. alpina* was investigated using ddRAD-seq, with the aim of identifying ESUs, estimating the effective population sizes within Italian protected areas, and assessing the extent of genetic erosion over time. In parallel, a comparative genomic analysis was carried out on *Osmoderma* spp. to explore genomic and epigenomic differentiation between *O. eremita*, *O. cristinae*, and *O. italicum*, and to pinpoint genes potentially involved in local adaptation.

These genomic insights will enhance our understanding of the evolutionary history and current genetic diversity of these beetles and evaluate the effectiveness of existing conservation measures for old-growth forests. Ultimately, the results will inform the development of more targeted and effective conservation strategies for saproxylic insects.

Keywords: Genomics, saproxylic, Conservation, Evolution, Beetles

Pit-traps and pitfalls: reconstructing the evolutionary history of neuropteroid insects

Davide Badano

University of Siena, Italy

davide.badano@unisi.it

Neuropteroidea is an ancient insect clade that originated in the Permian and reached its peak diversity and morphological disparity during the Mesozoic. This group includes three orders: Raphidioptera (snakeflies), Megaloptera (fishflies and alderflies), and Neuroptera (lacewings, antlions, and allies). Although neuropteroids represent a minor component of modern insect communities, they are remarkable for their diverse ecologies and life histories. All neuropteroid larvae are predatory, but they exhibit striking specializations, ranging from freshwater sponge predators to social parasites and ambush hunters that construct elaborate traps, such as antlions. A key innovation driving lacewing diversity is the modification of larval mouthparts into a piercing-sucking apparatus linked to venom glands. Traditionally, larval morphology played a crucial role in inferring phylogenetic relationships and classification. However, molecular-based phylogenies have challenged this view, revealing complex patterns of convergent evolution across different lineages. Recent phylogenomic studies using genomic and transcriptomic data have profoundly reshaped our understanding of neuropteroid evolution, prompting a reassessment of key morphological traits and uncovering previously unsuspected affinities masked by ecological specializations and homoplasy. These advances provided a clearer phylogenetic framework and have identified major evolutionary radiations, including the transitions to soil and freshwater habitats.

Keywords: Evolution, Phylogeny, Lacewings, Morphology, Genomic

Breeding success of the critically endangered red-headed vulture (*Sarcogyps calvus*): an international partnership to save the species from the extinction

<u>Caterina Spiezio</u>¹, Saowaphang Sanannu², Chaianan Poksawat², Andrea Criscione³, Simon Bruslund⁴, Miriam Vadalà⁵, Camillo Sandri⁵

¹Fondazione Zoom, Natura Viva, Bussolengo, Italy, ²The Zoological Park Organization of Thailand, Thailand, ³University of Catania, Italy, ⁴Copenhagen Zoo, Denmark, ⁵University of Milano, Italy

caterina.spiezio@openature.com

Parco Natura Viva has been deeply involved in the conservation of the critically endangered red-headed vulture (Sarcogyps calvus), focusing on maintaining a genetic reservoir through exsitu breeding. After initial success in the late 1990s, consistent hatching failures occurred for different reasons despite continued efforts. In 2013, two eggs were incubated artificially after an initial period of parental incubation. Both chicks hatched successfully and were hand reared. This marked the discovery that the species required a longer incubation period, an average of 55 days, than previously reported. Between 2013 and 2020, nine more chicks hatched via artificial incubation. In the winter of 2020, for the first time, an egg was left with the parents, resulting in successful natural hatching and parent rearing under video monitoring from a video camera placed on the nest. This event marked a significant milestone in zoo-based conservation of the Red-headed vulture. In 2021, a second chick was successfully raised by the same pair. Thanks to the experience acquired between 2013 and 2020, Parco Natura Viva developed a standardized protocol for egg incubation and chick hand rearing. In 2023, this protocol was shared with colleagues from the Korat Zoological Park in Thailand, leading to the successful hand-rearing of a chick there. A National project in Thailand to have back this vulture species in the wild was born, and in 2021 Korat Zoological Park established an aviary in the wild at Sub Fa Pa Forest Protection Unit within the Huai Kha Khaeng Wildlife Sanctuary. A breeding pair was introduced in the aviary in 2022 and, in 2024, produced their first chick, which was successfully raised by its parents. This year, the same pair has laid and is raising a second chick, again under parental care. This collaborative, multi-step effort represents a hopeful model for the long-term conservation of S. calvus, connecting ex-situ expertise with in*situ* action.

Keywords: Asian vulture, Hand-rearing protocol, Parent rearing, in situ conservation, ex situ population

Genetic variability and differentiation of an endangered Mediterranean falcon (*Falco biarmicus feldeggii*) through a multi-marker approach: a support for conservation efforts

<u>Lorenzo Attili</u>¹, Luisa Garofalo¹, Antonella Pizzarelli¹, Giuseppe Puddu², Giampiero Tirone², Veronica Cippitelli², Stefano Picchi², Rita Lorenzini¹

¹Istituto Zooprofilattico del Lazio e della Toscana, Italy, ²Regione Lazio, Riserva Naturale Lago di Vico, Italy

lorenzo.attili@izslt.it

The European lanner falcon *Falco biarmicus feldeggii* (subgenus *Hierofalco*) is a medium-sized raptor that is rapidly heading for global extinction following a dramatic decline mainly caused by anthropogenic impacts. Currently, the global population size counts no more than 200 breeding pairs, with Italy, historically considered a stronghold for this taxon, currently hosting around 30-40 pairs, which is 20% of the pair number counted 40 years ago. To support and strengthen the efficacy of conservation efforts, we aimed at characterising the gene pool of the European lanner, examining the extent of its variability and differentiation from other falcon taxa inhabiting the Mediterranean area, which exhibit similar morphological traits.

We used a multi-marker molecular approach to investigate variation in the mitochondrial (mt) and nuclear DNA (Short Tandem Repeats, STRs) of 146 falcons sampled from different areas. Our results show that the European lanner is genetically distinct from other Mediterranean taxa as revealed by nuclear DNA, although no significant differences were found in mtDNA. Additionally, the use of STR markers provided a deeper assessment of the genetic diversity within falcon taxa. The combined system of DNA analysis employed proved to be suitable for investigations at various hierarchical levels, ranging from (sub)species to individuals.

The findings of this study proved to be highly effective in revealing the genetic differentiation and variability of this critically endangered European bird compared to other Mediterranean hierofalcons, thus providing a valuable tool for its future management and the development of strategies aimed at preserving both the species and its habitats.

Keywords: *Falco biarmicus*, Conservation, Mediterranean, Endangered, Genetic distinctiveness.

MuVal – The future of tradition: an immersive journey through Valnerina

Francesca Maria Sarti¹, Glenda Giampaoli², Vjola Luarasi³

¹University of Perugia, Italy, ²Director of Hemp Museum - Sant'Anatolia di Narco, Italy, ³Visual Museum Experience - MuVal - Sant'Anatolia di Narco, Italy

francesca.sarti@unipg.it

MuVal is an innovative project that transforms cultural and agricultural heritage into an interactive, multisensory experience. By integrating traditional know-how and agrobiodiversity, MuVal aims to create a sustainable and resilient future. Located in the Valnerina region, known for its high-quality agricultural traditions, the project seeks to counteract depopulation and revitalize rural territories through immersive technologies and educational methodologies.

The MuVal project is structured into thematic areas utilizing immersive technologies such as virtual reality and interactive installations. The Immersive Room provides a visual tour of Valnerina's most symbolic locations, while the Interactive Room, equipped with Oculus Meta Quest 2, facilitates a deeper understanding of local products and traditional farming techniques. The core of the project is dedicated to narrating agricultural expertise and highlighting the significance of agrobiodiversity, encompassing native crops, traditional practices, and local knowledge.

MuVal effectively bridges past and present by integrating advanced technological tools with traditional agricultural knowledge. This approach fosters awareness of environmental sustainability and territorial resilience, promoting local agricultural resources as strategic assets against depopulation. By offering an engaging and educational experience, MuVal stimulates community participation and facilitates knowledge transmission across generations, ensuring the preservation of Valnerina's rich heritage while fostering innovation. MuVal represents a model for sustainable rural development, demonstrating how technology and tradition can coexist to support local communities. By enhancing agricultural and cultural heritage through interactive experiences, this project stands as a virtuous example of resilience, education, and sustainable development, providing a replicable framework for similar initiatives worldwide.

Keywords: AgriTech heritage, Immersive sustainability, Cultural regeneration, Rural innovation, Biodiversity empowerment

Characterization of heterozygosity-rich regions in Sicilian horse breeds

<u>Morena Carlentini¹</u>, Serena Tumino¹, Giorgio Chessari¹, Salvatore Mastrangelo², Andrea Criscione¹, Donata Marletta¹, Salvatore Bordonaro¹

¹University of Catania, Italy, ²University of Palermo, Italy

morena.carlentini@phd.unict.it

Heterozygosity-rich regions (HRRs) are genomic regions of continuous heterozygosity, which may harbor functional genes related to the population's fitness response. The Sicilian horse breeds Sanfratellano (SAN), Siciliano (SIC) and Purosangue Orientale Siciliano (PSO) are known for the adaptability to a wide range of climatic conditions, sometimes even challenging. This study aimed to investigate HRRs distribution in a total of 220 horses (63 SAN; 93 SIC; 64 PSO) genotyped with the Illumina Equine 80K array. The consecutive runs method was used to detect HRRs and the top 0.1% of the SNP in RUNs were considered to define HRR islands per breed. The analysis identified 1944 HRRs in PSO (NHRR 30.38 ± 5.74), 1499 in SAN (NHRR 23.79 ± 5.59) and 2817 in SIC (NHRR 30.29 ± 7.91). The longest HRRs were observed on ECA7 across all three breeds. A total of 16, 16 and 11 HRR islands were identified in PSO, SAN and SIC, respectively. Gene annotation in HRR hotspots showed loci involved in immune response (SAN, PSO and SIC), environmental adaptation (SAN), fertility (SAN and SIC), and sports performance (PSO and SIC). The ECA7 hotspot (from 50.45 to 50.90 Mbps) was shared by the three Sicilian breeds (breeds recurrence >25%) harboring genes involved in the development and differentiation of muscle and bone tissues. QTL annotation, using markers in HRR islands, detected health traits in SAN, as well as growth and performance traits in all breeds. The investigation of the regions of the genome-wide consecutive heterozygous sites could be useful to reveal the traits linked to the balancing selection processes of Sicilian equine breeds and support their conservation plans.

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Keywords: HRRs, Heterozygosity, Horse, Molecular markers, SNPs, Animal genetics

Ecology of the lasca *Protochondrostoma genei* (Bonaparte 1939) in the Chiarò di Cialla Creek (Northeast Italy): new insights from a biodiversity hotspot affected by human impacts and alien species

<u>Marco Bertoli</u>¹, Matteo Maglitto¹, Andreah Sala¹, Marino Prearo², Paolo Pastorino², Elisabetta Pizzul¹

¹University of Trieste, Italy, ²Veterinary Medical Research Institute for Piemonte, Liguria and Valle D'Aosta, Italy

marbertoli@units.it

Freshwater hydrological networks can host precious biodiversity hotspots but are also among the most threatened environments and inhabiting native fish fauna can be critically endangered by human activities presence of alien species. Therefore, proper knowledge is of pivotal importance to protect/restore these species, manage their habitats and keep biodiversity hotspots safe.

In this study we investigate the ecology of the lasca *Protochondrostoma genei*, listed in the Annex II of the European Habitat Directive 92/43/EEC and among the endangered species in the Red List of Italian Vertebrates. Our study area was the Chiarò di Cialla Creek, partially included in a Site of Community importance (pSIC - IT3320041) and hosting other species listed in the Annexes of the Habitat Directive. Electrofishing sampling activities were carried out in 2024 throughout the whole creek, to analyze lasca population structure and fish community composition. Within the watercourse stretch included in the pSIC, main mesohabitats and substrate types were recorded, while values of main chemico-physical parameters were measured. The presence of anthropogenic impacts was checked. Distribution of alien species along the whole watercourse was checked, as the invasive common nase *Chondrostoma nasus* (negatively affecting the lasca population) was detected, and the brown trout *Salmo trutta* inhabits the upper watercourse stretch as consequence of introduction for fisheries.

Our results highlighted a well-structured lasca population inhabiting mainly pools and glides, while in riffles the occurrence was lower than in other habitats. Unfortunately, the lasca shares its habitats with common nase, which increased its density in the last years.

The present work provides new information about *P. genei*, that can be helpful to arrange management actions in the area and in other watercourses. Genetical investigations are now required to check potential hybridization between the lasca and common nase.

Keywords: Fish ecology, Conservation, Habitat preferences, Invasive species

Genetic characterization and conservation strategies for Mediterranean trout (*Salmo ghigii*) in Italian freshwater ecosystems

<u>Francesco Perini</u>, Francesca Lorenzoni, Antonella Carosi, Irene Cardinali, Hovirag Lancioni, Massimo Lorenzoni, Fatemeh Zarei, Emiliano Lasagna

University of Perugia, Italy

francesco.perini@unipg.it

The Mediterranean trout (Salmo ghigii) is a freshwater species of high conservation concern due to habitat degradation and genetic introgression from non-native Atlantic trout (Salmo *trutta*). As part of the LIFE IMAGINE project (LIFE19 IPE/IT/000015), the fish farm of Borgo Cerreto (Valnerina, Umbria, Italy) has been converted to produce Mediterranean trout, using wild breeders selected by genetic analysis. Subsequently, animals from various rivers in Central Italy were sampled to enhance the number of wild breeders. This study employed molecular markers, including nuclear LDH-C1 polymorphisms, mitochondrial control-region (mtDNA), and microsatellites (STR), to characterize wild populations across multiple Italian river basins. A total of 189 fin clips were stored in 99 % ethanol at -18°C until DNA extraction. Among these, 113 samples were obtained from Borgo Cerreto (BO) representing the breeders in the genetic center, while the others were collected from rivers in Umbria: seven samples from Argentina River (AR), 46 from Fosso delle Rote (RO), 21 from Fosso di Sensati (SEN), and 33 from Vigi River (SEL). All samples underwent LDH-C1 polymorphism genotyping using PCR-RFLP method. Only samples identified as LDH-C1*100/*100 were used for mtDNA genotyping. Ultimately, 141 samples were analysed for the mtDNA control region, and 15 samples using STRs. The results underscore the importance of reproduction center, where all animals presented the Adriatic haplotype. Conversely, all AR samples exhibited introgression with the Atlantic haplotype as well as in SEN animals, while 30% of the RO animals and the SEL population were Adriatic. These findings highlight the need for conservation measures such as genetic monitoring, and controlled breeding programs to preserve native genetic diversity. The integration of genetic tools with ecological assessments will be fundamental for the long-term viability of an ecologically and culturally valuable species such as *S. ghigii*.

Keywords: Genetic population, Biodiversity, Fish, Umbria

Genomic insights into runs of homozygosity and heterozygosity of Sicilian cattle breeds

<u>Serena Tumino</u>¹, Andrea Criscione1, Morena Carlentini¹, Giorgio Chessari¹, Aurora Antoci¹, Salvatore Mastrangelo², Santina Di Bella³, Gaetano Cammilleri³, Salvatore Bordonaro¹, Donata Marletta¹

¹University of Catania, Italy, ²University of Palermo, Italy, ³Istituto Zooprofilattico Sperimentale della Sicilia "A. Mirri", Italy

serena.tumino@unict.it

Genomic autozygosity (ROH) and heterozygosity (HRR) patterns were investigated in Sicilian Modicana (38 MOD) and Cinisara (26 CIN) cattle. Eighteen additional breeds (640,279 SNPs - a total of 442 animals: B. t. taurus, B. t. indicus, and admixed) framed the results within species diversity. ROH and HRR were detected using the consecutive run method. The top 0.1% of SNPs in runs formed ROH and HRR islands. 38,797 ROH segments were detected ranging from 437 (Piemontese) to 4189 (Jersey). FROH ranged from 0.018 (Piemontese) to 0.187 (Hereford); MOD showed intermediate (0.086), while CIN showed among the lowest (0.041), similar to indicine breeds. BTA5, BTA7, BTA14, and BTA21 accounted for 45% of ROH islands. Genes involved in epigenetics and reproduction were found in the most shared ROH islands on BTA21 and BTA23 across taurine, indicine, and admixed breeds, including CIN. In MOD, BTA6 harboured genes linked to milk traits and disease resistance. 771 HRR segments were detected, from 9 (Gir) to 87 (Beef Master), with admixed breeds showing the highest number and length per individual. Among taurine breeds, Hereford, MOD and CIN exhibited the highest mean of HRR per individual (2.80, 2.18, and 2.00), along with the highest mean HRR lengths (0.304, 0.263 and 0.295 Mb). BTA3, BTA7, BTA15, and BTA18 harboured 57% of HRR islands. The HRR hotspot on BTA3, shared by 11 breeds, including the Sicilian ones, highlighted genes linked to immunity and growth. An HRR island on BTA7, shared by Sicilian and three admixed breeds, harboured genes related to immunity and heat tolerance. These findings provide insights into the environmental adaptation of Sicilian cattle breeds.

This study was carried out within the Agritech National Research Center and received funding from the European Union Next-GenerationEU (PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR)-MISSIONE 4 COMPONENTE 2 INVESTIMENTO 1.4 - D.D.1032 17/06/2022 CN00000022) and by IZSS - Project ARCAS PSR Sicilia 14/20 Op. 10.2b

Keywords: ROH, HRR, Adaptation, Sicilian cattle, Diversity

Discovering unexpected pollinators suitability in urban environment

<u>Gianni Gilioli</u>, Fabio Gatti, Anna Simonetto

University of Brescia, Italy

gianni.gilioli@unibs.it

Bees (Apoidea) are of particular interest as they are especially vulnerable to biodiversity loss and are primary providers of pollination services, which are vital for the productivity and stability of agricultural and natural systems worldwide. Anthropogenic land-use change is a major driver of bees abundance and biodiversity decline, reducing landscape heterogeneity and ecological connectivity, and resulting in habitat fragmentation and degradation. Although many studies have addressed bees' population decline in human modified ecosystems, assessing the capacity of urban ecosystems to support functionally viable pollinator communities remains complex.

To address this knowledge gap, we developed a framework for assessing urban ecosystem suitability for pollinators integrating: i) high-resolution geospatial mapping of potential pollinator habitats, ii) a multidimensional suitability index, and iii) metrics describing spatial configuration and connectivity of habitat patches, all implemented within a GIS-based cartographic database. The methodology was applied to a case study of Brescia (northern Italy) to assess pollination suitability of this city and to evaluate the potential impacts of the new municipal policy for biodiversity conservation and climate change mitigation.

The analysis revealed a complex and heterogeneous habitat mosaic within the urban area, highlighting an unexpected potential of urban and peri-urban environments to support pollinator communities. The multi-scale approach enables assessment of both individual patch contribution and overall spatial configuration - key components of pollination suitability. Scenario analyses, based on various levels of implementation of the biodiversity conservation policy, showed how the designed strategies results in changes on habitat suitability across land-use types. The developed methodology represents a valuable tool for designing and implementing pollinator-friendly urban planning strategies.

Keywords: Bees, Urban ecosystem, Pollination service, Biodiversity conservation, Urban planning

Enrichment procedures for the selection and isolation of promising polycyclic aromatic hydrocarbons (PAHs) - degrading fungal strains: towards a Nature Based Solution (NBS) soil restoration

Anna Poli^{1,2}, Andrea Lara Marchitelli¹, Giovanna Cristina Varese^{1,2}, Valeria Prigione^{1,2}

¹University of Torino, Italy, ²NBFC, National Biodiversity Future Center, Palermo, Italy

anna.poli@unito.it

Soil hosts diverse microorganisms, including fungi, whose interactions underpin important ecosystem services. Anthropogenic activities (e.g. industrial processes, traffic pollution etc.) threaten soil health by accumulating xenobiotics like PAHs. Bioaugmentation of autochthonous fungal strains capable of degrading PAHs is a promising Nature Based Solution (NBS) for soil remediation. This work led to the isolation and identification of fungal strains from enriched cultures performed on a contaminated soil.

Three consecutive enrichments were performed using four individual PAHs and a mixture of them as sole carbon source to foster the growth of specialized fungal communities. Following solid screening, isolates were purified and identified using a polyphasic approach. In parallel, metabarcoding analyses were performed to assess fungal community dynamics across enrichment steps.

Among 102 isolates (12 genera and 18 species) recovered, the most represented classes were Sordariomycetes, Eurotiomycetes, and Dothideomycetes, with Hypocreales, Cladosporiales, and Eurotiales as the dominant orders. Metabarcoding analyses yielded similar results. Biodiversity indices calculated for each sample revealed that both contaminant type and enrichment progression significantly reduced the number of OTUs, indicating a strong selection for specialised communities and, interestingly, the number of pathogenic species increased as result of the selective pressure. Additionally, strains of *Cladosporium allicinum, Geotrichum candidum, Paracremonium* sp., and *Penicillium chrysogenum* were positive to biosurfactant production assays, suggesting a potential to enhance PAHs bioavailability.

This study demonstrates effective strategies for isolating PAH-degrading fungi and underscores their potential as bioremediation agents, supporting their use in restoring contaminated soils. To this aim, the most promising strains are currently being selected though miniaturized screenings.

Keywords: Xenobiotics, Bioaugmentation, Mycoremediation, Nature Based Solutions

The effect of biodiversity on phenolic content and antioxidant activity of sprouts from fruit-tree species

<u>Beatrice Flacinelli</u>¹, Ombretta Marconi¹, Elisabetta Bravi¹, Angelica Galieni², Franco Famiani¹, Paolo Benincasa¹

¹University of Perugia, Italy, ²Research Centre for Vegetable and Ornamental Crops, Council for Agricultural Research and Economics [CREA-OF], Italy

beatrice.falcinelli@unipg.it

Seeds from fruit-tree species represent a relevant by-product of the juice industry and a potential source of bioactive compounds such as phenols and other antioxidants. Sprouting could be an intriguing idea to enhance the content of these compounds. This work reviews results from three experiments carried out by our group to evaluate the sprouting performances and the phytochemical and antioxidant content of seeds and sprouts from 4 genotypes of pomegranate (Punica granatum cv Akko, Dente di Cavallo, Mollar de Elche, and Wonderful), 3 genotypes of olive (Olea europea cv. Arbequina, Leccino, and Moraiolo) and 5 *Citrus* species (bitter orange; *C. aurantium*; blonde orange, *C. sinensis* cv. Biondo comune; sweet orange, C. sinensis; lemon, C. limon (L.) cv. Femminello; mandarin, C. reticulata cv. Tardivo di Ciaculli). Seeds of each species were separated from ripe fruit by hand, washed with tap water, and incubated in plastic trays containing sterile cotton wetted with distilled water. According to a completely randomized design with 3 replicates, the trays were incubated in a growth chamber at T>20°C in a light:dark regime of 16:8 h for olive and pomegranate and of 12:12h for Citrus species. For olive, a month of stratification in dark at 14°C was needed before the beginning of sprouting. Sprouts were harvested at the complete cotyledon expansion and just before the emission of the first true leaf. Pomegranate gave the most stricking result, since i) germination in most cultivars was high and quite fast (one to two weeks); ii) sprouts had a good taste and texture and iii) their phenolic content and antioxidant activity were extremely higher than in seeds, with differences among cultivars. Sprouts from Citrus species and olive also showed high and genotype dependent phenolic and antioxidant content, but the low germination performances and the bitter taste make them not actually edible, and more suitable to the extraction of food additives, cosmetics or pharmaceutics.

Keywords: Sprout, Fruit-tree, Germination, Phytochemical, Antioxidant activity

An updated Plant Landscape Map of the Oreto river basin (Palermo, NW Sicily)

<u>Giulio Barone</u>, Emilio Di Gristina, Giuseppe Venturella, Gianniantonio Domina, Enrico Bajona, Raimondo Pardi

University of Palermo, NBFC, National Biodiversity Future Centre, Italy

giulio.barone01@unipa.it

The Oreto River is a 12 km watercourse that flows through the municipalities of Palermo, Monreale, and Altofonte. Although there are other tributaries further upstream, its source is located to the south in the territory of Altofonte. Passing through the city of Palermo, the river flows into the Tyrrhenian Sea. Along its watercourse it crosses the so-called "Conca d'Oro", a large plain rich in water resources and fertile soil. The Oreto River represents an important reservoir of biodiversity. In fact, its upper section is the locus classicus for *Carex panormitana* Guss. and hosts the westernmost population of *Platanus orientalis* L. However, in the post-war period, the area has undergone progressive transformation due to urban expansion of the city of Palermo and its neighbouring towns. This change in the landscape, together with widespread pollution and illegal construction, has led to the near-total loss of natural areas, particularly in the lower part of the river. In 1990, a plant landscape map of the entire Oreto River basin was published, also aimed at planning actions for the naturalistic redevelopment of the area. This survey reports the evolution of the plant landscape in the Oreto River basin over the past 35 years. An updated plant landscape map, produced through photointerpretation and supported by new field investigations, is presented. Additionally, a comparative analysis between the map provided in 1990 and the new one was carried out. It revealed a general deterioration in the quality of the area's natural state and specifically, a drastic reduction of semi-natural areas was recorded, with agricultural land giving way to urban expansion. Moreover, post-war reforestation efforts have been significantly reduced due to the numerous wildfires that have occurred in recent years. Populations of C. panormitana near the city of Palermo showed a decline, while those in the upper sections increased. No variations were observed in the P. orientalis population.

Keywords: Rivers, Land use, Urban expansion, Biodiversity, Sicily

Impact of ski slope management on soil properties and biodiversity in mountain grasslands

<u>Ilaria Fracasso</u>, Zinabu Marsie Gebru, Rapahel Tiziani, Sara Casagrande Bacchiocchi, Tanja Mimmo, Luigimaria Borruso, Camilla Wellstein

Free University of Bozen, Italy

ilaria.fracasso@unibz.it

Some areas of the Dolomites are subject to intensive management practices of ski resorts, which involve the use of artificial snow, snow grooming, and grazed or mowed vegetation. These factors may significantly alter soil physical and chemical characteristics, as well as micro- and mesofauna diversity.

We collected samples along an altitudinal gradient ranging from 1586 to 2066 m above sea level at five different sites. At each site, we collected 10 soil samples from the ski slopes and 10 samples from adjacent areas that were not subjected to alpine ski management practices. We measured soil pH, total organic carbon (TOC), total nitrogen (TN), texture, and aggregate stability. Additionally, we evaluated the micro- and mesofauna communities by amplifying the Cytochrome c oxidase I (COI) gene.

Most samples displayed comparable soil texture and aggregate stability values across ski slopes and adjacent areas. Nevertheless, ski slopes exhibited a higher pH compared to the surrounding area and a lower TOC and TN content. The lower TOC and TN concentrations could be related to increased surface erosion, which removes the topsoil rich in C and N, possibly due to the management and maintenance of the ski slope. Soil micro- and mesofauna alpha diversity, measured through species richness, did not show differences between slope and control areas. However, beta diversity revealed significant differences in soil micro and mesofauna communities, suggesting that while the overall number of species may remain stable, ski slope management may alter species composition. These findings highlight the impact of ski area management practices on soil health and biodiversity, with potential consequences that remain uncertain and require further investigation.

Keywords: Mountain land use, Ski slope management, Soil biodiversity, Soil properties

Novel aerobic 1,2-DCA degrading consortia from a contaminated aquifer for enhanced bioremediation purposes

<u>Laura Scirè Calabrisotto</u>¹, Elisa Maria Petta¹, Giovanna Carpani², Alberto Vassallo³, Marcello Tagliavia⁴, Valentina Catania¹, Paola Quatrini¹

¹University of Palermo, Italy, ²Environmental and Biological Laboratories, Eni S.p.A., Italy, ³University of Camerino, Italy, ⁴Institute for Biomedical Research and Innovation, IRIB-CNR, Italy

laura.scirecalabrisotto@unipa.it

Anthropized environments are a source of unexplored microbial diversity and functions that can contribute to address emergent environmental threats in a sustainable way. 1,2-dichloroethane (1,2-DCA) is a toxic groundwater contaminant that can be aerobically and anaerobically biodegraded by specialized bacteria. The main aerobic catabolic pathways is hydrolytic dechlorination, mediated by the key enzyme DhlA. The aim of this study was to isolate and characterize novel degrading bacteria from an unexplored 1,2-DCA contaminated aquifer to exploit for enhanced bioremediation purposes.

Enrichment cultures from groundwater samples were set up on mineral medium amended with 1,2-DCA as sole carbon source. The degradation abilities of enriched consortia were tested by Cl- release assay and Gas Chromatography-Mass Spectrometry. The consortia were PCR-screened for the dhlA gene. The consortia composition was studied by Ion Torrent 16S rRNA gene sequencing. Whole genome sequencing was performed by Nanopore technology.

Four stable 1,2-DCA-dechlorinating consortia with similar composition were obtained. All consortia consisted of known aerobic 1,2 DCA-degrading genus *Ancylobacter* and other genera with unclear role. The consortia degraded up to 1000 ppm 1,2-DCA in three days. The dhlA gene, identical to that of all other known aerobic 1,2-DCA degraders, and other genes involved in 1,2-DCA hydrolytic dechlorination were found and located on *Ancylobacter* chromosome in all consortia.

The consortia can efficiently degrade 1,2-DCA to a concentration that was not tested yet for other known 1,2-DCA hydrolytic degraders. The dhlA gene, located on plasmids in other known 1,2-DCA degraders, was located on a chromosome and it was confirmed to be highly conserved and likely acquired by horizontal gene transfer. The consortia can be exploited in bioremediation as a nature-based solution relying on the sustainable use of biodiversity.

Keywords: Dechlorinating bacteria, Aerobic dechlorination, Haloalkane dehalogenase gene, Groundwater bioremediation

A strategic tool for agrobiodiversity: the national portal of genetic resources for food and agriculture

<u>Antonella Trisorio</u>

CREA - Centro di ricerca Politiche e Bioeconomia, Italy

antonella.trisorio@crea.gov.it

Agrobiodiversity is essential for enhancing the resilience of agricultural production systems and ensuring greater adaptability to climate change. However, genetic erosion and loss of biodiversity continue unabated. Among the actions supporting the conservation and enhancement of agrobiodiversity, information and its proper management plays a key role. In implementation with Article 5 of Law 194/2015, the National Portal of genetic resources for Food and Agriculture (GRFA) was created to establish an interconnected database system on GRFA; to disseminate information on GRFA and monitor their conservation status. The portal is a web platform, established at the Ministry of Agriculture, which, among other things, integrates and makes interoperable the IT systems of the National Register and the National Network of GRFA, created in implementation of Articles 3 and 4 of Law 194/2015. As a project of national interest, the Portal was developed in close coordination with relevant institutions, including regional representatives to accommodate their specific IT and organizational needs. The development process of National Register and National Network included: identifying all stakeholders involved in the registration procedure and their roles; implementing the registration workflow; and defining the system for management, updates and consultation, as well as structuring the related databases and mutual connections. Key features of the system are flexibility, allowing adaptation to different regional models; modularity, enabling the system to evolve to meet future needs; interoperability, ensuring data exchange across systems; and cooperation, supporting collaborative implementation. The Portal enables a comprehensive overview of GRFA, supports monitoring of conservation status of GRFA, enhances knowledge sharing, strengthens stakeholder cooperation, and fosters international dialogue, making it a strategic tool for national policies on GRFA conservation and enhancement.

Keywords: Agrobiodiversity, Genetic Resources for Food and Agriculture (GRFA), National portal, Information system, Conservation

The role of organic districts in nature and biodiversity protection and climate change mitigation. The example of the biodistricts in the Lazio Region

<u>Raffaella Pergamo</u>¹, Barbara Giorgi², Manal Hamam¹, Antonio Manzoni¹, Giulia Pastorelli¹, Luigi Servadei¹

¹CREA - Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria, Italy, ²Biodistretto dei Laghi di Bracciano e Martignano, Italy

raffaella.pergamo@crea.gov.it

Biodistricts in the Lazio Region are an innovative model based on organic farming and sustainability, promoted through Law no. 11/2019 to enhance sustainable agricultural production, protect the environment, and boost rural territories. The Climate Change Working Table, activated by these biodistricts, fosters synergies among institutions, farms, and research bodies, contributing to the region's sustainability efforts.

The study examines 5 biodistricts in Lazio, focusing on the Climate Change Working Table's role in assessing the effectiveness of actions for biodiversity, climate change mitigation, and sustainable water management. It also explores the challenges posed by climate change, particularly in relation to water resource use and biodiversity protection in these biodistricts. Lazio's biodistricts serve as effective tools for protecting biodiversity and water resources

while mitigating climate change. Their activities have reinforced territorial governance and promoted practices with lower environmental impacts. The Climate Change Working Table has been key in fostering cooperation among stakeholders, encouraging resilient agricultural practices and the protection of natural resources.

The biodistricts in Lazio contribute significantly to ecological transition and climate resilience. The Climate Change Working Table represents an innovative governance model, fostering collaboration. Key discussions include restoring degraded ecosystems, creating corporate water reservoirs to address the water crisis, and developing financial tools like water credits. Challenges include the need for sufficient funding and better institutional coordination. Moving forward, increasing financial support and cooperation will be vital to sustaining these strategies over time.

Keywords: Bidioversity, Sustainability, Climate change, Water resources

From diversity to multifunctionality: Integrating marginal area and cover crops for enhanced agroecosystem performance

Ilaria Bruno, Cristiana Peano

University of Torino, Italy

i.bruno@unito.it

Biodiversity can contribute to the multifunctionality of the system. A possible technique that can be used for enhancing ecosystem functions is the use of cover crops and spontaneous species, as diversification not only increases but also harnesses the functional biodiversity of the system. Since wild or sown species are an interface between the above and below ground environments, if managed correctly, we can enhance specific ecosystem services and boost the multifunctionality of agroecosystems. This requires careful consideration of the complementarity among various functional traits.

In specialised fruit-growing sector, it can also be achieved through the inclusion of marginal areas, which, despite not being productive, can be included for the sustainability of the systems; the areas are represented by the inter-row and field edges. The first area has the most important surface in the orchards; it is represented by 2.5 and 4.5 meters in width and multiplied by the tree rows.

The case studies analysed show the evolution of 3- and 2-year cover crop mixtures sown in specialised apple orchards in south-western Piedmont. The choice of species was based on an analysis of relevant functional traits for the targeted agroecosystem.

The study aims to optimize the self-assessed design indicator named Vegetation-based Ecological Functions Sustainability Index (VEFSI), which is used to assess the development of these species in relation to the ecological functions they perform.

The index evaluates five ecological functions: nitrogen fixation, soil coverage, pollination, attraction of pollinators and enhancement of soil structure. For index calculation we considered the number of species and both relative and total coverage for each species.

Our goal is to highlight how cover crops with varying degrees of diversity perform and the ecological functions they provide to improve the agroecosystem condition.

Keywords: Fruit growing sector, Functional traits, Multifuncionality, Ecological functions, Cover crops

Physiology and endophytic communities of *Xylella*-resistant and susceptible olive tree cultivars

<u>Luigi De Bellis</u>, Alessandro Frontini, Marzia Vergine, Mariarosaria De Pascali, Erika Sabella, Andrea Luvisi

University of Salento, Italy

luigi.debellis@unisalento.it

Xylella fastidiosa subsp. *pauca* (Xfp) causes significant physiological changes in olive trees culminating in symptoms such as leaf scorch, wilting, and dieback. The bacterium colonizes the xylem vessels, disrupting water transport and causing hydraulic failure.

Olive trees of cultivars Leccino (resistant) and Cellina di Nardò (susceptible) were sampled in productive orchards close to Lecce. We measured physiological parameters, stress markers (both metabolites and enzymes), and the microbial community composition by Next Generation Sequencing (NGS).

Results indicated differences among cultivars, with a general decrease of pigment content and relative water content and a general increase in stress markers and carotenoids in presence of infection. Cellina microbiome appeared to fluctuate depending on Xfp titer, while Leccino microbiome showed greater refractoriness to the pathogen, and a higher abundance and diversity of putative beneficial endophytes.

Xfp alters the organization of the olive tree microorganism community determining changes in the plant physiology. Healthy plants harbor a more diverse and abundant array of microorganisms, whereas infected plants exhibit a shift towards less varied communities, potentially dominated by pathogenic microorganisms. Identifying beneficial microorganisms associated with the resistant Leccino cultivar (e.g from genus *Enterobacter*), underscores the importance of cultivar characteristics in disease resistance and highlights the possibility for effective biocontrol agents in sustainable agricultural practices.

Keywords: Xylella fastidiosa, Olive tree, Resistant and susceptible cultivar, Microbiome

Structural and metabolic changes in Xylella fastidiosa resistant and susceptible olives

<u>Alessandro Frontini</u>, Luigi De Bellis, Marzia Vergine, Mariarosaria De Pascali, Erika Sabella, Andrea Luvisi

University of Salento, Italy

alessandro.frontini@unisalento.it

Xylella fastidiosa subsp. *pauca* (Xfp) is regarded as one of the most serious plant pathogens, affecting a variety of agriculturally important host species, including olive trees. The research aim is to examine both olive cultivars and wild olives as sources of knowledge on disease resistance.

Olive trees of the cultivars Leccino (resistant) and Cellina di Nardò (susceptible), together with oleaster genotypes were sampled in different localities of Salento Apulia, Italy. Structural and metabolic changes in wood-forming processes will be investigated to detect histological and structural anomalies in xylem tissue mainly hybridizing thin xylem sections (45 μ m) of one-year-old olive or wild olive branches with the FISH (Fluorescence In Situ Hybridization) KO210 probe specific for *X. fastidiosa* (Xf).

In the representative images on the right, oleaster vessels are largely single or in pairs in noninfected (-Xfp). In contrast, in infected oleaster (+Xfp), the vessels are clustered together and positioned adjacent to each other, aligned along the section's ideal radii; in this scenario, numerous xylem vessel occlusions by Xf cells are visible, as evidenced by the probe's red signal emission. Comparably images were obtained by analyzing sections of branches of the varieties Leccino and Cellina di Nardò.

The dominance of single vessels permits the bacterium to remain limited to only one vessel, slowing disease progression and potentially making the host plant more tolerant/resistant to the pathogen. In any case, it is possible that the production of more xylem vessels close to each other is a response to the infection, and thus a way of conveying more water to the leaves, with an effort that paradoxically may aggravate the infection because *Xylella* can colonize nearby vessels. Subsequent investigations will allow us to determine whether 'single' xylem vessels represent a stretch of resistance.

Keywords: Olive, Xylella fastidiosa, Xylem structure, Resistant and susceptible cultivars

Solanum aethiopicum gr. gilo accessions and their potential use as eggplant rootstock

<u>Beppe Benedetto Consentino</u>, Lorena Vultaggio, Gaetano Giuseppe La Placa, Fabiana Mancuso, Pietro Bellitto, Salvatore La Bella, Leo Sabatino

University of Palermo, Italy

beppebenedetto.consentino@unipa.it

Herbaceous grafting is an agamic plant propagation technique involving the union of two plants, the rootstock, selected for its tolerance to biotic and/or abiotic distresses, and the scion selected for yield and quality traits. *Solanum torvum* represents the most widely used rootstock for eggplant. Nevertheless, the employment of other rootstock genotypes and their interspecific hybrid could be a useful alternative to improve eggplant performances and to valorise the biodiversity. In our study we tested six different grafting combinations [ungrafted, self-grafted, grafted onto: *S. torvum*, *S. melongena* gr. gilo × *S. aethiopicum*, *S. aethiopicum* gr. gilo (accession 1) or *S. aethiopicum* gr. gilo (accession 2)] using the cultivar "Scarlatti" as scion. All genotypes tested as potential rootstocks did not adversely affect fruit quality characteristics. Additionally, fruit glycoalkaloids content was always below the recommended limit in all grafting combinations. The study underlined that the use of interspecific hybrid rootstocks secured high yield performance. The results also indicated that the use of *S. melongena* × *S. aethiopicum* gr. gilo interspecific hybrid could be an encouraging option to the most used *S. torvum*. Herbaceous grafting is a key tool to ensure or increase fruit yield and quality under optimal or stressed conditions. Grafting success is a further important aspect when testing new combinations of scions and rootstocks. In our study, grafting success was over 89% in all rootstock-graft combinations with a peak of 99% when using *S. torvum* and *S. melongena* × *S. aethiopicum* gr. gilo rootstocks. From these results, it is evident that the genotype choice is an important step in identifying the appropriate rootstock for fruiting vegetables. This choice may be improved by exploiting the variation among the accessions of a specific species.

Keywords: *Solanum melongena*, Herbaceous grafting, Biodiversity use, Biodiversity valorisation, Accessions

Multilevel assessment of soil biodiversity after application of biostimulant based on arbuscular mycorrhizal fungi in three cropping systems

Francesco Vitali¹, Gabriele Berg², Samuel Bickel², Gaia Bigiotti¹, Loredana Canfora¹, Corrado Costa³, Lorenzo D'Avino¹, Sara Del Duca⁴, Antonia Esposito¹, Ewa Furmaczyk⁵, Anne D. Jungblut⁶, Hester J. van Schalkwyk⁶, Dawid Kozacki⁵, Alessandra Lagomarsino¹, Eligio Malusà⁵, Andrea Manfredini¹, Antonio Gerardo Pepe¹, Maria Grazia Tommasini⁷, Sara Turci⁷, Nadia Vignozzi¹, Simona Violino³, Stefano Mocali¹

¹Research Centre for Agriculture and Environment, Council for Agricultural Research and Economics (CREA-AA), Italy, ²Graz University of Technology, Austria, ³Research Centre for Engineering and Agro-Food Processing, Council for Agricultural Research and Economics (CREA-IT), Italy, ⁴Research Centre for Genomics and Bioinformatics, Council for Agricultural Research and Economics (CREA-GB), Italy, ⁵The National Institute of Horticultural Research, Poland, ⁶Natural History Museum, Department of Sciences, UK, ⁷RI.NOVA Soc. Coop. (Research and Innovation in Agriculture), Italy

francesco.vitali@crea.gov.it

Complex and multilayered communities of soil biota underpin ecosystem services in healthy soils. Agricultural practices are key drivers of soil biological diversity; they can lead to its degradation but also have the potential for inducing its enhancement. Microbial-based plant biostimulants represent a promising alternative solution to chemical fertilization with great potential of positive impacts on soil biodiversity. Biostimulants containing arbuscular mycorrhizal fungi (AMF) can improve nutrient uptake and soil structure. To better understand their effect and evaluate in situ application outcomes, we applied a multilevel assessment of their impact on soil biota for three cropping systems covering apples, strawberries and tomatoes.

AMF-based biostimulants were compared with untreated controls in field trials located in the northeastern Emilia-Romagna region in Italy, in northern Mediterranean agricultural environmental zone. We assessed the soil microbial communities and activity by way of the 16S rRNA gene bacterial diversity, metabolic activity (Biolog Ecoplates), gene abundance (qPCR), as well as soil nematode and microarthropod communities, hydrolytic enzyme activity, and potential CO₂ and N₂O production.

The three cropping systems differed in most measured variables, with apple orchards showing the highest values for most of them, followed by strawberry. PCA ordination indicated that plant-parasitic nematodes characterized tomato, while N-cycle genes characterized strawberry. The AMF treatment did not increase yields for any of the crops, nor induced its decrease; but a marked increase of several biodiversity indices and functional biological parameters, especially in the strawberry cropping system, was identified.

The integrated assessment suggests that microbial biostimulants can support sustainable soil management by enhancing biodiversity and ecosystem functioning, relevant for long-term improvement of cropping systems.

Keywords: Soil biodiversity, Microbial-based plant biostimulants, Multilevel biota assessment

Insect taxonomic and functional diversity: opportunities from genetic approaches

Matteo Montagna, Matteo Brunetti, Giulia Magoga

University of Napoli Federico II, Italy

matteo.montagna@unina.it

Characterizing insect biodiversity is essential for understanding ecosystem functionality and resilience, including the impact of climate change, agricultural practices, and land-use intensification. DNA-based methods, particularly DNA metabarcoding, provide efficient and high-throughput solutions for insect biodiversity assessment, enabling accurate taxonomic and functional characterization. This approach relies on well-curated reference databases of genetic markers (e.g., COI, 12S rRNA) built from morphologically identified specimens, thus integrating taxonomic and molecular biology expertise. Properly formatted databases with high-quality reference sequences ensure seamless integration into bioinformatic pipelines and accurate taxonomic assignment, strengthening biodiversity monitoring efforts. A key advantage of DNA metabarcoding is its broad applicability to various environmental samples, including bulk insect, soil, water, and air samples, allowing large-scale biodiversity assessments across different ecosystems. Although these approaches rely on short genetic fragments (a few hundred nucleotides), recent advancements demonstrate their potential to also retrieve preliminary population genetics information. Additionally, DNA-based approaches, combined with functional trait databases, represent an efficient way to study the ecosystem services provided by insects, such as pollination and pest control. However, challenges remain in protocol standardization, database completeness, and methodological biases. Addressing these limitations will further enhance the reliability of DNA-based approaches, supporting their adoption in biodiversity conservation and ecosystem management strategies.

Keywords: Molecular taxonomy, DNA metabarcoding, Environmental DNA, DNA-barcoding databases

Hoverfly (Diptera, Syrphidae) biodiversity in Italian National Parks

Daniele Sommaggio, Lara Maistrello, Michele Cesari, Giovanni Burgio

University of Modena and Reggio Emilia, Italy

daniele.sommaggio@unimore.it

The Italian fauna of Syrphidae (Diptera) is the second richest in Europe, yet our understanding of hoverfly distribution remains fragmented. Currently, 21.4% of Italy's terrestrial area is under protection, with 5.3% within 25 National Parks. Despite the critical role of Syrphidae in ecosystem services like pollination and biological control, research on their presence in National Parks is still insufficient. In recent years, some National Parks have initiated projects to enhance knowledge of hoverfly fauna, revealing notable differences between parks. While certain parks have limited species records, others show remarkable diversity. For instance, the Dolomiti Bellunesi National Park (DBNP) boasts 211 species, thanks to five years of focused research.

These efforts have significantly expanded the Italian hoverfly fauna, with species such as *Anasimyia lunulata, Syrphus rectus,* and *Helophilus hybridus* recorded for the first time in the DBNP, and *Eumerus narcissi* identified in the Arcipelago Toscano National Park. Standardized sampling protocols allow comparisons of conservation status among parks, as demonstrated by DBNP and Val Grande National Parks. In Alpine Parks hoverflies have been included in research focusing on pollinator distribution along altitudinal gradients, revealing a unimodal distribution of hoverflies with peak at middle altitude (1400-1600 m). Molecular approaches have advanced the understanding of population differentiation in species like Merodon cinereus, making it a promising model for studying climate-induced changes.

This research highlights the urgent need to expand knowledge of hoverflies in all Italian National Parks, which are crucial biodiversity hotspots and key to conserving this important group of insects.

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Keywords: Syrphidae, Italian National Parks, Pollinators, Climatic change, Altitudinal gradients

Using biosolutions in fruit orchards against the invasive *Halyomorpha halys* to reduce pest control impact on biodiversity

Adriana Poccia¹, Elena Chierici¹, Elisa Marchetti², Gabriele Rondoni¹, Eric Conti¹

¹University of Perugia, Italy, ²Agri2000Net Srl – Bologna, Italy

adriana.poccia@dottorandi.unipg.it

Biodiversity plays a crucial role in maintaining ecosystem resilience, including natural pest regulation. However, the introduction of invasive species, such as the brown marmorated stink bug (*Halyomorpha halys*), can disrupt ecological balance by altering native species dynamics and reducing biodiversity. Native to East Asia, *H. halys* has rapidly spread across North America and Europe, feeding on over 300 cultivated plant species and causing significant economic losses. In Italy, this pest has particularly affected fruit orchards, including pears. Although H. halys is commonly controlled with synthetic insecticides, increasing concerns over environmental impact have encouraged the development of more sustainable approaches, such as the use of natural compounds and biological control agents. In laboratory trials, various organically registered products (e.g., azadirachtin, sulphur, calcium polysulfide) showed significant lethality against *H. halys* nymphs. Diatomaceous earth, either alone or alternated with sulphur or calcium polysulfide, provided comparable control in field trials when compared to conventional strategies based on neonicotinoids (e.g., acetamiprid), with reduced effects on non-target beneficials like the egg parasitoid Trissolcus japonicus. Further research evaluated the repellency of three compounds against *H. halys*. Repellent activity was confirmed under laboratory conditions. Field experiments conducted in pear orchards showed that repellentbased dispensers effectively reduced *H. halys* presence in treated plots and mitigated fruit damage. These findings support integrated pest management (IPM) strategies that limit chemical inputs while enhancing biodiversity conservation and ecological sustainability in agroecosystems.

Keywords: Brown marmorated stink bug, Integrated pest management, Hemiptera, Natural compounds

Funerary archaeoentomology: a discipline to investigate biodiversity, local extinction and new arrivals

Stefano Vanin

University of Genova, Italy

stefano.vanin@unige.it

Archaeoentomology is a branch of environmental archaeology that focuses on insects and other arthropods, contributing alongside other disciplines to reconstruct a more complete view of past events, climate, and landscape. Funerary archaeoentomology, as defined by Huchet in 1996, focuses on the arthropods associated with human remains of archaeological interest or with elements involved in funerary rituals, such as offerings.

In recent years, several studies have been conducted on Italian archaeological sites covering around 5,000 years and various contexts. Sardinian necropolises, Egyptian mummies stored in Italian museums, and offerings in public collections are among the oldest samples from which insects have been isolated. Mummified and skeletonized bodies of kings, saints, and common people also represent an important source of insects. It is worth mentioning that more than 80% of the studies deal with burials that occurred in the modern era, especially in crypts under churches or related to the remains of World War I soldiers.

In all cases, the majority of the findings are insects in the orders Diptera and Coleoptera, while among the Arachnida, mites represent the most important taxon. Cases of local extinction (e.g., *Phormia regina*, Diptera: Calliphoridae), new potential species introduction (e.g., *Hermetia illucens*, Diptera: Stratiomyidae), ectoparasites associated with humans and other animals (Siphonaptera and Psocodea), food and wood pests (Coleoptera: Curculionidae, Ptinidae, Dermestidae, Cleridae, and Tenebrionidae), and the distribution of several flies (Diptera: Phoridae, Muscidae, Fanniidae, Calliphoridae, and Sarcophagidae) are reported and discussed. This study, having a historical perspective based on well documented and relaible dating, allows a temporal analysis of the entomofauna evolution also depending on human activities, trades and travels.

Keywords: Insects, Funerary archaeoentomology, Past reconstruction, Diptera, Coleoptera

The use of archaeoentomology and cartography to investigate the landscape transformation in the modern era

Giuseppina Carta¹, Omar Larentis², Alessandro Leto³, Davide Badano⁴, Stefano Vanin¹

¹University of Genova, Italy, ²University of Trento, Italy, ³Pian di Marte, Italy, ⁴University of Siena, Italy

giuseppina.carta@edu.unige.it

Archaeoentomology is an interdisciplinary discipline that focuses on insect remains from archaeological contexts, providing deeper insights into human-environment interactions from a historical perspective. This study aims to analyze variations in land use by examining insect assemblages from archaeological contexts and comparing them with contemporary species records, based on historical (e.g., Catasto Chiesa, 1727-1734) and modern land-use cartography. Archaeological contexts offer well-dated or easily datable material, providing a reliable chronological framework.

Since 2022, this research has been conducted at the Pieve di San Cristoforo church in Pian di Marte (Umbria, Central Italy), employing pitfall and Malaise traps alongside direct hand collections. Five hypogean crypts (18th-19th century) containing human remains were analyzed as part of a multidisciplinary project, with a particular focus on the entomofauna associated with the bodies. Two chambers, located on the northeastern side of the church, have drainage channels connecting them to the external environment. However, these channels were sealed around the end of the 18th century. Before their closure, they likely allowed access to predatory and opportunistic insect species unrelated to cadaveric fauna. Ground beetles (Carabidae: *Carabus, Pterostichus, Nebria, Trechus,* etc.) and leaf beetles (Chrysomelidae) were sampled. These taxa, with their specific habitat and food preferences, are recognized as reliable bioindicators of soil conditions and vegetation.

The results indicate that, despite significant variations in land use near the church, the ground beetle fauna has not been strongly affected. This could be explained by the survival of small wooded patches that served as refuge areas for Carabids. On the other hand, leaf beetles reveal the past abundance of elm trees, which no longer exist in the area. However, some local toponyms testify to the historical presence of these trees.

Keywords: Insects, Carabidae, Chrysomelidae, Land-use, Past reconstruction
Session: Insect biodiversity in the modern era

Small creatures, big impact: unveiling the power of nematode diversity in the Mediterranean ecoregion

Barbara Manachini¹, Federica Semprucci²

¹University of Palermo, Italy, ²University of Urbino Carlo Bo, Italy

barbara.manachini@unipa.it

Studying the biodiversity of nematode communities in Mediterranean regions is crucial for several reasons, especially given the unique ecological and agricultural characteristics of these areas. The Mediterranean climate supports a wide variety of habitats that harbor rich assemblages of nematode species. This biodiversity plays a key role in maintaining ecological balance and ensuring the functionality of both terrestrial and marine ecosystems.

Examples from natural and agricultural terrestrial habitats will be provided, where nematodes are known to contribute significantly to nutrient cycling and soil health. In Mediterranean orchards, vineyards, and olive groves, beneficial nematodes can help regulate pest populations, reducing the reliance on chemical pesticides. By integrating nematological knowledge into land management practices, farmers can improve soil structure and fertility, supporting a more sustainable form of agriculture with reduced environmental impact.

Furthermore, the study of nematode communities extends beyond land into the meiofauna of the Mediterranean Sea, where they are essential components of benthic food webs. Their biodiversity reflects the health of marine ecosystems, making them valuable indicators of environmental change. Understanding the dynamics of marine nematode communities can inform conservation strategies and the sustainable management of marine resources, particularly in the face of anthropogenic stressors such as overfishing and pollution.

In conclusion, evidence suggests that the integrated study of nematode biodiversity in Mediterranean areas is vital for advancing sustainable agriculture and preserving the ecological integrity of both terrestrial and marine environments. By recognizing the diverse roles nematodes play, we can enhance ecosystem resilience, support food security, and promote environmental sustainability goals that align with broader biodiversity conservation and ecosystem management efforts.

Keywords: Sustainable agriculture, Nematode communities, Meiofauna, Biological control, Ecological indices

Phenotypic and genomic assessment of sugar assimilation in the pomegranate yeast *Hanseniaspora valbyensis*

<u>Maria De Angelis</u>¹, Rosangela Limongelli¹, Fabio Minervini¹, John Morrissey²

¹University of Bari Aldo Moro, Italy, ²University College of Cork, Ireland

maria.deangelis@uniba.it

Among non-conventional yeasts, *Hanseniaspora* is known for its high capacity to produce aroma compounds during fermentation. Its apparent reduced ability to completely utilise sugars in some ecosystems (e.g., grape must) may be explained by growth impairment due to sensitivity to ethanol or antimicrobials produced by other yeasts. Although the capacity of *Hansenisapora* species (e.g. *Hanseniaspora valbyensis*) to grow on fructose was previously reported, no fructose-specific transporters were identified. This study aimed to characterize fermentation behavior and scout potential fructose transporters of *H. valbyensis* biotypes, isolated from pomegranate.

The capacity of *H. valbyensis* to assimilate diverse sugars was first assessed using agar minimal medium (MM) supplemented (at 2%) with glucose, fructose, lactose, xylose, maltose, or sucrose. Subsequently, growth, sugar consumption and metabolite production were investigated during liquid cultivation with three different carbon sources: glucose, fructose, glucose and fructose. Well characterised strains of *Saccharomyces cerevisiae* and *Kluyveromyces marxianus* were used as references. Whole genome analysis was performed to identify potential sugar transporters of *H. valbyensis*, and a phylogenetic tree was built.

H. valbyensis grew at highest level on MM plates containing glucose or fructose. Among the yeast species under investigation, it was the only one able to consume fructose and glucose after cultivation on MM broth, thus suggesting potential fructophilic behavior. The analysis of the phylogenetic tree showed that some sugar transporters of *H. valbyensis* were close to Ffz1 fructose facilitator of *Zygosaccharomyces bailii*. Ffz transporters are phylogenetically distinct from all the other previously characterized hexose transporters and more similar to drug transporters. Further research will focus on the role of this candidate Ffz1-like transporter in *H. valbyensis*.

Keywords: Hanseniaspora valbyensis, Sugar

From by-product to innovation: exploiting biodiversity of *Yarrowia lipolytica* strains to valorize cheese whey and develop adjunct cultures for improved cheese ripening and quality

<u>Davide Gottardi</u>, Lorenzo Siroli, Margherita D'Alesandro, Giacomo Braschi, Francesca Patrignani, Rosalba Lanciotti

University of Bologna, Italy

davide.gottardi2@unibo.it

Cheese whey represents an important dairy by-product which contains valuable components that can be recovered or used as microbial growth substrates. This study explores the potential of using cheese whey to cultivate Yarrowia lipolytica biomasses for application as adjunct cultures in cheesemaking. Y. lipolytica strains were screened on three types of cheese whey for growth, lipolytic activity, and proteolysis. The best-performing strains, RO3. and Y3, were scaled up in a 20L fermenter and applied to the cheese surface. RO3. was further incorporated into both milk and cheese surface in an industrial-scale (500L) cheesemaking process. The cheeses were stored at 6°C for 35 days and analyzed for microbiological (plate counts), chemical (water activity, pH, color), proteolytic (SDS-PAGE), lipolytic (Folch method with GC), and volatile molecule profiles (SPME-GC-MS), alongside sensory evaluations. The tested strains exhibited strain-dependent behavior in hydrolytic profiles and growth capabilities reaching up to 8.77 log CFU/mL in caciotta whey after 72 h. When scaled up in a 20L fermenter, RO3. and Y3 reached 7.97 and 7.68 log CFU/mL, respectively, after 48 h. These biomasses were applied to the cheese surface and showed a ripening acceleration by enhancing proteolysis and increasing unsaturated fatty acid content (25% for RO3. vs. 19% in the control). Moreover, they stimulated the development of ripened cheese aroma compounds (e.g., butanoic, hexanoic, and decanoic acids). RO3. was further tested in cheesemaking by incorporating it into both milk and cheese surface. This approach reinforced and enhanced the results observed with surface application alone, differentiating the product from the benchmark in less than 12 days of ripening. This study highlights that the selection of specific Y. lipolytica strains and development of tailored protocols for production represent a promising approach for upcycling a dairy by-product into innovative ingredients and foods.

Keywords: *Yarrowia lipolytica*, Cheese whey, Innovative cheese, Adjunct culture, by-product valorization

Yeast biodiversity in brewing: a comprehensive screening of 30 strains of *Saccharomyces cerevisiae* isolated from different ecological niches

<u>Giovanni De Francesco^{1,2},</u> Gianmarco Mugnai³, Pietro Buzzini¹, Benedetta Turchetti¹, Valeria Sileoni⁴, Vincenzo Alfeo¹, Ombretta Marconi^{1,2}

¹University of Perugia, Italy, ²Italian Brewing Research Centre, Perugia, Italy, ³University of Padova, Italy ⁴Universitas Mercatorum, Italy

giovanni.defrancesco@unipg.it

Yeasts biodiversity significantly influences the quality of fermented beverages, including beer, wine, and spirits. This study investigates different *Saccharomyces cerevisiae* strains isolated from diverse ecological niches (natural and industrials environments) to identify novel yeasts that can enhance flavour, aroma, and overall beer quality.

Thirty *S. cerevisiae* strains were evaluated for brewing capacity using standardized 12 Plato barley malt wort in micro-fermentation trials. The fermentative abilities were evaluated on a micro fermentation scale by analysing the main qualitative parameters (e.g. alcohol, attenuation, pH), the volatile profile by GC-MS (high alcohols, esters, aldehydes), and the sugar profile by HPLC (sucrose, glucose, maltose, maltotriose, dextrins).

The screening work demonstrated remarkable diversity among yeast strains of the same species but originated from different habitats. Alcohol content analysis enabled the identification of weakly fermenting strains (0.7 % v/v alcohol) isolated from natural and oligotrophic habitats, medium fermenting strains (2.5-4 % v/v alcohol), highly fermenting strains (up to 5.5 % v/v alcohol) mainly derived from industrial and nutrient-rich niches. Strains exhibiting low alcohol production demonstrated limited maltose utilization, making them promising candidates to produce low-alcoholic beers. Other strains fermented maltose but not maltotriose, suitable for full-body beers. Unexpectedly, three strains fermented maltotriose but not maltose, indicating an original metabolic trait compared to brewing yeasts currently available on the market.

GC-MS analysis confirmed substantial heterogeneity in volatile aromatic profiles among the strains, with esters ranging from 0.5 to 21 mg/l, higher alcohols from 25 to 218 mg/l, diacetyl from 0 to 400 μ g/l, and aldehydes from 14 to 87 mg/l. Future work will focus on selecting the most performant strains for scale-up to a 25-liter pilot scale.

Keywords: Yeast biodiversity, Beer, Low-alcohol beer

Microbial resources for sustainable meat productions in the green deal era

Michela Pellegrini, Debbie Andyanto, Emma Gridello, Giuseppe Comi, Lucilla Iacumin

University of Udine, Italy

michela.pellegrini@uniud.it

Nitrate and nitrite salts are widely used for improving the quality and safety in fermented meat products. They are effective against both cells and spores of *Clostridium botulinum*, prevent lipid oxidation, and promote the red colour of meat products. However, the association between this additives and health-related issues and the consequent awareness for foods without synthetic additives has led to explore new ways to ensure the safety and extending shelf-life. Lactic acid bacteria (LAB) and Coagulase-Negative Catalase-Positive Cocci (CNCPC) are known for their safety and fermentation capacity and are promising due to their in vitro antioxidant

for their safety and fermentation capacity and are promising due to their in vitro antioxidant activity and the production of enzymes such as Nitric Oxide Synthase (NOS), which converts L-arginine into Nitric Oxide (NO). NO binds to myoglobin, producing nitroso-myoglobin (NO-Mb) responsible for meat products red colouration.

Several strains of *Staphylococcus* spp. and Lactic Acid Bacteria were characterized for their ability to produce Nitric Oxide via Nitric Oxide Synthase (NOS) pathway or NOS-like enzymes.

The strains that showed higher NOS activity were used for the production of low-nitrite fermented sausages, evaluating their ability to stabilize the red colour of meat through the production of nitrosomyoglobin and for their proteolytic and antioxidant activity. The effect on physico-chemical parameters, microbial population, volatilome as well as sensory characteristics was evaluated.

The results suggest that using starter cultures with NOS activity could be a promising strategy for producing clean-label products without compromising the safety and sensory properties, representing a step forward in the search for sustainable solutions for meat preservation, opening new perspectives for the food industry.

Development of a new brewing strain with improved aroma through hybridization and UV mutagenesis

<u>Chiara Nasuti</u>¹, Viola Ceramelli Papiani¹, Davide Tagliazucchi¹, Kristoffer Krogerus², Lisa Solieri¹

¹University of Modena and Reggio Emilia, Italy, ²VTT Technical Research Centre of Finland, Finland

chiara.nasuti@unimore.it

Yeasts are fundamental in beer production, influencing fermentation, flavor, and stability. To meet consumer demand, we developed a novel, GMO-free yeast hybrid between a sourdough strain of *Saccharomyces cerevisiae* and a cryotolerant *S. eubayanus* x *S. bayanus* via spore-to-spore hybridization. Microfermentations showed improved brewing traits in one hybrid but also the undesired Phenolic Off-Flavor (POF+) phenotype, caused by the conversion of ferulic acid into 4-vinyl guaiacol (4VG). To eliminate this trait, we applied UV mutagenesis, optimizing irradiation conditions (50 cm distance, 30 s exposure) to achieve 8-22% mortality. Nystatin treatment, which selects slow-growing mutants, reduced the mutation success rate (13.3% without vs. 0.4% with nystatin). Mutants were screened on YPDA with 4 mM ferulic acid and analyzed via Ferulic Acid Conversion Index (FACI) and Cinnamic Acid Sensitivity Index (CASI). POF- candidates exhibited low FACI and high CASI values, confirming reduced 4VG production. Further microfermentations confirmed that selected mutants retained improved brewing traits without the POF+ phenotype. This study demonstrates that hybridization combined with UV mutagenesis is an effective, GMO-free strategy for developing superior brewing yeasts.

Keywords: Yeast hybridization, Phenolic off-Flavor, UV mutagenesis, Brewing yeast improvement

Climate changes, habitat transformation and germination behavior. A complex story from three Mediterranean plants of conservation interest: *Muscari gussonei*, *Petagnaea gussonei* and *Poterium spinosum*

Giuseppe Bonanno, Vincenzo Veneziano

University of Catania, Italy

bonanno.giuseppe@unict.it

Knowing the optimum germination temperatures of endangered plants, as well as the magnitude of climate changes (e.g., rising temperatures) across the spatial range of these species, is essential to assess the level of threat for such species and, consequently, to implement tailored and enduring conservation programs. These analyses should be also integrated by the study of land-cover changes, which can act as an indicator of landscape fragmentation and, therefore, as a proxy of gene flow across metapopulations of species of conservation interest. This study, in particular, investigated both the germination behavior of Muscari gussonei, Petagnaea gussonei and Poterium spinosum, and the trends of climate and land-cover changes occurred in the distributional areas of these species. M. gussonei and P. gussonei are two endangered and narrowly distributed endemic plants from Sicily (Italy), whereas *P. spinosum* is another biogeographically important species with a highly scattered range across south-eastern Sicily. All the studied plants showed the same narrow germination optimum of 10-15 °C, but different final germination percentage (FGP): 82-98% in M. gussonei, 10-38% in P. gussonei, 5-61% in fruits and 21-68% in seeds of P. spinosum. These optimum germination temperatures are low and limited and, therefore, make the three species much more vulnerable to ever-rising temperatures, which specifically increased by up to 2 °C in the period 1931-2020. Similarly, the analysis of CORINE Land Cover classes showed highly fragmented landscapes, where forest and seminatural areas (class 3) declined, and agricultural areas (class 2) increased. The ongoing climate changes will make the suitable germination temperatures harder to be reached by plants with low and narrow germination optimum, such as *M. gussonei*, *P. gussonei* and *P. spinosum*, whose survival is further threatened by a complex fragmented territory with declining natural areas.

Keywords: Mediterranean endemic plants, Global warming, CORINE Land Cover, Germination performance, in situ and ex situ conservation, Sicily

Shading lights on *Silybum* genus biodiversity: chemodiversity, genetic and genomic characterization of a wide germplasm collection

<u>Laura Bassolino</u>^{1,2}, Marianna Pasquariello^{1,2}, Tommaso Martinelli^{1,3}, Roberta Paris^{1,2}, Salvatore Esposito², Damiano Puglisi^{1,2}, Gabriele Magris⁴, Mario Liva⁴, Michele Morgante^{1,4}, Anna Moschella², Pasquale De Vita^{1,2}, Pecchioni Nicola²

¹NBFC, National Biodiversity Future Center, Palermo, Italy, ²CREA-Research Centre for Cereal and Industrial Crops, Italy, ³CREA-Research Centre for Plant Protection and Certification (CREA-DC), Italy, ⁴University of Udine, Italy

laura.bassolino@crea.gov.it

Silvbum marianum (L.) Gaertn., also known as milk thistle, is an herbaceous medicinal plant of the Asteraceae family native to the Mediterranean basin. The species is a weed but is cultivated since past for silymarin production, a high-value complex of flavonolignans accumulating in achenes with hepato-protective and anti-inflammatory properties. The Silybum genus also includes *S. eburneum*, but its classification is often misreported in the literature and knowledge about it is limited. Thanks to the NBFC-spoke 3 project, the S. marianum germplasm collection available at CREA-CI Bologna was implemented with 83 wild Silybum accessions of diverse geographical origins, by sampling campaigns or from seed GeneBanks, to characterize the genus biodiversity at biochemical, morphological, and genetic levels. Targeted metabolomics revealed that *S. marianum* is characterized by three diverse chemotypes A, B, and C, while *S.* eburneum accessions exhibit a unique chemotype (D) with isosilychristin as the major flavonolignan component. Flower and leaf morphology were identified as distinctive traits and combined with DNA barcoding based on the ITS2 sequence allowed us to clearly differentiate the two Silybum species. To investigate the genetics of silymarin biosynthesis, the genome of chemotype B accession was de novo assembled into 17 chromosomes using a combination of Oxford Nanopore long and ultra-long reads. The approach yielded a final assembly of ~ 721 Mb of which 6 chromosomes were telomere-to-telomere, with the longest sequence of 62.1 Mb. The genome completeness was assessed with BUSCO which identified a high proportion of complete single-copy orthologs (> 99%) indicating a highly complete and contiguous genome. Genome annotation using RNAseq data of different tissues is still ongoing. Our work paved new knowledge on Silvbum genus biodiversity and resources that will facilitate its exploitation in nutrition and human health sciences.

Keywords: Silybum, silymarin, Chemotypes, Genetic resources, Genome assembly

The potential of the terpene profile of Mediterranean fir species in the chemotaxonomic study and the conservation prospects

<u>Waed Tarraf</u>¹, Tolga Izgu¹, Carla Benelli¹, Gabriele Cencetti², Marco Michelozzi², Alfonso Crisci¹

¹Institute of BioEconomy (IBE), CNR, Italy, ²Institute of Biosciences and Bioresources (IBBR), CNR, Italy

waed.tarraf@ibe.cnr.it

Some fir species in the Mediterranean have restricted geographical distributions and are often endemic and endangered, typically found in relict areas, except for Abies alba. Among these threatened species, Abies pinsapo (Spanish fir) is classified as endangered by the International Union for Conservation of Nature (IUCN), and A. nebrodensis (Sicilian fir) is included in the Red List of IUCN as one of the most critically endangered conifers in the Mediterranean region. Conifers have evolved various physical and chemical defences against biotic and abiotic stress; for instance, the variation of terpenes significantly affects insect behaviour and herbivory. The relationships between the quantity and composition of terpenes have been extensively studied in different parts of coniferous plants, except seeds, where there has been less focus. Therefore, this study aimed to examine the features and terpene profiles of seeds collected from the critically endangered Sicilian and Spanish fir and the common European silver fir species. After X-ray analysis, only the empty seeds were used for morphometric measurements and terpene isolation. The results of GC-MS analysis reported the dominance of monoterpenes in all the species, while A. nebrodensis revealed the considerable presence of sesquiterpenes. Statistically significant differences were found in most of the detected terpenes, and only 3 (α -pinene, limonene, and boranyl acetate) out of 25 compounds showed no statistical differences between species. For a clear discrimination, the linear discriminant analysis was more effective in separating the Abies species. The current findings confirmed the potential and suitability of the terpene profile in the chemotaxonomic studies between species from the same family. Moreover, the identified compounds will enable future research on plant defense against biotic stress to reduce the risk of species extinction caused by pests and diseases.

Keywords: Sicilian fir, European silver fir, Spanish fir, Threatened species, Conifers, Chemotaxonomic markers, Empty seeds

Conservation status of Annex I habitats in Italy: first overview from the Fifth National Report under Article 17 of the Habitats Directive

Daniela Gigante¹, A.T.R. Acosta², M. Aleggrezza², C. Angiolini², S. Assini², G. Bonari², G. Buffa², M. Caccianiga², M.C. Caria², E. Farris², A.R. Frattaroli², L. Gianguzzi², G. Giusso del Galdo², M. Malavasi², G. Spampinato², D. Viciani², M. Barcella², D. Ciaramella², L. de Simone², V. di Cecco², G. Galdenzi², M. Gennai², A. La Mantia², L. Lorenzato², F. Manelli², G. Miraglia², A. Morabito², S. Pisanu², G. Rivieccio², A. Selvaggi², A. Sini², M.G. Sperandii², G. Tesei², G. Bacchetta², G. Bacilliere², G. Bazan², R. Bolpagni², L. Brancaleoni², S. Cannucci², M. Castello², G. Ciaschetti², D. Ciccarelli², R. Copiz², M. Cutini², M. D'Agostino², M. Dalle Fratte², L. di Martino², E. Fanfarillo², E. Fantinato², S. Fascetti², T. Fiaschi², L. Filesi², B. Foggi², L. Forte², R. Gerdol², R. Guarino², G. La Bella², C. Lasen², C. Marcenò², M. Mariotti², F. Mascia², G. Mei², N. Merloni², A. Morabito², C.M. Musarella², G. Oriolo², G. Patera², E.V. Perrino², A. Petraglia², B. Petriccione², N. Postiglione², M. Puglisi², S. Sciandrello², A. Stanisci², A. Stinca², S. Strumia², V. Tomaselli², B. Valle², R. Venanzoni², M. Villani², G. Zangari², P. Angelini³, E. Carli³, L. Casella³, F. Pretto³, S. Bagella¹

¹University of Perugia, Italy, ²SISV - Italian Society of Vegetation Science, Pavia, Italy, ³ISPRA - Istituto Superiore per la Protezione e la Ricerca Ambientale, Roma, Italy

daniela.gigante@unipg.it

Under Article 17 of the "Habitats" Directive (92/43/EEC), Member States periodically have to assess and report on the conservation status of Annex I habitats. The reports include data on habitat conservation status, trends, pressures, and threats. The results of reporting address policy evaluation and biodiversity strategies. Italy's V national report (period 2019-2024), coordinated by the Italian Society of Vegetation Science (SISV) and the University of Sassari, with co-coordination by the Italian Institute for Environmental Protection and Research (ISPRA) on behalf of the Ministry of the Environment and Energy Security (MASE), is nearing completion. A multidisciplinary team of regional and thematic experts validated and integrated data on habitat distribution and conservation status submitted by Italian Regions and Autonomous Provinces. Distribution maps, based on the ETRS89-LAEA5210 10x10 km grid, were created and made available via a dedicated WebGIS developed by ISPRA for data entry. validation, and management. Additional datasets, including the Natura 2000 database released by MASE in Dec 2024, were also utilized. The assessment covers 124 terrestrial and inland water habitats across Alpine, Continental, and Mediterranean biogeographical regions. Analytical efforts address data gaps and inconsistencies through robust methodologies and scientific dialogue. Emphasis is placed on traceability and integration of multiple sources, such as peer-reviewed literature, phytosociological surveys, and unpublished expert materials. This extensive knowledge base underpins a long-term strategy to ensure continuity in future reporting cycles. Following European Commission validation, maps, datasets, and associated documentation will be publicly accessible on ISPRA's national reporting portal. This forwardlooking process marks a crucial step toward a science-based monitoring system for conserving Annex I habitats in Italy.

Keywords: Biodiversity, European Commission, Monitoring, Vegetation

Plant biodiversity and conservation of endemic species of the Dolomites and Southeastern Alps

<u>Camilla Wellstein</u>¹, Francesco Rota², Philipp Kirschner³, Gabriele Casazza⁴, Juri Nascimbene⁵, Pau Carnicero⁶

¹Free University of Bozen, Italy, ²Swiss Federal Institute for Forest, Snow and Landscape Research WSL, Birmensdorf, Swizerland, ³University of Innsbruck, Austria, ⁴University of Genova, Italy, ⁵University of Bologna, Italy, ⁶University of Barcelona, Bellaterra, Spain

camilla.wellstein@unibz.it

The Southeastern Alps are not only a biodiversity hotspot but also host the highest proportion of endemic plants in the Eastern Alps. During the climatic changes of the Pleistocene, long-term stable habitats - so-called refugia - probably facilitated the emergence of endemic biodiversity in the area. In two projects, we investigated, first, the evolutionary history of nine key plant species endemic to the Southeastern Alps by sequencing large parts of their genomes using RADseq data. We infer how recurrent climatic changes have influenced the evolutionary history of these target species, how glacial cycles have generated unique evolutionary lineages, and how this unique genetic diversity has evolved and is distributed in time and space. Our results show that, depending on the respective ecology, the species found peripheral refugia in the southern and southeastern areas, showed patterns of nunatak, i.e. unglaciated mountain tops, survival or a combination thereof. Our results also allow the identification of evolutionarily unique populations and lineages within each species to inform conservation efforts. Second, we assessed potential future climatic refugia of these key species, using high-resolution (50 m) downscaled climate data and topographic factors to identify areas of climatic stability under different climate change scenarios. Future climate projections suggest moderate to severe range contractions, with lower elevations being most affected. Stable and newly suitable habitats were primarily at higher elevations, but the Dolomites' high-altitude plateaus exhibited rapid climate change velocity, potentially limiting long-term persistence. Integrating all our results advances our knowledge of why areas such as the Southeastern Alps are hotspots of endemism, how the endemic key species might develop under ongoing climate change and how both aspects should be combined for conservation efforts in mountain landscapes.

Keywords: Endemic alpine plants, Phylogeography, Intraspecific diversity, Climate change, Species distribution models

Occurrence and distribution of yeast communities related to honeybees system: an ecological overview

<u>Silvia Gattucci</u>, Alice Agarbati, Laura Canonico, Laura Moretti, Maurizio Ciani, Francesca Comitini

Università Politecnica delle Marche, Italy

s.gattucci@pm.univpm.it

Pollination is one of the most important ecosystem services, and honeybees (Apis mellifera) play a crucial role in this process. They are essential for biodiversity and food production and, due to their complex society, serve as a great model of social behavior. The aim of the study was to increase the knowledge regarding to the yeasts related to the honeybee system. For this reason, flowers, bee gut and hive products such as bee pollen, bee bread and propolis were sampled and analyzed.

A total of 27 yeasts genera and 51 species were identified. Basidiomycetes were predominant in flowers, while *Aureobasidium* sp., *Filobasidium* sp., *Meyerozyma* sp., and *Metschnikowia* sp., were found in all environments. Fermenting yeasts, such as *Debaryomyces* sp., *Saccharomyces* sp., *Starmerella* sp., *Pichia* sp., and *Lachancea* sp., were mainly found in the gut, whereas most species identified in bee products were absent in gut mycobiota. Moreover, the yeast species *Meyerozyma guilliermondii*, *Debaryomyces hansenii*, *Hanseniaspora uvarum*, *Hanseniaspora guilliermondii*, and *Starmerella* roseus were detected in the bee gut during both summer and winter sampling, suggesting their role as a stable eukaryotic component of the core gut microbiota. 3 strains of *Meyerozyma guilliermondii* and 4 strains of *Meyerozyma caribbica* exhibited probiotic traits. These results contribute to understanding the yeast community as a component of the bee gut microbiota and its relationship with the environment. Moreover, honeybee ecosystem represents a valuable tool for a source of probiotic and functional yeasts.

Keywords: Yeasts, Honeybee, Honeybee gut microbiota, Bee bread, Bee pollen

Enhancing soil bacterial community profiling: PMA treatment and long-read sequencing across biogeographic regions and land uses

<u>Sara Del Duca¹</u>, Antonella Lamontanara¹, Andrea Manfredini¹, Giulia Conti², Roberta Farina¹, Loredana Canfora¹, Luigi Orrù¹

¹CREA, Italy, ²University of Torino, Italy

sara.delduca@crea.gov.it

In the context of the BIOservicES project, climate chambers are used to simulate future climate conditions and study their impact on soil health. A climate change field experiment began in July 2024 in European semi-natural areas of the Alpine, Atlantic, Boreal, and Mediterranean regions. These four experimental areas are continuously monitored to link multi-level soil biodiversity and land-use types to soil ecosystem services over three years. In recent decades, total DNA extraction and sequencing for the assessment of environmental microbial communities has been performed ignoring relic DNA from non-viable cells. In this scenario, propidium monoazide (PMA), a DNA-intercalating agent that selectively penetrates membrane-compromised or dead bacterial cells, enables the targeted removal of relic DNA before downstream analyses. This approach facilitates the differentiation between viable and total bacterial communities within samples. The present work provides a preliminary evaluation of PMA's potential in studying soil bacterial communities, combining PMA staining with Oxford Nanopore Technology to analyze the full-length bacterial 16S rRNA gene.

DNA was extracted from 120 soil samples, subjected to PMA treatment and untreated control, and sequenced. The findings revealed region-specific variations in the correlation between viable and total bacterial community structures, suggesting differential capacities of soils to preserve relic DNA. Land-use intensity significantly influenced both viable and total bacterial communities, with a slightly reduced effect on total communities. Further in-depth analyses of sequencing data, coupled with quantitative PCR assays, could provide valuable insights into the functional roles of the viable soil bacterial community compared to the total community. Additionally, incorporating future soil sampling data will enable a more comprehensive exploration of the impacts of climate change and land-use practices on soil bacterial dynamics.

Keywords: Vital bacterial community, Oxford Nanopore Technology, Environmental microbiology, Soil health

Plant Growth-Promoting Yeasts (PGPYs) as a sustainable solution to mitigate saltinduced stress on zucchini plant growth

Debora Casagrande Pierantoni, Chiara Ruspi, Angela Conti, Laura Corte, Gianluigi Cardinali

University of Perugia, Italy

debora.casagrandepierantoni@unipg.it

Among the long-term sustainable solutions to mitigate saline stress on plants, the use of plant growth promoting microorganisms (PGP) is considered very promising. While most of the efforts have been devoted to the selection and use of bacterial PGPs, little has been proposed with yeast PGP (PGPYs). In this study, three PGPY strains belonging to *Naganishia uzbekistanensis*, *Papiliotrema terrestris* and *Solicoccozyma phenolica* were employed singularly and in a consortium to mitigate salt stress of zucchini (*Cucurbita pepo*). The results demonstrated that these yeasts, when applied to salt-amended soil, mitigated the growth inhibition caused by NaCl. Among the three species, *N. uzbekistanensis* and *P. terrestris* showed the most significant improvements in plant performance, with *N. uzbekistanensis* exhibiting hormetic effects under salt stress by improving root length and dry plant biomass. In general, the root system was the most affected part of the plants due to the presence of the yeasts. The entire rhizosphere bacterial microbiota was significantly influenced by the addition of PGPYs, while the mycobiota was dominated by the introduced yeasts. Metabolomic fingerprinting using FTIR revealed modifications in hemicellulose and silica content, indicating that PGPY inoculation impacts not only the plant but also the soil and rhizosphere microorganisms.

Keywords: PGPYs, Salt-stress, Zucchini, Rhizosphere microbiome, Rhizosphere mycobiome

Cascade effect of microplastic aerial deposition affects tomato growth, root metabolome and exudome, and rhizosphere microbiome

<u>Oussama Bouaicha</u>¹, Fabio Trevisan¹, Raphael Tiziani¹, Martin Brenner², Wolfram Weckwerth², Elisabetta Onelli³, Alessandra Moscatelli³, Tanja Mimmo¹, Luigimaria Borruso¹

¹Free University of Bozen, Italy, ²University of Vienna, Austria, ³University of Milano, Italy

Oussama.Bouaicha@unibz.it

Here, we evaluated the impact of microplastics (MPs) aerial deposition on the physiology of tomato plants (Solanum lycopersicum L.) and rhizosphere microbial communities. Tomato plants were grown in soil and hydroponics for 31 days. After 15 and 21 days, leaves were sprayed with polyethylene microspheres (PEMS; 790-4999µm; 10-100-1000 mg L-1) or MilliQ water (Control), avoiding direct contact of MPs with the growing media. After 31 days, tomato plants, soil, and root exudates were sampled. Fresh and dry biomass, elemental composition, and root metabolome were assessed on soil-grown plants, while root exudates were collected from hydroponically grown plants. The concentration of nutrients in the shoots was determined using an inductively coupled plasma-optical emission spectrometer (ICP-OES). Gas chromatography-mass spectrometry (GC-MS) was used to evaluate root metabolome and exudome, while rhizosphere microbial diversity was investigated via DNA metabarcoding of the bacterial 16S rRNA gene and fungal ITS2 region. In shoots, PEMS aerial application significantly reduced the water content and increased most of the element concentrations (p < 0.05). In addition, PEMS caused leaves' ultrastructure deformation. In roots, PEMS significantly decreased the content of serine and tryptophan, 5,6-Dihydrouracil, lactic and tartaric acid, and palmitic and stearic acid. Similarly, in root exudates, the relative abundance of organic acids (i.e., malic, succinic, and citric acid), amino acids (i.e., aspartic acid and isoleucine), and carbohydrates (i.e., gluconic and threonic acid) decreased in PEMS-treated plants. Consistently, PEMS had a profound impact on rhizobacterial diversity (i.e., alpha and beta diversity) but not rhizofungal diversity. These findings highlight the potential impact of airborne PEMS on plant physiology and the rhizosphere bacterial community, underscoring the need for further research in this area.

Keywords: Microplastics, Root exudates, Microbial diversity, Rhizosphere

Characterisation of *Pseudomonas syringae* pv. *syringae* Italian strains causing severe wilting in eggplants

<u>Michela Paglialunga</u>¹, Benedetta Orfei¹, Anna Scian¹, Theo H.M Smits², Cayo Ramos³, Giuseppe Carannante⁴, Vittorio Mario Stravato⁴, Roberto Buonaurio¹, Chiaraluce Moretti¹

¹University of Perugia, Italy, ²Zurich University of Applied Sciences ZHAW, Switzerland, ³Universidad de Málaga, Spain, ⁴GENISTA s.r.l, Fondi, Italy

michelapaglialunga16@gmail.com

The study of bacterial plant pathogen diversity is a crucial aspect for understanding how bacterial populations evolve in response to changes in agricultural systems, global trade and climate. Pseudomonas syringae is an evolutionarily diverse bacterial species complex and a preeminent model for studying plant pathogen interactions due to its remarkably broad host range. We focused on two bacterial strains isolated in Italy from eggplants (Solanum melongena L.) showing unusual and severe wilting symptoms. Phylogenetic analysis based on the housekeeping genes gapA, rpoA and recA revealed that the two strains are identical and clustered together with 22 Pseudomonas syringae pv. syringae strains infecting herbaceous plants. The genome of one of the strains, named DAPP-PG 773, was sequenced on an Illumina MiSeq platform using indexed paired-end 250-nucleotide v2 chemistry. A total of 7.907.342 pairs of reads were obtained, representing approximately 182-fold coverage of the genome and comprising 142 contigs. The assembled genome size was 6.06 Mb and the G/C content was 59.4%. Annotation of the DAPP-PG 773 draft genome sequence was carried out using Bakta yielding 5262 CDS. Phenotypic tests revealed that our strains produced exopolysaccharides, biofilm and N-acyl-homoserine lactones and very low level of indole-3-acetic acid; they had motility by swimming and swarming. Pathogenicity tests conducted on Solanaceae species highlighted the ability of the DAPP-PG 773 strain to infect exclusively eggplant plants, colonizing the xylematic vessels. Since genome analysis using EDGAR 3.2 platform revealed that the strain clustered with other P. syringae pv. syringae strains belonging to the 2b-a clade causing disease on Cucurbitaceae species, we conducted additional pathogenicity tests on squash plants, which confirmed the ability of the DAPP-PG 773 strain to systemically infect this plant species as well.

Keywords: Pseudomonas, Eggplant, Squash, Systemic disease, Genome analysis

The environmental context of honey bee gut microbiota: insights from the endemic Maltese subspecies, *Apis mellifera ruttneri*

<u>Simone Cutajar</u>¹, Chiara Braglia¹, Loredana Baffoni¹, Diana Di Gioia¹, David Mifsud², Daniel Alberoni¹

¹University of Bologna, Italy, ²University of Malta, Malta

simone.cutajar4@unibo.it

Understanding how microbial communities connect across ecological compartments is key to preserving biodiversity and enhancing ecosystem resilience. This study explores the link between soil, plant, and pollinator microbiomes by investigating the gut microbiota of *Apis mellifera ruttneri*, the endemic Maltese honey bee, in relation to environmental microbial sources.

Previous work indicated that *A. m. ruttneri* harbours a greater proportion of environmental microbes compared to *A. m. ligustica*, but the drivers of this pattern remain unclear. To disentangle genetic and environmental influences, colonies of both subspecies were co-located in experimental apiaries in Malta and Italy, representing Mediterranean and continental climates.

Monthly samples of worker bees and pollen were collected over a year, and 16S rRNA gene sequencing was used to characterize the microbial communities. Comparative analyses revealed that *A. m. ruttner*i exhibited a higher prevalence of environmental bacteria, including taxa typically associated with soil, such as Bartonellaceae, *Apilactobacillus*, and *Pseudomonas*. In contrast, *A. m. ligustic*a displayed a microbiota dominated by host-associated *Lactobacillus* and *Bombilactobacillus*. Despite similar core taxa, their relative abundances differed markedly, indicating that environmental factors are a major influence on honey bee gut microbiota composition.

These findings suggest that *A. m. ruttneri* hosts a microbiota shaped by long-term exposure to the ecological conditions of the Maltese landscape, highlighting the importance of the environment in pollinator-microbe interactions. By demonstrating the microbial distinctiveness of local subspecies, we highlight the need to consider microbial ecology in pollinator conservation strategies, particularly in the face of climate and land-use change.

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Keywords: Honey bee microbiota, Pollinator conservation, Environment pollinator interactions, Microbiome adaptation, Endemic species

Microbial drivers of nectar flows: the case study of sunflower

Daniele Alberoni, Chiara Braglia, Loredana Baffoni, Diana DI Gioia

University of Bologna, Italy

daniele.alberoni@unibo.it

Over the past decade, beekeepers in southern Europe have faced mounting challenges due to declining honey yields. Despite being a major nectar source for beekeeping, sunflower (*Helianthus annuus*) has shown declining nectar production, likely driven by increasing climate pressures such as drought and heatwaves. Compounding the issue, declining soil microbial diversity in agricultural lands may disrupt plant microbiome interactions essential for nectar production. Soil microorganisms play a key role in mobilising micronutrients like manganese and magnesium, making them crucial for nectar synthesis. Naturally occurring in soils, Plant Growth-Promoting Bacteria (PGPB) are commonly used as biofertilisers to promote plant growth and stress tolerance, yet their role in nectar-related physiological processes remains unclear.

To address this, a field trial in Italy was conducted using hybrid and non-hybrid sunflower cultivars. Selected PGPB from the bacterial genus Bacillus and family Lactobacillaceae were inoculated into experimental plots. Two hundred sunflowers were sampled across treatments. Gene expression of SWEET sugar transporters was determined via RT-qPCR. Simultaneously, root samples were collected and subjected to high-throughput sequencing to assess epiphytic microbial communities.

Results revealed that sunflower genotype significantly influenced rhizosphere microbial colonisation. Some PGPB strains also affected expression levels of genes encoding SWEET sugar transporters. These findings offer preliminary insights into how PGPB may regulate nectar production and, by extension, plant pollinator interactions. Overall, this research highlights how climate change can impact ecological interactions not directly related to honey bee biology, yet still influencing its productiveness and health.

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Keywords: Sunflower, Microbiome, Bio-fertilizers, PGPB, Nectar-flow

The challenges and opportunities of the EU Nature Restoration Law and the role of research. The national project for the development of a catalogue and planning support tool for Nature-Based Solutions

Luigi Servadei¹, <u>Chiara Catalano^{2,3}</u>

¹CREA, Council for Agricultural Research and Analysis of Agricultural Economics, Rome, Italy, ²CNR IRET - Terrestrial Ecosystem Research Institute, Italy, ³NBFC – National Biodiversity Future Center, Italy

chiara.catalano@cnr.it

The adoption of the Nature Restoration Regulation (EU) No 2024/1991 represents a decisive step in Europe's strategy to protect biodiversity and strengthen ecosystem resilience. The legislation sets binding targets for the restoration of degraded terrestrial and marine ecosystems, requiring Member States to accelerate conservation policies and the integration of Nature-Based Solutions (NbS) into spatial and sectoral planning processes.

In this scenario, research assumes a fundamental role not only as a monitoring and evaluation tool, but as a stimulus to guide planning, support innovation in practices and strengthen the capacity of public institutions. The opportunities opened by the Regulation for the world of research are manifold, such as the development of ecological indicators, the modelling of impact scenarios, the experimentation of adaptive approaches, the construction of interoperable databases and integrated decision-making tools.

In this regard and within the framework of the National Biodiversity Future Centre, the NbS CataTool is a multi-stakeholders Decision Support System aimed at facilitating the selection of effective, adaptive and coherent Nature-based Solutions (NbS).

The CataTool classifies NbS and real-world case studies according to ecosystems and functional criteria distinguishing them across urban, terrestrial and marine domains. It is structured around two interlinked databases: the 'NbS Database' and the 'Case Study Database'. The first is a catalogue of over 100 theoretical NbS derived from existing catalogues and scientific literature. The second hosts more than 100 georeferenced NbS case studies from across Italy, sourced from European repositories and NBFC demonstration sites. Both databases use expert defined Key Performance Indicators to evaluate and compare solutions offering measurable insights to support informed decisions and develop concrete guidelines for evidence-based implementation of Regulation (EU) No 2024/1991.

Keywords: Nature, Restoration, Biodiversity, Research, Nature-based solutions

The role of integrated LIFE programmes in restoring ecosystems: a case study from the "Integrated management and actions for a green and Innovative nature" Project

Luisa Paolotti, Fabio Maneli, Antonio Boggia, Roberto Venanzoni, Lucia Rocchi

University of Perugia, Italy

luisa.paolotti@unipg.it

The Nature Restoration Act is a major legislative effort supporting the Global Biodiversity Framework, the European Green Deal, and the EU Biodiversity Strategy. It aims to restore at least 20% of the EU's land and sea areas by 2030, and all ecosystems needing restoration by 2050. Member States must submit National Restoration Plans to the European Commission by mid-2026, detailing how they will meet these goals.

Restoration of ecosystems is not new in Europe. These efforts often rely on Payments for Ecosystem Services (PES), where public funds compensate landowners for ecological improvements. PES schemes create incentives for sustainable practices by assigning economic value to ecosystem services, that are the benefits which ecosystems provide to humans (e.g., clean water, biodiversity, recreation). These services are central for integrating ecological and economic policies, moving beyond the traditional view of environmental protection versus development.

PES address the market failures caused by externalities (unpriced social or environmental impacts) by aligning private and public interests. PES are voluntary transactions between a service provider and a beneficiary, where compensation is given for maintaining or enhancing a defined ecosystem service. Two configurations are possible:

- 1. PES involving direct payments between local beneficiaries and service providers.
- 2. PES-like, funded by public institutions, without direct market exchanges

This study presents the PES-like scheme, aimed at preserving and restoring a rare habitat in Umbria (alkaline fens - Natura 2000 habitat type 7230). Interventions include mowing and clearing of invading vegetation; removal of the surface layer of the soil, including reed litter; interventions aimed at maintaining the surface water table; planting of species typical of habitat 7230. Local community has been involved to make it part of the restoration process.

Keywords: Ecosystem services, Payments for ecosystem services, Ecosystem restoration

The LIFE IMAGINE UMBRIA project for the conservation of insect species of community importance in Umbria

<u>Matteo Pallottini</u>, Barbara Caldaroni, Antonia Concetta Elia, Enzo Goretti, Gianandrea La Porta, Silvana Piersanti, Manuela Rebora

University of Perugia, Italy

matteo.pallottini@unipg.it

Life Imagine Umbria project (LIFE19 IPE/IT/000015, 2020-2027) supports the development of a management strategy for the Natura 2000 network in the Umbria region (Italy). Its main objective is to maintain and improve the conservation status of habitats and species protected under the Habitats and Birds Directives, in specific target Natura 2000 Sites. To address this challenge, effective ecological restoration projects have been carried out, focusing on selected species of Odonata (Coenagrion castellani and Lindenia tetraphylla), Coleoptera (Cerambyx cerdo, Lucanus cervus, Osmoderma eremita, and Rosalia alpina) and Lepidoptera (Eriogaster catax, Euphydryas provincialis, and Melanargia arge) listed in the annexes of the Habitat Directive. For *C. castellani*, the project focused on maintaining the riparian vegetation of small watercourses (e.g. channels and ditches) and implementing best practices for their management. For L. tetraphylla, it involved actions to preserve and promote the growth of *Phragmites australis* and the typical lake vegetation formation known as reedbeds, utilizing technologies such as artificial floating islands. Best practices for enhancing the habitats of C. cerdo, L. cervus, and R. alpina focused on measures aimed at increasing the presence of senescent trees and associated forest necromass. For *O. eremita*, the main approach involved creating and installing artificial cavities to increase the presence of microhabitats suitable for larval development. For the lepidopteran species E. catax, best practices involved creating artificial ecotonal strips rich in shrubs, predominantly Prunus spinosa. Finally, best practices for *E. provincialis* and *M. arge* focused on safeguarding grasslands by limiting the settlement of shrubs, trees, and alien or synanthropic vegetation. The project aims to implement demonstrative actions for ecological management and habitat restoration to counteract the decline of these species and improve their conservation status.

Keywords: LIFE Programme, Habitat directive, Conservation, Best practices, Insects

Tipping points of biodiversity and sustainability of South Tyrol traditional pasture systems (BIOPAS)

Franziska Zimmermann, Ilaria Fracasso, Luigimaria Borruso, Thomas Zanon, Camilla Wellstein

Free University of Bozen-Bolzano, Italy

franziska.zimmermann@unibz.it

Traditional alpine pastures are high nature value ecosystems shaped by extensive livestock grazing dating back to pre-roman times. However, recent changes in grazing management have altered biodiversity, soil properties, and ecosystem functions, threatening long-term sustainability. While intensification has occurred in lowland areas, less accessible pastures face abandonment, leading to shrub and tree encroachment and biodiversity loss. In sheep farming, management has shifted from flocking and accompanied grazing to mainly free-range grazing, creating a more heterogeneous impact on pasture habitats. To anticipate and mitigate these effects, it is crucial to identify potential ecological tipping points and their indicators.

This study examines the impact of different grazing management types - (I) homogeneous rotation grazing, (II) heterogeneous free-range grazing, and (III) pasture abandonment - on vegetation, soil biodiversity, and sheep grazing behaviour in South Tyrol. We select three plots per management type across six sites, assessing plant indicator species of reduced management, vegetation composition, and soil biodiversity (bacteria, fungi, protozoa, micro-and mesofauna) alongside physico-chemical soil properties. At the site scale, we track sheep movement using GPS sensors to analyse grazing patterns and their link to vegetation changes. We hypothesize that reduced grazing management alters biodiversity in South Tyrol's pasture systems, leading to a stepwise shift in vegetation and soil communities. We expect to identify threshold values for biological and ecological parameters connected to soil and plant diversity that signal tipping points in pasture conditions. Our findings will contribute to sustainable management recommendations for mountain pasture ecosystems in South Tyrol and facilitate their application by sharing insights with farmers and stakeholders.

Keywords: Traditional pasture systems, Grazing management, Alpine biodiversity, Ecological tipping points, South Tyrol

POSTER ABSTRACTS

Session: Impact of climate change on biodiversity

MultiForDiv: a trait-based, multi-taxon analysis of forest understory biodiversity

<u>Maura Francioni</u>¹, Zuzana Fačkovcová², Silvia Giusto², Anna Andreetta³, Giorgio Brunialti⁴, Giandiego Campetella¹, Roberto Canullo¹, Stefano Carnicelli⁵, Marco Cervellini¹, Francesco Chianucci⁶, Simone Di Piazza², Luisa Frati⁴, Paolo Giordani², Nicola Puletti⁶, Mirca Zotti², Stefano Chelli¹.

¹University of Camerino, Italy, ²University of Genova, Italy, ³University of Cagliari, Italy, ⁴University of Siena, Italy, ⁵University of Florence, Italy, ⁶CREA-Research Centre for Forestry and Wood, Italy

maura.francioni@unicam.it

Forest ecosystems provide essential ecosystem services but face increasing threats from global changes. Although conservation of forest biodiversity is prioritized in international and national policies, many components, especially those in the understory (vascular plants, fungi, lichens) remain overlooked. These organisms are crucial for forest functioning and sensitive to environmental change.

The MultiForDiv project investigates spatio-temporal patterns and drivers of forest understory biodiversity using a multi-taxon, trait-based approach. This research integrates long-term data collected in the Italian permanent plots of the ICP Forests LII network distributed across all the national territory.

Analyses on the vascular plants reveals significant species richness declines over the last 25 years. Using linear mixed models, forest structural variables, soil pH, and climate features are identified as key drivers of diversity, with biome-specific responses. Preliminary results on epiphytic lichens suggest temporal stability in species richness. Functional traits of epiphytic non-vascular communities - including lichens and bryophytes - are explored. The relationships among air, bark and cryptogams thermal and hydric regimes under different environmental conditions are disentangled based on IR and NIR spectrum signatures and measured photosynthetic parameters. This allows to better understand their energy balance and their contribution to forest microclimate regulation and ecosystem functioning. Soil microfungal diversity is investigated through functional traits (including xerotolerance, thermotolerance, and solubilization of phosphates) to explore their responses to environmental variables.

This trait-based, multi-taxon approach reveals group-specific responses to environmental conditions, highlighting the need to integrate diverse biological components for a better understanding of forest biodiversity dynamics and effective forests management.

Keywords: Multi-taxon, Trait-based, Forest monitoring, Permanent plot

Evaluation of gastrointestinal motility and sensory preference characteristics of cucumber and fruits of "Barattiere" and "Scopatizzo"

<u>Massimiliano Renna</u>, Mohamad Khalil, Adriano Didonna, Gianni Pietragalla, Pietro Santamaria, Piero Portincasa

University Aldo Moro, Bari, Italy

massimiliano.renna@uniba.it

The Puglia region (Southern Italy) is a treasure trove of horticultural agrobiodiversity, renowned for its melon production (Cucumis melo L.), particularly unripe melons, such as Scopatizzo and Barattiere, consumed as an alternative to cucumbers (Cucumis sativus L.) for their sensory traits and better digestibility. Although consumers often misuse the term "digestibility", literature lacks comparative data on the digestibility of cucumbers versus unripe melons. This study investigated the gastrointestinal motility by simultaneous combined measurements of gastric, gallbladder emptying, and orocecal transit time in response to the ingestion of cucumber, Scopatizzo, and Barattiere fruits for two hours following the meal ingestion. Moreover, the Visual Analogue Scales were used to quantify homeostatic (hunger, satiety) and rewarding (wanting liking, and learning) control of food intake and gastrointestinal symptoms (i.e. nausea, fullness, epigastralgia, meteorism). Finally, a cross-sectional populationbased survey was conducted to assess demographic, socioeconomic, and sensory preference characteristics related to the consumption of cucumber, Scopatizzo, and Barattiere. Cucumber showed the highest reports of mild digestive discomfort (16.3%) and complete maldigestion (11.5%), whereas Barattiere and Scopatizzo were better tolerated. In the clinical study, Scopatizzo and Barattiere scored higher in rewarding food control compared to cucumber. No significant differences were observed for homeostatic control (i.e. appetite and satiety). All fruits produced similar agreeability, mild gastric emptying (max antral area ~7 cm²), and mild gallbladder emptying (ejection volume \sim 20%), without gastrointestinal symptoms and microbial fermentation. In conclusion, the promotion of Scopatizzo and Barattiere could provide consumers with highly palatable and digestively favorable alternatives to common cucumbers.

Keywords: Agrobiodiversity, Cucumis, Digestibility, Local varieties, Puglia region

Fermentation of carob juice for the production of innovative low-alcohol beverages with high health benefits

<u>Francesco Grieco</u>¹, Giuseppe Romano¹, Francesco Tedesco², Maria Tufariello¹, Valentina Petrelli³, Francesco Loperfido³, Aronne Galeotti³, Giuseppe Maggi³, Pasquale Venerito⁴, Carmela Gerardi¹

¹Istituto di Scienze delle Produzioni Alimentari, CNR, Lecce, Italy, ²University of Salento, Italy, ³Fondazione ITS Academy AgriPuglia, Locorotondo, Italy, ⁴CRSFA Centro di Ricerca, Sperimentazione e Formazione in Agricoltura Basile-Caramia, Locorotondo, Italy

francesco.grieco@cnr.it

Fermentation of fruit juices from minor species, such as carob (*Ceratonia siliqua*), is an attractive proposition for the development of innovative products. This fruit has a unique composition that includes high levels of bioactive compounds, sugars and polyphenols. This study describes a biotechnological approach to enhance this species, with great potential for food innovation in the fermented beverage market.

Carob juice was fermented with the two starter strains of wine-derived *Saccharomyces cerevisiae*. At the end of the fermentation process in the obtained juice, the following were quantified: 1) the content of total polyphenols, 2) the antioxidant capacity, 3) the content of sugars and organic acids, and 4) the presence of volatile compounds. The juice was also analyzed with untargeted analytical technologies using an 80 MHz NMR and an E-nose GC-FID for liquid and VOCs components, respectively.

The results obtained indicate that the fermentation process enhances the functional properties of carob juice particularly in total polyphenol content and antioxidant capacity. Chemical analysis showed specific metabolic differences between the two strains, which may influence the organoleptic profile of fermented carob juice.

The high concentrations of esters, alcohols, acids and phenols in the fermented juices revealed the complex aroma and sensory profile of the final product suitable for specific food applications.

Fermentation of carob juice has been shown as an optimal approach to develop functional lowalcohol beverages enriched with prebiotic and antioxidant compounds. This bio-technological approach might lead to the enhancement of local biodiversity to create typical regional products using sustainable technologies to enhance these minor species and expand offerings in the fermented beverage market.

Keywords: Ceratonia siliqua, Fermented beverage, Local biodiversity

Future of crop biodiversity: the case of the germplasm bank preserved by CREA-CI in Bologna and Rovigo (Italy)

<u>Roberta Paris</u>, Andrea Carboni, Ilaria Alberti, Manuela Bagatta, Andrea Del Gatto, Massimo Montanari, Daniela Pacifico

CREA - Research Centre for Cereal and Industrial Crops, Italy

roberta.paris@crea.gov.it

The exploitation of industrial crops at the Cereal and Industrial Crop Centre of Bologna and Rovigo dates to the beginning of the last century and has seen the development of a germplasm bank consisting of 2237 accessions. This collection reflects the multidisciplinary approach of geneticists, agronomists, biologists and chemists to the study of wild relatives and landraces collected in Italy or Europe, breeding lines and populations, as well as ancient or modern varieties, many of which were developed by our breeders.

Main crops are grain legumes (different species with 1250 accessions), sugar beet (*Beta vulgaris* L., 381 accessions), flax (*Linum usitatissimum* L., 283 accessions), sunflower (*Helianthus annuus* L., 95 accessions), hemp (*Cannabis sativa* L., 90 accessions), several species of the Brassicales order (75 accessions), potato (*Solanum tuberosum* L., 45 accessions) and castor bean (*Ricinus communis* L., 18 accessions).

Each of these crops has been studied with different approaches: genetic and genomic studies enabled the explanation of qualitative and quantitative traits as well as structure and diversity; chemical analyses allowed the characterization of primary and secondary metabolites important for the pharmaceutical, food and chemical industries.

With species-specific insights, we clarify how an *ex-situ* germplasm bank, characterised by physiological, agronomic, chemical, genetic data is the *conditio sine qua non* to face the future challenges of a modern agriculture. Able, therefore, to propose effective solutions for: 1. Fighting genetic erosion and biodiversity loss concerns (i.e. over-reliance on a restricted number of commercial varieties, climate change and habitat destruction endangers the genetic diversity of wild species, ecotypes and landraces, which is essential for breeding resilient crops); 2. Ensuring a concrete and active resource to address the challenges of quality, health and environmental sustainability in terms of global food security.

Keywords: Germplasm, ex-situ conservation, Industrial crops, Breeding, Diversity loss

Genetic and metabolic diversity of Broccoli-Rabe Landraces ('*Brassica rapa*' L. subsp. 'sylvestris') with a focus on glucosinolate pathways

Giulio Testone¹, Alice Pajoro², Stefano Pavan³, Riccardo Aiese Cigliano⁴, Gabriella Sonnante⁵, Maria Gonnella⁶, Anatoly Petrovich Sobolev¹, Giuseppe Scioli¹, Lorenzo Pin¹, <u>Donato Giannino¹</u>

¹CNR- Institute for Biological Systems, Italy, ²CNR- Institute of Molecular Biology and Pathology, Italy, ³University Aldo Moro, Bari, Italy, ⁴Sequentia Biotech, Barcelona, Spain, ⁵CNR-Institute of Biosciences and Bioresources, Italy, ⁶CNR-Institute of Sciences of Food Production, Italy

donato.giannino@cnr.it

'Brassica rapa' L. is a diploid (2n=20, genomic formula = AA, haploid genome size ca. 425 Mb) and mostly allogamous species including broccoli-raab ('B. rapa' subsp. 'sylvestris'), known in Italy as "cima di rapa" or "friariello". Due to limited investments, no broccoli-raab official cultivars are registered in Italy or the EU. Broccoli-raab breeding and seed propagation are traditionally managed by farmers, who selected improved populations often classified by cultivation cycle length (short, medium, long, e.g. 40-90-120 days). A CNR-UNIBA collaboration is developing the first broccoli-raab reference genome together with morphological, genomic and metabolic characterization of several broccoli-raab populations. We investigated the genetic diversity of 48 populations (41 of Apulian origin, conserved at the CNR Mediterranean Germplasm Genebank, and 7 from seed industries) by whole genome resequencing of DNA pools (each consisting of 5 plants) and read mapping against the 'B. rapa' cv 'Chiifu' genome (field mustard), while awaiting the specific broccoli-raab genome. Overall, polymorphism distribution varied along chromosomes, with A2 and A6 showing regions of highest variation. The number of SNPs ranged from 1,048,015 to 1,380,244, with the lowest in population '3202' (Putignano, BA) and the highest in '113' (Monopoli, BA). Remarkably, Principal Component Analysis and structural genetic diversity surveys separated populations from the province of Lecce from those of other Apulian provinces, which clustered together. Finally, an in-depth analysis of the glucosinolate pathway genes identified polymorphisms potentially relevant in GWAS analyses targeting various flavour traits. NMR profiling of populations grown in Apulia allowed quantification of over 40 metabolites in florets associated with pungency, sweetness and acidity.

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Keywords: Broccoli-raab population diversity, Fingerprinting by whole genome resequencing, Glucosinolates, NMR metabolic profiling

Genetic diversity and phylogenetic relationships of ancient and monumental olive trees of Crete Island: implications for sustainability and breeding purposes

<u>Livia Polegri</u>¹, Nicolò Cultrera¹, Valentina Passeri¹, Lorenzo Cruciani¹, Roberto Mariotti¹, Panagiotis Kalaitizis², Konstantinos Blazakis², Athanasia Maria³, Stilianos Arhondakis³, Soraya Mousavi¹

¹CNR Institute of Biosciences and Bioresources, Perugia, Italy, ²Department of Horticultural Genetics & Biotechnology, Mediterranean Agronomic Institute, Crete, Greece, ³Dourou, BioCoS PC, Crete, Greece

liviapolegri@cnr.it

Olive (*Olea europaea* L.) possesses a rich genetic heritage, with its diversity closely linked to its geographical distribution. Monumental olive trees hold significant cultural and ecological value and serve as a vital genetic reservoir for future advancements in oliviculture. An in-depth exploration of the island of Crete led to the collection of over 300 samples from olive trees located in provinces of Chania, Rethymno, Heraklion and Lasithi. Sample included 57 monumental, 35 ancient and 47 feral plants. To distinguish between grafted and non-grafted individuals, leaves were collected from both the canopies and rootstocks. Genetic relationships were investigated using 17 well-known Greek cultivars from ELGO-DIMITRA collection, along with 400 olive cultivars from 20 Countries worldwide.

SSR and cp-SSR analysis of all samples enabled the identification of 156 genotypes most of which were traceable to the olive cultivars Throumbolia, Koroneiki and Mastoidis. The application of plastid markers allowed the identification of six distinct lineages among Cretan genotypes, with the majority belonging to the E1.1 chlorotype. Ten monumental and uncultivated olive trees showed the E1.N4 chlorotype, a lineage recently discovered in the Cretan germplasm. The phylogenetic study, which included 400 olive cultivars from across the Mediterranean Basin, revealed that a large group of rootstocks from monumental olive trees formed a distinct cluster, separate from the rest of the germplasm.

Our research highlights that the uniqueness of the Cretan olive germplasm is primarily associated with its monumental trees. Given the high risk of extinction due to natural and human factors, the conservation and propagation of this germplasm are essential. This study offers tangible outcomes and directly contributes to conservation strategies for the Cretan germplasm, both ecologically and productively, supporting the future of regional olive cultivation and potential genetic improvement efforts.

Keywords: Ancient olive trees, Breeding for Climate Changes, Genetic biodiversity

Integrative genomic approach unravels genotypic diversity in the potato-leaf phenotype of Italian tomato landraces

<u>Lorenzo Mancini</u>, Barbara Farinon, Ludovica Fumelli, Maurizio Enea Picarella, Andrea Mazzucato, Fabrizio Olivieri

University of Tuscia, Italy

lorenzo.mancini@unitus.it

Italy is a secondary diversity centre for tomato (Solanum lycopersicum L.). The country hosts cultivation areas characterized by diverse environmental conditions and likewise different use and storage practices. These factors, linked with the selection activity, have led to the formation of an important genetic reservoir of tomato landraces, carrying peculiar plant and fruit traits. This study aimed to investigate the genetic origin of the potato leaf (PL) phenotype found in four Italian landraces: "Spagnoletta" (SPA) from Lazio, "Giagiù" (GIA) and "Patanara" (PTN) from Campania and "Pomodoro di Mola" (MOL) from Apulia. First, an allelism test was carried out by crossing the PL genotypes to assess the involvement of the Potato leaf (C) gene in the phenotypic expression. Then, both SCAR, dCAPS marker and Sanger sequencing analyses on C gene were performed. Two American PL accessions, (LA2374 and PC711571) carrying the traditional rider mutant allele of the C gene on chr6, as well as a Red Setter PL mutant line (affected in the Aux/IAA9 gene), were used as controls for the PL trait. The cv Nagcarlang (NAG) was used as the wild-type leaf control. The allelism test revealed that a mutation in the C gene is responsible for the PL phenotype in the four Italian landraces. SCAR marker analysis permitted to distinguish the Italian tomato landraces from the two American C gene rider mutant lines. On sequencing data publicly available, a private SNP mutation was found in SPA. dCAPS marker analysis confirmed the identity of the SNP in SPA. Sanger sequencing of C revealed the presence of two further mutations not previously reported in tomato in this gene within Italian landraces. These results highlight the potential utility of the C alleles in agri-food traceability and genetic distinctiveness. Such efforts could further enhance our understanding of biodiversity while strengthening connections between genetic traits and their land of origin.

Keywords: Tomato, Italian agrobiodiversity, Qualitative traits, Molecular markers, Landraces

SAVEGRAIN-CER a project for the collection, characterization and safeguard of agricultural diversity of cereal species in the Apulia region

<u>Gaetano Laghetti</u>¹, Luigi De Bellis², Rita Accogli², Alessio Aprile², Pasquale De Vita³, Domenica Nigro⁴, Giuseppe De Mastro⁴, Luigi Tedone⁴, Barbara Laddomada⁵, Emanuela Blanco¹, Giacomo Mangini¹, Pasquale Luca Curci¹, Marcella Urbano¹, Paolo Direnzo¹, Rosella Giunta¹, Francesco Losavio¹, Mariano Zonna¹, Gabriella Sonnante¹

¹IBBR-CNR, Italy, ²DiSTeBA, Italy, ³CREA, Foggia, Italy, ⁴University of Bari, Italy, ⁵ISPA, CNR, Lecce, Italy

gaetano.laghetti@cnr.it

Germplasm conservation is crucial for preserving knowledge of plant species. Human intervention, favoring some genes and eliminating others, has eroded genetic diversity.

Cereal landraces, traditionally selected by local farmers over time and well adapted to the climatic conditions of the Apulia region (southern Italy), are currently threatened by genetic erosion/extinction, because of the gradual replacement with modern, high-yielding cultivars.

To address this issue, within the framework of the Rural Development Programme of Apulia 2014-2020, Measure 10.2.1, the Apulia Region is funding the project titled "Biodiversità dei cereali antichi pugliesi per la sostenibilità e la qualità (SAVEGRAIN-CER)". The project, coordinated by IBBR-CNR, is being carried out in collaboration with public research institutions, universities, and private companies operating in the Apulia Region.

The main objectives of SAVEGRAIN-CER are: i) the collection of historical data; ii) the classification and conservation of Apulian cereal landraces; iii) their morphological, genetic and bio-agronomic characterization; iv) the assessment of qualitative traits.

Launched in 2023, the initiative has already recovered over 100 accessions of cereals, including bread wheat, durum wheat, barley, oats, and hulled wheat. These materials originate from diverse Apulian agroecosystems, including biodiversity hotspots and traditional farming landscapes. Collected germplasm is duplicated for ex-situ conservation at the IBBR-CNR Mediterranean Germplasm Bank (https://www.ibbr.cnr.it/mgd/) and maintained on-farm by custodian farmers to ensure dynamic in-situ preservation.

To date, over 20 landraces have been proposed for their inclusion in the Apulia Regional Register of Plant Genetic Resources.

Preliminary findings underscore the agroecological resilience and cultural value of Apulian landraces, positioning them as cornerstones for sustainable agriculture and regional identity.

Keywords: Agricultural diversity, Plant genetic resources, Landraces, ex-situ and on farm conservation, Cereals

The BiodiverSO project as a model for preserving the biodiversity of vegetable crops in Puglia (Southern Italy)

<u>Pietro Santamaria</u>, Angelo Signore, Adriano Didonna, Onofrio Davide Palmitessa, Massimiliano Renna

University of Bari, Italy

pietro.santamaria@uniba.it

The Puglia region, rich in agro-biodiversity, demonstrates how local vegetable varieties integrate with modern horticulture. However, its crop genetic diversity has declined due to rural abandonment, an aging farming population, and lost generational knowledge. This contribution summarizes the objectives, methodologies, and outcomes of the "Biodiversity of Puglia 's Vegetable Crops (BiodiverSO)" projects, funded by the Puglia Regional Administration under the Rural Development Program, aim to recover, characterize, conserve, and enhance local vegetable varieties.

In the first project edition (2013-2018), eight work packages were implemented. Among key achievements we highlight recognition and promotion of "Carota di Polignano" (*Daucus carota* L.), a local carrot variety with yellow, purple, and orange roots, and sanitization of eight globe artichoke varieties from some viruses (AILV, ArLV, TICV) via meristem-tip culture and in vitro thermotherapy.

In the second edition (2022-2025), activities expanded to ten work packages with two extra actions for dissemination. Notable progress was made for two landraces of unripe melons (*Cucumis melo* L.) used like cucumbers: "Scopatizzo" yielded 5.3 kg/plant (26.2 fruits) in hydroponics within 71 days; "Barattiere" showed resistance to Tomato leaf curl New Delhi virus making it a promising rootstock for susceptible cucurbits.

For both project editions, a computerized database "the BiodiverSO Management System (BMS)" was developed to ensure accurate and efficient management and processing of project data.

The results underscore that while some local varieties were replaced by modern ones before reaching their full potential, their genetic value remains critical for future crop improvement programs.

In conclusion, the BiodiverSO project serves as a model initiative for the protection and recovery of vegetable varieties at risk of genetic erosion, facilitating the identification and valorization of Puglia's diverse plant germplasm.

Keywords: Genetic erosion, Local varieties, Protection, Recovery, Valorization

The relationship between biodiversity and a cooperative of floriculture producers: a pilot case study in Italy

Myriam Arcidiacono, Anna Mensuali

Scuola Superiore Sant'Anna, Pisa, Italy

m.arcidiacono@santannapisa.it

The European Union is the world 's largest floriculture market, with a production valued at around 9.4 billion and over 33,000 companies operating on 55,600 hectares. This economic sector has a relationship with environment and biodiversity characterized by inner contradictions, since it generates both a positive and a negative impact on it. We selected and wrote a case study investigating the characteristics and implications of the relationship between biodiversity and business, focusing on "Flora Toscana", an Italian cooperative of floriculture producers.

The iniziative was carried out within the framework of the European National Biodiversity Future Center, task 7.5.5. Interviews and site visits were conducted in order to write the case study.

The negative and positive impacts of Flora Toscana on environment and biodiversity, together with the dependence relationship of the cooperative on biodiversity, were analysed and described, outlining their indirect and direct effects. Based on the data provided by the cooperative and the conducted interviews, the path taken over time by the cooperative members towards biodiversity management was described, as well as the results of the initiatives taken so far to reduce the environmental impact of the production activities.

The study showed that Flora Toscana consistently draws on the extensive repertoire of flowering plants provided by biodiversity to meet the pressing demand of new plant varieties characteristic of the floriculture sector. Nevertheless, the company has shown to understand the value of biodiversity through the environmental certifications achieved, as well as the growing number of initiatives undertaken to reduce the environmental impact and to guarantee a sustainable use of biodiversity.

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Keywords: Ornamental plants, Business, environmental impact, Agro-biodiversity, Green economy

Unveiling intra-varietal genetic diversity in olive cultivars through whole genome resequencing and assembly

<u>Edoardo Franco</u>¹, Andrea Porceddu², Mario Santona², Chiara M. Posadinu², Gianni Nieddu², Valentina Marrassini¹, Giuseppe Quaratiello¹, Maria Cristina Valeri¹, Luciana Baldoni¹, Ornella Calderini¹, Domenico Rau²

¹Institute of Biosciences and Bioresources, CNR, Perugia, Italy, ²University of Sassari, Italy

edoardofranco@cnr.it

The Italian olive germplasm represents the largest basin of species variability, with hundreds of varieties preserved in traditional olive groves and in thousands-year-old trees. Despite extensive research on inter-varietal diversity, intra-varietal variation remains poorly explored, as olive cultivars are commonly assumed to be genetically uniform due to vegetative propagation. However, standard markers, such as simple sequence repeats (SSR), are unable to detect subtle intra-varietal differences, as they cover limited genomic regions. This issue also affects other clonally propagated crops such as grapevine.

To address this, two Italian olive cultivars were selected as models: "Frantoio", widely spread under various synonyms across Italian regions, and "Bosana", predominant in Sardinia and also present elsewhere under different names.

In order to detect somatic mutations, the genomes of 17 clones (9 from cv. Bosana and 8 from cv. Frantoio) were sequenced using Illumina 150PE technology at ~100X depth and aligned to the cv. Arbequina reference genome. Somatic mutations were identified using FreeBayes to infer genetic relationships among clones of each group. In the meantime, high-quality de novo genome assemblies of both cultivars are under generation using PacBio HiFi long reads and HiC-based scaffolding, in order to capture full genomic variability.

A first overview of the genome somatic differences among clones of the two cultivars has been obtained.

These findings provide insight into the origin and differentiation of clones within each cultivar, offering a basis for understanding intra-varietal diversity in clonally propagated trees.

This study highlights the genetic distinctiveness of territorial clones within the same cultivar, shedding light on their local adaptation and evolutionary trajectories. Such insights may support the valorization and conservation of region-specific olive germplasm.

Keywords: Biodiversity, Olive, Clonal diversity, de novo assembly, Somatic mutations

Session: Innovation in vine and wine microbiology

Biodiversity of culturable yeast population isolated for two consecutive years from hypogean wine cellars located in Southern Italy

Angela Capece¹, Rocchina Pietrafesa¹, Gabriella Siesto¹, Giorgia La Rocca¹, Francesco Tedesco¹, <u>Patrizia Romano²</u>

¹University of Basilicata, Italy, ²Universitas Mercatorum, Italy

pot2930@gmail.com

The hypogean wine cellars can be considered production and aging sites of traditional wines. These ecosystems could also be the keepers of yeasts responsible for transformation of grape must into wine, which in the past were certainly entrusted to the naturally present yeasts and not to the use of commercial starters. The yeasts resident in these habitats can be defined "ancient yeasts", selected over the time in each traditional cellar; this population might be a source of indigenous yeasts, poorly explored until now. In this study, the cultivable yeast population sampled over two consecutive years from hypogean cellars located in Southern Italy, mainly in Basilicata region, was studied. The yeasts were identified by restriction analysis of ITS region, followed by sequencing of D1/D2 domain of 26S rDNA. The genetic diversity among Saccharomyces cerevisiae strains were evaluated by amplification of inter-delta region, while all wine yeasts were submitted to a technological screening, such as the resistance to antimicrobial compounds present during vinification (i.e. sulphur dioxide, ethanol, copper sulphate), production level of hydrogen sulphide. The cultivable yeast population isolated from this habitat is characterized by different species, which also varied depending on the analyzed site. The majority of yeasts was composed by wine-associated species, such as S. cerevisiae, Hanseniaspora spp., Wickerhamomyces anomalus, Pichia spp., Candida spp. High genetic polymorphism among S. cerevisiae isolates and high variability for technological traits was found. The preliminary results obtained confirmed the suitability of this approach to capture and preserve the microbial biodiversity associated to these ancient sites.

This work was supported by the project ViCaM, "Vite e vino dal Campo ai Musei - Le due Culture in un bicchiere" - FSC di Ricerca e Innovazione - Regione Basilicata Fondo di Sviluppo e Coesione - N° 142046/128D

Keywords: Traditional wine cellars, Wine yeasts, New starters

Session: Innovation in vine and wine microbiology

Investigating the microbiome of a Barbera vineyard by a shotgun metagenomic approach

Paola Di Gianvito, Vasileios Englezos, Ilario Ferrocino, Luca Cocolin, Kalliopi Rantsiou

University of Torino, Italy

paola.digianvito@unito.it

Vineyard microbiome is deeply interconnected with the plant and serves as a reservoir of genes and functions, to the extent that it is considered part of the holobiont. In this study, the dynamics of fungal and bacterial communities were characterized in a conventionally managed Vitis vinifera cv. Barbera vineyard using shotgun sequencing. Samples of rhizosphere soil, leaves, and grapes were collected at different time points, from fruits development to harvest. A clear distinction between the phyllosphere and rhizosphere microbiota was observed for both bacterial and fungal communities. The specificity of certain species in different compartments was confirmed, as well as the presence of a core microbiome. Regarding the bacterial community, Stenotrophomonas maltophilia was the only core species, while LEfSe analysis revealed an enrichment of genera known for their plant growth-promoting (PGP) properties or their roles in carbon and nitrogen fixation. The fungal core consisted of 21 species with both beneficial and detrimental effects in the vineyard. Additionally, an enrichment of saprobic fungi rich in carbohydrate- and biomass-degrading enzymes was observed across all compartments. Functional analysis revealed that the Barbera vineyard microbiome was primarily involved in carbohydrate and amino acid metabolism. KEGG pathway analysis highlighted the enrichment of genes related to valine, leucine, and isoleucine biosynthesis in all compartments. The rhizosphere microbiome exhibited a wide array of enriched pathways associated with organic matter decomposition, carbon, lipid, and nitrogen recycling, as well as energy metabolism. In fungi, an enrichment of pathways involved in xenobiotic degradation was also observed. This study expands our knowledge of the Barbera vineyard microbiome. These findings may be useful for designing a tailored microbiome to enhance plant health and promote productivity and wine quality.

Keywords: Barbera vineyard metagenome, Rhizosphere and phyllosphere microbiota, Functional genes, Metabolic pathway
Session: Innovation in vine and wine microbiology

Low-Temperature active dry yeast rehydration: nutrients for enhanced fermentation and membrane fluidity

Elisa Aiello¹, Carlo Montanini², Mattia Pia Arena¹, Andrea Pulvirenti¹, Maria Gullo¹

¹University of Modena and Reggio Emilia, Italy, ²AEB group, Brescia, Italy

elisa.aiello@unimore.it

Active dry yeasts (ADY) are vital in winemaking due to their durability, but successful rehydration-relying on optimal trehalose levels, time, temperature, pH, nutrients, and ergosterol-is essential for restoring function. Low rehydration temperatures, however, reduce membrane fluidity and may impair yeast performance. This study evaluated the effects of suboptimal rehydration temperatures on selected yeast strains of Saccharomyces cerevisiae and Torulaspora delbrueckii, preserved at the Unimore Microbial Culture Collection (UMCC), and assessed the efficacy of two rehydration nutrients-FERMOPLUS® Energy Glu 3.0 and FERMOPLUS® Energy Glu 4.0 (AEB S.p.A)-focusing on improving fermentation performance and stabilizing membrane fluidity. All tested strains, except for T. delbrueckii, exhibited enhanced initial fermentation performance upon treatment with both nutrients. Analyses of membrane fluidity revealed that yeast cells rehydrated at 20°C displayed reduced fluidity compared to those cultivated at 25°C for 24 hours, confirming a temperature-induced stiffening effect. Notably, cells treated with FERMOPLUS® Energy Glu 4.0 demonstrated less variation in membrane fluidity, suggesting a more effective stabilization of membrane properties under suboptimal conditions. Overall, this work provides valuable insights into optimizing ADY rehydration at low temperatures-conditions employed in the wine industry to save time and costs-and offers practical strategies to enhance fermentation performance, ultimately improving wine quality.

This work was funded by the European Commission - NextGenerationEU ("Strengthening the MIRRI Italian Research Infrastructure for Sustainable Bioscience and Bioeconomy", code IR0000005), by the European Union - NextGenerationEU ("National Biodiversity Future Center-NBFC", CUP E93C22001090001), and by AEB S.p.A ("Studio di Ceppi di Lievito di Interesse in Campo Enologico e Mantenimento delle Colture presso la Collezione UMCC", CUP E83C24002050007).

Keywords: Active dry yeast, Rehydration, Yeast strains, Membrane fluidity, Fermentation performance

Session: Innovation in vine and wine microbiology

Microbial biodiversity as a source of new yeast strains for winemaking

Daniele Oliva

Istituto Regionale del Vino e dell'Olio - Regione Sicilia, Italy

daniele.oliva@regione.sicilia.it

In the past 25 years, IRVO has studied microbial biodiversity in grapes and musts from various areas of Sicily and selected 7 yeast strains belonging to 4 genera, now on the market for the benefit of wineries.

Grape juice or spontaneously fermenting musts were plated, single colonies were isolated, their genera were determined by microbiological (colony morphology on WL Nutrient agar) and then by molecular methods (PCR-RFLP of the ITS region; amplification and sequencing of the D1/D2 region of the 26S rDNA). Laboratory tests were performed to determine fermentative vigor without and with sulfites and the production of ethanol, glycerol, volatile acidity, β -glucosidase, and H₂S. Strains with the best characteristics were used as starters in vinifications of 100 L, and the wines were analyzed for chemical-physical parameters and VOC (by GC-MS) and by sensorial analyses. Best strains were finally used in industrial vinifications.

From late spontaneous fermentations made in southeastern Sicily, 918 *Saccharomyces* colonies were isolated, and two strains were selected for red wines, one for white wines, and one for bottle fermentations. From grape musts collected in western Sicily through the analysis of over 2,500 yeast colonies, one *Starmerella bacillaris* (syn. *Candida zemplinina*) strain, in sequential fermentation with *S. cerevisiae*, was able to produce red wines with higher glycerol concentrations. One *Lachancea thermotolerans* strain produced lactic acid and wines with higher total acidity. From grapes harvested on the small island of Linosa, south of Sicily, through the analysis of over 3,800 yeast colonies, one *Kluyveromyces marxianus* strain was identified for its ability to produce beta-glucosidase activity, as well as for the production of greater quantities of esters.

Yeast populations present in Sicily have proven to be an excellent source of strains usable in the wine industry to improve the quality of wines.

Keywords: Wine, Fermentation, Yeast, Saccharomyces, non-Saccharomyces

Characterization of yeast strains isolated from agricultural soils for their potential in biodegradation of glyphosate

<u>Francesca Emili</u>¹, Veronica Spinelli¹, Andrea Ceci¹, Benedetta Turchetti², Pietro Buzzini², Domenico Davolos³, Anna Maria Persiani¹

¹University of Rome, La Sapienza, Italy, ²University of Perugia, Italy, ³Department of Technological Innovations and Safety of Plants, Products and Anthropic Settlements (DIT), INAIL Research Area, Rome, Italy

francesca.emili@uniroma1.it

Glyphosate (GP) is the most used herbicide in agriculture. Its prolonged use has led to the frequent occurrence of GP and its main metabolite, AMPA, in the environment, posing risks to ecosystems and human health. Yeasts, due to their metabolic plasticity, represent promising candidates for soil bioremediation. This study aimed to isolate and characterize yeasts able to degrade GP and AMPA using them as nutritional source. Soil samples were collected from a wheat field with a history of GP use in Marsciano (PG), and isolation in enrichment condition with GP and AMPA as sole P source was carried out. Yeast strains were identified through molecular approach and will be deposited in the Culture Collection DBVPG of the University of Perugia. Out of 25 isolates, 17 were identified as the black yeast *Exophiala alcalophila* Goto & Sugiy (Herpotrichiellaceae). Screening in 96-wells plates were performed for all the strains in P-free mineral medium with GP or AMPA at 2.5, 5 and 10mM and growth was monitored by measuring OD600 twice daily for 7 days. Preliminary results showed different growth patterns among treatments. Most of E. alcalophila strains showed increased growth values at the highest AMPA concentration compared to the negative control (C-), which suggests their ability to use AMPA as P source. Moreover, since the growth value at 10 mM exceeded twice that of the positive control (C+), this may even stimulate yeast growth. However, the presence of GP reduced the performance of these strains. Instead, other strains not yet identified showed higher growth values with GP compared to C-, and reduced growth with AMPA. In conclusion, our results suggest that yeasts may degrade GP and AMPA, highlighting their potential for the bioremediation of GP- and AMPA-contaminated agricultural soils.

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Keywords: Glyphosate, Bioresources, Bioremediation, Yeasts, Agricultural soils

Exploring the cultivable mycobiota associated with Mediterranean *Cymodocea nodosa* for ecological and biotechnological applications

<u>Valeria Paola Prigione</u>¹, Anna Poli¹, Marina Carrasco-Acosta², Pilar Garcia-Jimenez², Giovanna Cristina Varese¹

¹University of Torino, Italy, ²Universidad de Las Palmas de Gran Canaria, Spain

valeria.prigione@unito.it

Marine fungi occupy a broad spectrum of ecological niches and are widespread across diverse marine habitats. Analogously to their terrestrial counterparts, marine taxa associate with both abiotic substrates such as sediments and the water column and biotic hosts across all trophic levels, functioning context-dependently as parasites, pathogens, saprotrophs, or mutualistic symbionts. Despite reports of their presence are increasing, comprehensive understanding of their abundance, diversity, and functional roles in marine ecosystems remains limited, raising questions about their ecological significance and potential as reservoirs of biomolecules with biotechnological applications.

To address these questions and gain deeper insights into their abundance, diversity, and ecological functions, we isolated and identified the cultivable mycobiota associated with *Cymodocea nodosa*, a seagrass species that plays a crucial role as an ecosystem engineer in upper sublittoral areas, littoral zones and coastal lagoons. Samples were collected from two meadows along the southern Spanish Mediterranean coast: one located in a littoral area and the other in a coastal lagoon, each with distinct mean annual salinities (37.5 psu and 43.5 psu, respectively) and characterized by a different degree of anthropogenic disturbance. The epiand endophytic communities isolated from both roots and leaves were then compared. In total, more than 60 taxa (mainly Ascomycota) were identified. Notably, different species from strictly marine genera, such as *Paralulworthia* and *Cumulospora*, were the only endophytes isolated exclusively associated with the roots of both meadows. The results provide a framework for understanding the role of seagrasses-associated marine fungi that could be a source of novel molecules of biotechnological interest.

Keywords: Marine fungi, Seagrasses, Ecological applications, Biotechnological potential

Fungi in Multi-Taxon analysis: updates from the PRIN MultiForDiv Project

<u>Silvia Giusto</u>¹, Anna Andreetta², Giorgio Brunialti³, Giandiego Campetella⁴, Roberto Canullo⁴, Marco Cervellini⁴, Stefano Chelli⁴, Francesco Chianucci⁵, Zuzana Fackovcová¹, Maura Francioni⁴, Luisa Frati³, Paolo Giordani¹, Nicola Puletti⁶, Mirca Zotti¹, Simone Di Piazza¹

¹University of Genova, Italy, ²University of Cagliari, Italy, ³University of Siena, Italy ⁴University of Camerino, Italy, ⁵University of Florence, Italy, ⁶CREA, Research Centre for Forestry and Wood, Italy

silvia.giusto@edu.unige.it

Temperate forests in Europe provide essential ecosystem services, such as carbon storage, water regulation, and habitat provision. However, they face significant threats from climate change and human disturbances. Biodiversity conservation is a priority of national and international policies, yet many aspects of forest diversity, particularly understorey plants, and fungi (including lichens) remain poorly understood. This project investigates the patterns and drivers of multi-taxon forest diversity in Italian forests using sites from the International Cooperative Programme on Forests LII network. The study focuses on soil fungal diversity, key players in nutrient cycling and forest resilience. In particular, we studied the vital soil microfungal component. Soil samples from ten Italian plots were analyzed using dilution plating to quantify and identify fungal strains. Functional traits such as xerotolerance and thermotolerance were assessed to explore their ecological roles and responses to environmental variables. Five plots were analyzed, revealing 1289 colony-forming units (CFUs) and 140 morphotypes. Molecular analysis refined genus identification. The most represented genera were Penicillium (55%), Trichoderma (9%), and Aspergillus (6%). Significant differences in fungal distribution among plots suggest the influence of soil type, forest composition, and organic matter. For instance, the TOS2 plot (Tuscany), dominated by holm oaks and sandy colluvial soil, showed higher fungal presence (248 CFUs) than BOL1 (Bolzano), dominated by Norway spruce and podzolic soil on drift (168 CFUs). The dominant genus also varied: Penicillium in TOS2 and Umbelopsis in BOL1. Culture-based tests on Penicillium and Aspergillus strains were conducted to characterize their functional traits. These findings will provide insights into their contributions to organic matter decomposition, symbiosis, and vegetation interactions, enhancing our understanding of forest ecosystem dynamics.

Keywords: Microfungi, Soil, Fungal biodiversity, Global change

Genetic biodiversity of summer truffle (*Tuber aestivum* Vitt.) from ten regions of Italy

<u>Niccolo' Militello</u>, Giovanna Soffritti, Maria Elena Antinori, Lorenzo Stagnati, Edoardo Puglisi, Matteo Busconi

Università Cattolica del Sacro Cuore, Italy

niccolo.militello@unicatt.it

Truffles are hypogeous ascomycetes belonging to the order Pezizales. They form symbiotic relationships with the roots of various plants, contributing to plant health. Even though some truffles are highly appreciated for their aroma and flavour, the yields of natural truffle grounds are decreasing, and their life cycle is not completely understood.

Tuber aestivum Vitt. is widespread in Italy and interest in this species is growing because climate change is threatening its natural truffle grounds with a severe risk of biodiversity loss. Studying the DNA of *T. aestivum* is pivotal for understanding summer truffle biodiversity, deepening our knowledge of its life cycle and characterising the genetic variability of wild populations locally adapted to different environmental conditions. Genome sequencing can also help to understand the plant-truffle symbiosis, the formation of the fruiting body and the aroma formation, thus providing data that could help to preserve the biodiversity of summer truffle. Moreover, shotgun sequencing can be used to enhance insight into the role of bacterial biodiversity in the development of the distinctive flavour of *T. aestivum* by identifying the bacterial species associated with the fruiting body of summer truffles and the bacterial genes involved in the development of truffle aromatic and sensory characteristics.

One hundred DNA samples were extracted from the gleba of summer truffles coming from ten Italian regions (Apulia, Basilicata, Calabria, Campania, Emilia Romagna, Lazio, Marche, Piedmont, Tuscany, and Umbria). Shotgun sequencing is being employed to analyse the genetic diversity of truffles and the biodiversity of the bacteria associated to the gleba. By analysing and comparing a heterogeneous population of truffles we aim to highlight the implications of our findings for truffles biodiversity and spreading.

Keywords: Truffle, Tuber aestivum Vitt., Biodiversity, Whole genome sequencing, Aroma

Genome-based exploration of *Mrakia*: sequencing all type strains to unlock fermentative traits of this promising non-conventional yeast (NCY) genus

<u>Francesca Di Cesare</u>¹, Benedetta Turchetti², Daniele Andreani², Gioele Lazzari¹, Eugenio Parente³, Giovanna Felis¹, Nicola Vitulo¹

¹University of Verona, Italy, ²University of Perugia, Italy, ³University of Basilicata, Italy

francesca.dicesare@univr.it

In recent years, the fast progress of next-generation sequencing (NGS) and integrated omics has transformed the study of microbial diversity. This has sparked new interest in non-conventional yeasts (NCYs) and sped up the development of their genetic and functional tools for biotechnological use. Among these, the genus *Mrakia* - comprising 20 psychrophilic and psychrotolerant species in the Basidiomycota phylum and typically isolated from cold and extreme environments - has gained attention for its unexplored biotechnological potential. Some strains have shown promising fermentative abilities, and *Mrakia gelida* has been successfully used in the production of a low-alcohol beer prototype, supporting the relevance of this genus in the development of fermented products.

In this study, we generated high-quality genome and transcriptome data for 20 *Mrakia* typestrains, preserved in different international Culture Collections. We used a hybrid sequencing method with Oxford Nanopore long reads and Illumina short reads to get high-contiguity genome assemblies. Average nucleotide identity (ANI) was used to perform a phylogenomic analysis and explore genome-based relationships among the 20 Mrakia type strains. The ANI analysis identified two clusters: *M. gelida* is closely related to *M. robertii* and *M.* sp.1 (ANI 86%), forming a subcluster with *M. psychrophila*, *M. blollopis*, and *M. frigida* (ANI 82%). This group is less related to *M. stelviica* and *M. montana* (ANI 87%).

Gene prediction and functional annotation were carried out with the support of transcriptomic data, allowing the identification of confidently supported coding sequences. We focused on genes linked to alcoholic fermentation, aiming to understand the genetic base of fermentative traits in *Mrakia*.

The genomic framework developed here offers the most complete resource currently available for this genus and provides a basis for future research into the biotechnological application of NCYs in sustainable food systems.

Keywords: non-conventional yeast, Genomics, Food biotechnology, Bioprospecting

Microbiome of Zelkova sicula, a critically endangered relict tree of Sicily, Italy

<u>Giulia Cosimi</u>¹, Giuseppe Garfi², Giorgio Schiera¹, Giancarlo Perrotta³, Paola Quatrini¹

¹University of Palermo, Italy, ²Istituto di Bioscienze e Biorisorse (IBBR), Italy, ³Dipartimento Dello Sviluppo Rurale e Territoriale, Regione Siciliana, Italy

giulia.cosimi@unipa.it

Zelkova sicula is a bioclimatic relict and a critically endangered tree, incapable of sexual reproduction: today only two small populations are known in the Iblei Mountains (Siracusa, Italy), Pisano (ZS1) and Ciranna (ZS2). We investigated the microbial interactions of *Z. sicula* to characterize its microbiome and to identify key beneficial symbionts to improve the conservation strategies in progress. We investigated bacterial and fungal endophytes and focused on arbuscular mycorrhizal fungal (AMF) symbionts as they are recognized as beneficial for most terrestrial plants and helpful in reproduction processes.

Fine roots, bulk and rhizosphere soil were sampled from the two populations ZS1 and ZS2. Physical-chemical analysis and metabarcoding sequencing of Bacteria, Fungi and Microarthropods communities were conducted on bulk soil; AMF spores were counted after wet-sieving extraction from rhizosphere soils and molecularly identified. Root samples were stained in trypan blue to assess endomycorrhizal status and DNA was extracted from roots for metabarcoding analysis of endophytes.

ZS2 site revealed higher soil pH, lower organic carbon content and higher spore density in respect to ZS1. Bulk soil Bacteria communities differed between the two sites. Higher AMF colonization rate and higher AMF biodiversity were detected in rhizosphere soil and individuals of ZS2; this result was confirmed by the greater number of AMF's OTUs detected by metabarcoding. Among AMF we identified five genera and two species: *Funneliformis geosporum* in the root of *Z. sicula* and *Claroideoglomus etunicatum* as the most abundant in soil of both populations.

We report for the first time AMF symbiosis in *Z. sicula*. Considering the importance of AMF for the surviving of this rare and endemic tree, the management of these symbionts could be exploited for conservational purposes, improving both in vivo and in vitro propagation.

Keywords: Zelkova sicula, Arbuscular mycorrhizal fungi, Microbiome, Endangered species

Session: Parallel session: New frontiers in the studies of animal biodiversity

Comparative analysis reveals a shared core gut microbiota in livestock with genusspecific modulation by dietary polyphenols

<u>Massimo Trabalza-Marinucci</u>¹, Federica Mannelli¹, Gabriele Acuti¹, Katia Cappelli¹, Valentina Stefanetti¹, Maria Pia Franciosini¹, Domenico Pietro Lo Fiego², Davide Pravettoni³, Alessandro Priolo⁴, Claudio Forte⁵, Samanta Mecocci¹

¹University of Perugia, Italy, ²University of Modena and Reggio Emilia, Italy, ³University of Milan, Italy, ⁴University of Catania, Italy, ⁵University of Turin, Italy

massimo.trabalzamarinucci@unipg.it

Despite differences between monogastric and ruminant species, studies confirm the presence of a shared gut core microbiota, which modulates digestion, development, immunity, and hostmicrobe symbiosis. Genera such as *Prevotella, Lactobacillus, Faecalibacterium, Bifidobacterium,* and *Clostridium* consistently appear across species. Dietary components, such as polyphenols, can shape microbiota profiles. In this study, four experiments were set up to evaluate gut microbiota diversity and modulation in the presence of dietary polyphenols from hazelnut skins (HSP) in chickens, pigs, lambs and cattle. For each species, animals were divided into two groups: a control group fed a conventional diet and a treated group receiving the same diet supplemented with HSP.

Rumen, small intestine and cecum contents were collected and stored at -80 °C. The microbiota was assessed through 16S rRNA gene sequencing, targeting the V3-V4 hypervariable regions, and bioinformatic analysis using the QIIME2 pipeline and custom R scripts.

Comparative analysis revealed 16 bacterial genera common across all studied species. *Prevotella* and *Faecousia* were the most abundant genera across species and gut compartments. This shared core microbial profile provided a reference framework to assess the modulatory effects of HSP. *Prevotella* was markedly influenced by HSP presence, especially in the ruminants' caecum, which was the anatomical district showing the highest degree of microbial variations. The rumen and the monogastric small intestine core microbiota were composed of 44 and 35 genera, respectively. Among them, *Cryptobacteroides* and *Ruminococcus* in the rumen, and *Alloprevotella* and *Rothia* in the small intestine, were the genera most affected by HSP. Certain microbial populations exhibited higher resilience, ensuring stability and functionality despite dietary changes. These resilient microbes are known to play a crucial role in digestion, immune modulation, and overall gut health.

Session: Parallel session: New frontiers in the studies of animal biodiversity

Small basin, big data: eDNA metabarcoding tracks vertebrate diversity and distribution in the Serchio river basin

<u>Gabriele Cananzi</u>

University of Florence, Italy

gabriele.cananzi@unifi.it

Effective biodiversity monitoring is vital for detecting species loss and early incursions of alien species, especially in freshwater systems under increasing pressure. Traditional monitoring methods in flowing water are often invasive, require taxonomic expertise, and involve handling organisms, which can cause mortality. Environmental DNA (eDNA) metabarcoding offers a non-invasive alternative by detecting genetic material that organisms release into their environment.

In this study, we applied eDNA metabarcoding at five sites within the Serchio River basin, an understudied watershed in Tuscany, central Italy. Water samples were filtered, and eDNA was extracted from rivers with varying flow regimes. This method identified 64 taxa, including protected native and invasive alien species, across major vertebrate groups. Species distributions matched ecological expectations.

We compared eDNA results with traditional monitoring techniques, including transect surveys (March 2021- October 2023) and electrofishing. eDNA metabarcoding detected higher overall species richness, though some taxa were uniquely identified by each method. Richness was typically greater in the river 's mainstem than in its tributaries, likely due to eDNA accumulation, suggesting that main channels may be strategic points for efficient biodiversity monitoring.

Overall, eDNA metabarcoding enabled a rapid, non-invasive assessment of vertebrate diversity in the Serchio River basin, capturing both aquatic and terrestrial species. This approach revealed valuable insights into regional gamma diversity and proved more time-efficient than conventional methods.

Keywords: Environmental DNA, River, Monitoring, Vertebrates

Session: Parallel session: New frontiers in the studies of animal biodiversity

The DNA bank of five Italian beef cattle breeds

Fiorella Sbarra¹, Daniele Colombi², Emiliano Lasagna², Andrea Quaglia¹

¹A.N.A.B.I.C., Italy, ²University of Perugia, Italy

sbarra@anabic.it

A DNA bank is a collection of biological animal samples from which DNA extraction is possible. The advantages of preserving genetic material are several: implementation of selective breeding programs with genomic selection, preservation of genetic diversity, products molecular traceability. Genomic selection is useful for young animals and for sex-limited traits, traits with low hereditability or expensive to measure. Since almost 20 years ANABIC (National Association of Italian Beef Cattle Breeders) has set up a DNA bank for the five Italian beef cattle breeds: Marchigiana (M), Chianina (C), Romagnola (R), Maremmana (MM), and Podolica (P). The DNA bank plays an important role in selection and valorization of these breeds, it is used for parentage testing, estimation of inbreeding to protect the biodiversity, molecular traceability of meat products and for genetic and genomic analyses to diagnose genetic diseases. The samples are catalogued and they are stored in different ways depending on conservation needs: hair roots, dried ear cartilage and nasal swabs are stored in boxes at room temperature, blood, meat, or ear cartilage with liquid preservative in a freezer at -20° C, extracted and purified DNA in a freezer at -80°. ANABIC has also a semen bank with around 38,000 doses as a germplasm reserve to use for planned mating aimed to recover particular lines and genotypes, or for scientific research. The total samples collected at the present time are 802,722: 291,818 M, 309,762 C, 76,378 R, 35,352 MM, and 89,412 P. Regarding sample type: 3,562 DNA samples, 18,753 whole blood samples, 8,949 FTA card, 314,772 hair roots, 454,796 ear tissue samples and 1,890 nasal swabs. The continuous maintenance and implementation of this DNA bank constitute a pillar of genetic characterization of these breeds and represent an important biodiversity tool for Italian beef cattle.

Keywords: Italian beef cattle, DNA bank

Session: Biodiversity, invasive species and multitrophic interactions

Pesticides and biodiversity conservation: how low pesticide doses affect foraging behaviour of two Scelionidae and Coccinellidae biocontrol agents

Gabriele Rondoni¹, Elena Chierici¹, Vito Antonio Giannuzzi¹, Jacques Brodeur², Eric Conti¹

¹University of Perugia, Italy, ²IRBV - UDEM, Montreal, Quebec, Canada

gabriele.rondoni@unipg.it

Biological control is a pest control strategy helping to reduce chemical pesticides and conserving invertebrate biodiversity. In agricultural systems, the susceptibility of natural enemies to pesticide applications may preclude successful control. Besides lethal effects, nonlethal effects due to exposition of the beneficial insects to chemicals are critical and can impair foraging behaviour. Here we present data on the behavioural and cognitive effects of low concentrations of an acetamiprid-based neonicotinoid insecticide on two biocontrol agents: the egg parasitoid Trissolcus japonicus (Hymenoptera: Scelionidae) and the predatory ladybird Harmonia axyridis (Coleoptera: Coccinellidae). In open arena bioassays, T. japonicus females exhibited positive responses to host chemical traces and reduced foraging time following associative learning. However, parasitoids exposed to the insecticide showed altered walking behaviour and prolonged memory retention, despite no immediate effect on learning ability. Harmonia axyridis males demonstrated the ability to associate plant-host cues with mating experience, but exposure to sublethal insecticide doses disrupted this behaviour and affected decision-making during foraging. These behavioural impairments, observed in both species, suggest that even low pesticide residues can interfere with foraging efficiency and reproductive performance. Such effects may reduce the establishment and effectiveness of natural enemies, particularly exotic species, such as *T. japonicus* introduced for the control of invasive brown marmorated stink bug, Halyomorpha halys. Therefore, sublethal impact of pesticides should be carefully considered in biological control strategies aimed at promoting biodiversity conservation in agricultural systems.

Keywords: Halyomorpha halys, Harmonia axyridis, Neonicotinoid, Trissolcus japonicus

Session: Biodiversity, invasive species and multitrophic interactions

Phenological and germination insights for managing the spread of invasive *Baccharis halimifolia* in the Venetian Lagoon

<u>Valeria Xotta</u>¹, Nebojsa Nikolic¹, Donato Loddo², Roberta Masin¹

¹University of Padova, Italy, ²Institute for Sustainable Plant Protection, CNR, Italy

valeria.xotta@studenti.unipd.it

The impact of invasive species on biodiversity deserves to be analysed, as they affect agriculture, forestry, and natural ecosystems.

Baccharis halimifolia L. is a dioecious shrub belonging to the Asteraceae family. It is listed among the invasive species targeted for eradication under European Regulation No.1141/2016. This species has now naturalized in six European countries and has been recorded in Italy along the coastal areas of the Veneto region and Tuscany. In recent years, it has rapidly expanded, especially invading conserved native coastal communities.

The main objective of this study is to investigate potential strategies for controlling this highly invasive species in the Venetian Lagoon, a natural environment strongly influenced by temperature variations and by both the quantity and quality of freshwater, brackish, and seawater. Analyses of both the phenology and germination responses of *B. halimifolia* are therefore essential for developing an effective control strategy for this species.

The study was conducted in the WWF Oasis of Valle Averto, a wetland nature reserve located in the Venetian Lagoon. Five different sites were selected within this area, and ten individuals of *B. halimifolia* were identified at each site. The development of phenological phases was monitored through weekly surveys and visual assessments. In addition, the growth and phenological responses of the species to different cutting heights were evaluated to support practical management strategies. This helps clarify how mechanical control methods affect its life cycle, facilitating the identification of the optimal intervention.

Seeds collected from the five sites are being tested in Petri dishes to assess their germination response to constant and fluctuating temperatures and different salinity levels.

Preliminary results suggest that a combination of tactics is necessary to ensure long-term management and to predict its current and potential distribution in the Venetian Lagoon.

Keywords: Invasive species, Phenological phases, Salinity, Germination

Biodiversity of fructophilic lactic acid bacteria isolated from raw honey sampled in Abruzzo region, Italy

Giovanna Felis, Ilaria Checchia, Veronica Gatto, Silvia Lampis, Elisa Salvetti

University of Verona, Italy

giovanna.felis@univr.it

Raw honey, collected directly from the comb, may host beneficial microorganisms such as fructophilic lactic acid bacteria (FLAB), which can have a positive impact on bee health.

The aim of the present study was to investigate the biodiversity of FLAB isolated from honey samples collected from two apiaries located in the Abruzzo Apennines, in central Italy, as possible source of new biotechnological properties to enrich VUCC-DBT (Verona University Culture Collection - Dept. Biotechnology) catalogue.

Eight honey samples were collected after 2-3 days or after 10 days in comb, both multifloral or derived from *Sulla coronaria* (L.) B. H. Choi & H. Ohashi.

Six different culture conditions were used, with either fructose or glucose as carbon sources and addition of tetracycline and ampicillin as selective agents. FLAB were present at up to 10^5 CFU/mL, and isolation was focused on bacilli compatible with FLAB morphology.

Overall, 133 isolates were obtained, which were dereplicated by RAPD-PCR and REP-PCR, and identified by partial 16S rRNA gene and pheS gene sequencing, which revealed they mainly belong to genera *Apilactobacillus*, and *Fructobacillus*.

Genetically unique isolates, as revealed by the combination of RAPD and REP-PCR profiles, deriving from the same honey sample were considered single strains and were further analyzed for antibiotic resistance to ampicillin and tetracycline through MIC assays and PCR detection of antimicrobial resistance genes. Remarkably, some *Apilactobacillus* strains were characterized by phenotypic tetracycline resistance and presence of tet resistance genes.

This study provides the first characterization of FLAB from raw Sulla coronaria honey, and further strain characterization will be focused on possible applications in beekeeping as well as in food fermentation.

Keywords: Fructophilic Lactic Acid Bacteria, Raw honey, Apilactobacillus, Fructobacillus

Implementation of a common Quality Management System for the Italian Microbial Resource Research Infrastructure (MIRRI-IT)

<u>Giancarlo Perrone</u>¹, Iolanda Perugini², Luciana De Vero¹, Benedetta Turchetti³, Gian Paolo Accotto⁴, Rosario Musumeci⁵, Elisa Mazzotta⁶, Valeria Prigione², Lavinia Guerra⁶, Alda Natale⁶, Giovanna Cristina Varese²

¹Institute of Sciences of Food Production (ISPA), CNR, Bari, Italy, ²University of Torino, Italy, ³University of Perugia, Italy, ⁴Institute for Sustainable Plant Protection, CNR, Torino, Italy, ⁵University of Milano-Bicocca, Italy, ⁶Istituto Zooprofilattico Sperimentale delle Venezie, Legnaro, Italy

giancarlo.perrone@cnr.it

Collaborations between different Microbial Resource Centres (mBRCs) and ethical sourcing practices are mandatory to guarantee biodiversity conservation, successful preservation and fair share of benefits arising from the exploitation of genetic resources (ABS). In this context, the European and Italian Infrastructures, MIRRI-ERIC and MIRRI-IT respectively, inter-operate actively in the design of standard guidelines to certify their biological materials and guarantee viability, purity, and identity according to internal standard operating procedures (SOPs). A common Quality Management System (QMS) is a challenging goal of the ongoing SUS-MIRRI.IT project (n. IR0000005), which aims to establish quality criteria and build a valid national network of mBRCs facing the needs of public and private actors in the fields of research and bioeconomy. Three working groups dealing with (i) Common Collections Procedures, (ii) Compliance with the Nagoya protocol, and (iii) Code of Conduct on Biosafety and Biosecurity, have joined forces to define a general and harmonized management system. The general flow chart of the QMS has been defined with guidelines and common harmonised procedures for accepting microbial cultures, their quality check, and the different protocols for microorganisms' (fungi, bacteria, virus, microalgae etc.) preservation and distribution. Regarding the legal compliance with the Nagoya protocol, starting from available Material Transfer Agreement (MTA) and Material Deposit Agreement (MDA) models, a common template and guidelines for the Italian mBRCs have been developed. Moreover, training and capacity-building activities have been carried out to ensure due diligence regarding ABS within the sensitive processes of mBRCs. Finally, a working group on Biosafety and Biosecurity, with experts on human, animal, and plant diseases, is implementing guidelines for handling microorganisms based on the risks they may pose to humans, animals, plants and the environment.

Keywords: mBRCs, Quality control, Nagoya protocol, Biosafety, Biosecurity

Managing and exploiting microbial diversity within the ITEM Culture Collection

<u>Katia Gialluisi</u>, Luciana De Vero, Giuseppe Petruzzino, Giuseppe Cozzi, Nicola De Simone, Pamela Anelli, Mario Masiello, Antonia Susca, Massimo Ferrara, Vittorio Capozzi, Antonio Moretti, Giancarlo Perrone

Institute of Sciences of Food Production (ISPA), CNR, Italy

katia.gialluisi@cnr.it

Culture Collections (CCs) and microbial Biological Resource Centres (mBRCs) have a vital role in preserving, characterizing, managing and exploiting microbial diversity. mBRCs are essential not only as ex situ conservatories for biodiversity but also to assure research purposes and promote appropriate exploitation of biological resources in different fields such as food, industry, medicine and environment. Within the Italian scenario of BRCs, ITEM is an internationally recognized and ISO 9001-certified culture collection hosted at ISPA-CNR (Bari, Italy).

ITEM holds more than 14,000 eukaryotic and prokaryotic strains of agricultural and food interest, including resources of interest for topics ranging from plant pathology to fermentations, from the study of microbiomes to food safety, all relevant in supporting the sustainable transition of agro-food production systems. Most strains belong to filamentous fungi with phytopathological and toxicological significance but also with beneficial traits of interest to develop bio-based applications. These fungi are related to the production of an enormous number of metabolites with biological interest. Yeasts and lactic acid bacteria are useful as starter cultures for fermented products, and as probiotic and biocontrol agents.

ITEM strengthened the potential of collection and scientific services to customers and stakeholders due to the support of the EU Project "Strengthening the MIRRI Italian Research Infrastructure for Sustainable Bioscience and Bioeconomy" (SUS-MIRRI.IT- N. IR0000005), which provided the acquisition of new specialized equipment for high-throughput strains identification and characterization, and the implementation of their long-term preservation. In addition, this resource centre implemented the new public and interoperable database BioloMICS (BioAware, catalogue online item.bio-aware.com), in which biological, molecular, chemical and structural information about microbial strains are available.

Keywords: Biological Resource Centres, Biodiversity, Microbial resources, Exploitation, SUS-MIRRI.IT

Microbial sourdough type I biodiversity preservation as label of MBDS-UNISSCC culture collection

Marilena Budroni, Roberta Coronas, Angela Bianco, Laura Sanna, Carla Cossu, Giacomo Zara

University of Sassari, Italy

mbudroni1@uniss.it

No patents or guidelines exist for spontaneous food-microbiome preservation methods. The SUS-MIRRI project addresses this by developing methodologies to preserve microbial biodiversity and microbiome of sourdough. For this reason, this research aims i) to preserve microbial communities associated to Sardinian sourdough through culture dependent and culture independent approaches; ii) to optimise microbiome preservation methods; iii) to implement the MBDS-UNISSCC collection (University of Sassari) by developing specific databases and methods to preserve microbiome samples. Each sourdough shows unique microbial profiles with specific physicochemical and microbiological parameters including pH, total titratable acidity, and microbial counts. 105 Sourdough samples collected from 64 small villages are preserved in the MBDS-UNISSCC collection at -80°C after backslopping. Descriptive records exist for 78 samples, regarding original preparation methods, provenance, time and temperature of fermentation and bakery production, that is mainly focused on traditional breads and baked goods. The microbial characterisation and optimisation of protocol for sourdough microbiome preservation could be extended to other sourdough type I samples, collected in a special section of MBDS-UNISSCC.

The preservation tests involved the entire matrix (4°C) and the microbiome extracted from the matrix (by extruding the flour) with the addition of glycerol at -80°C. Data analyses of the various storage times (0, 6 months, one year) including culture-dependent, culture-independent, phenotypic and technological methods are currently in progress. A dedicated database section is being developed for sourdough microbiomes within the MBDS-UNISSCC catalogue to comprehensively document this valuable biocultural heritage, ensuring traditional sourdough knowledge and microbial diversity are preserved for future generations.

Keywords: Sourdough, Microbial biodiversity, Microbiome preservation, Database, Microbial culture collection

Preserved microbiomes: a resource for biotechnological applications

Lara Signorello, Elisabetta Antonazzo, Anna Farina, Mattia Pia Arena, Maria Gullo

University of Modena and Reggio Emilia, Italy

lara.signorello@unimore.it

Fermented food microbiome refers to microbial communities, namely mixed cultures carrying out the transformation of suitable substrates into fermented products. The study of fermented foods and microbiomes allows to expand the knowledge of the microbial diversity, which inhabit the fermented ecosystems, to collect and characterize the microbial composition and to use the information for assembling controlled microbiomes. Long-term preservation of these communities is crucial. In this study, microbiomes from vinegar and Kombucha tea were preserved using ultra-freezing and freeze-drying for 12 months, and the microbial communities were evaluated via phenotypic and genotypic characterization. Microbiomes preserved by both methods exhibited a reduction of 1-2 logarithmic units in viable counts compared to the initial community; however, after a propagation period, counts recovered to levels comparable to the original samples. Chemical analyses showed that ultra-freezing did not affect the ability of microbiomes to ferment as titratable acidity levels were similar to those prior to preservation in both vinegar and Kombucha tea samples, whereas freeze-drying significantly reduced the capability of microbiomes to metabolize sugars and acidify the substrate. Furthermore, 30 yeast and 66 bacterial isolates (42 Gram-positive and 24 Gram-negative) were characterized. First, focusing on bacterial isolates, they were grouped into different clusters by molecular fingerprinting analysis, and 16S rRNA gene sequencing provided species-level identification. These findings highlight the possibility of preserving the food microbiome, thus safeguarding its biodiversity, deepening its characterization and enhancing its potential in biotechnological applications.

Part of this work was granted by the European Commission - NextGenerationEU, Project SUS-MIRRI.IT "Strengthening the MIRRI Italian Research Infrastructure for Sustainable Bioscience and Bioeconomy", code n. IR0000005.

Keywords: Fermented beverages microbiome, Cryopreservation, Freeze-drying, Microbial communities, Microbial biodiversity

Strenghening the UNICA-DSMSP culture collection through the SUS-MIRRI.IT project

<u>Maura Deplano</u>, Silvia Viale, Eleonora Civolani, Federica Mereu, Maria Barbara Pisano, Sofia Cosentino

University of Cagliari, Italy

mdeplano@unica.it

In the last decades, biodiversity preservation has gained growing attention, and many strategies, laws and regulations have been enacted with this purpose. CC and mBRCs are depositories of microorganisms that study and protect biodiversity and make microbial strains and associated knowledge more accessible to the scientific and industrial communities. UNICA-DSMSP is an internationally recognized microbial collection hosted at the Dept. of Medical Sciences and Public Health of the University of Cagliari.

Since the year 2022, UNICA-DSMSP collection has been involved in the project SUS-MIRRI.IT, which aims at improving civil infrastructure and acquiring state-of-the-art laboratory equipment in order to identify and characterize microbial strains, implementing quality management system according to international standards, creating the Italian integrated catalogue of microorganisms, developing new services and training activities aimed at the public and private needs at territory level.

Thanks to the SUS-MIRRI.IT project (granted by NextGenerationEU, National Recovery and Resilience Plan, Code IR0000005), the collection has been able to: acquire cutting-edge laboratory equipment pivotal for characterizing and preserving so far about 600 strains of the collection, mainly represented by LAB and yeasts isolated from various food products; achieve the ISO 9001:2015 certification; implement new services and training activities; set up a disaster plan by storing a copy of the strains in a facility at about 200 km from Cagliari; improve the online accessibility of data trough harmonization of the local database with the national one.

Taking part to the SUS-MIRRI.it project has allowed to improve the management and sustainability of UNICA collection, therefore contributing to the preservation of resources to be exploited for both research purposes and biotechnological applications.

Keywords: Culture collection, SUS-MIRRI.IT, Biodiversity preservation

The SUS-MIRRI.IT project: research, services, and training for sustainable bioscience and bioeconomy by the MIRRI-IT Research Infrastructure

<u>Maria Gullo</u>

University of Modena and Reggio Emilia, Italy

maria.gullo@unimore.it

SUS-MIRRI.IT, funded by the NextGenerationEU programme with a total budget of about 17,000,000, is a project coordinated by the University of Turin and involves 24 Italian Operative Units. The mission is to strengthen the Italian Microbial Resource Research Infrastructure (MIRRI-IT) by the acquisition of cutting-edge equipment, infrastructural improvements, recruitment of high-qualified staff, to valorize microbial resources with associated (meta) data, and to implement top-level services for academia and industry. The project consists of 6 Work Packages (WPs): WP1 drives management, governance, and sustainability; WP2 is involved in microbial Culture Collections consolidation; WP3 focuses on digital activities for the creation of the single-entry point to the National Database of microbial resources and services; WP4 aims to study the biotechnological valorization of microbiomes; WP5 deals with the implementation of offered services and training courses; WP6 is dedicated to communication and dissemination actions. The strategic impact of SUS-MIRRI.IT is to promote partnerships, to encourage aggregation of skills, structures, and bioresources, promoting the transition towards the green economy, and contributing to the sustainability and safety of the environment.

To date, 50 researchers, PhD students, and technicians have been hired; about 80% of the funds for innovative technologies have been used; the online platform with the catalogue of Italian microbial resources holding 37,000 strains of bacteria, filamentous fungi, yeasts, microalgae and viruses has been launched; 29 advanced Training courses have been delivered; 56 new services ranging from microbiological analyses to user-tailored consultancies have been set up; 55 scientific papers have been published. All project updates are communicated by SUS-MIRRI.IT website and social media. An important recently achieved goal is the creation of Italian National Node of the European consortium MIRRI-ERIC, MIRRI-IT.

Keywords: Bioresources, Culture collections, Microbial Resource Research Infrastructure, MIRRI-IT, SUS-MIRRI.IT

Analysis of the genetic variability among Italian local pig breeds

Manolo Cappelloni¹, Maurizio Gallo¹, Alberto Cesarani²

¹ANAS, Italy, ²University of Sassari, Italy

m.cappelloni@anas.it

Within the SUIS.2 project, the Italian pig breeders association (ANAS) conducted a study on Italian native pig breeds that are currently managed with genetic conservation programs: Sarda (SR), Casertana (CT), Mora Romagnola (MR), Cinta Senese (CS), Apulo Calabrese (AC), and Nero Siciliano (NS). The aim of the study was to evaluate the genetic variability of these breeds and, in particular, to analyze their pedigree to investigate the genetic contributions of the founders to the current populations. Using PEDIG software, the following parameters were calculated: pedigree completeness, number of equivalent founders that equally contribute to the genetic variability, and effective number of ancestors (the minimum number of ancestors able to explain the whole genetic variability).

The numbers of animals in the pedigree (rate of pedigree completeness) were: 7,718 (93.02%) for SR, 15,535 (98.72%) for CT, 35,583 (99.86%) for MR, 154,535 (99.9%) for CS, 60,758 (98.06%) for AC, and 75,121 (97.19%) for NS. The number of founders ranged from 21 in MR to 1367 in NS; the number of ancestors ranged from 22 in MR to 1391 in NS. When looking at the effective founders and ancestors, the numbers were lower as expected: effective founders ranged from 3 (MR) to 27 (CT), whereas effective ancestors ranged from 3 (MR) to 25 (CT). It is interesting to note that CS had the largest number of animals in the pedigree, but it had only 66 (11 effective) founders and 77 (10 effective) ancestors. The number of ancestors able to explain 50% of the total variability was very low (<10) for all breeds, except NS (49).

Results of the present study demonstrate that the Italian autochthonous breeds derive from a low number of ancestors and, thus, are characterized by low genetic variability and high levels of inbreeding. ANAS activity is focused on the management of the mating schemes to maintain good genetic variability in the populations.

Keywords: Italian native pig breeds, Genetic conservation

"BERE A SAPERSI": a journey through knowledge, flavors, and Umbrian biodiversity

<u>Beatrice Strinati</u>¹, Michele Capaccioni², Renzo Torricelli², Alberto Palliotti¹, Francesca Maria Sarti¹, Gianluigi Cardinali¹

¹University of Perugia, Italy, ²"Bere a Sapersi" outreach initiative, Italy

beatrice.strinati@dottorandi.unipg.it

Launched in April 2023, "Bere a Sapersi" promotes Umbrian agri-food biodiversity by blending taste culture, scientific dissemination, and sustainability. Through events in wineries, restaurants, and farms, the initiative explores regional products, highlighting the deep connection between territory, traditions, and innovation. Umbria's extraordinary biodiversity is reflected in ancient legumes like lenticchia di Castelluccio, traditional cereals (farro di Monteleone di Spoleto), and unique vegetables like sedano nero di Trevi and aglione del Trasimeno. Native livestock breeds, including Sopravissana sheep and Suino Nero Cinghiato, enrich this heritage. Since 2019, the Ape ligustica has been listed in the Regional Register, playing a vital role in pollination and ecosystem balance. In the wine sector, rare native grape varieties such as Tostolello, Dolciame, Grero, Cornetta, Vaiano, and Lacrima have been rediscovered and reintroduced. Completing the regional ecosystem are microorganisms responsible for traditional food transformations, among Italy's first officially registered microbial genetic resources. During the events, producers and researchers showcase biodiversity's role in sustainable agriculture and food production. Guided tastings reveal how biological diversity enhances gastronomy, economy, and local development. Since 2023, many participating restaurants have introduced newly discovered native products into their menus, expanding market opportunities and raising awareness of Umbrian excellence. The growing network of producers, chefs, and consumers proves that biodiversity is a resource to protect and promote, not only for its environmental value, but also for its cultural and economic impact. More than an event, "Bere a Sapersi" is an invitation to awareness, where BENE and SAPERE intertwine, giving voice to Umbrian traditions and encouraging responsible consumption, conscious choices, and appreciation of authentic local products.

Keywords: Event, Territory, Traditions, Innovation, Agri-food biodiversity

Conservation genomics tools for biodiversity monitoring in three Italian freshwater fish species: Italian chub (*Squalius squalus*), Italian barbels (*Barbus spp.*) and vairone (*Telestes muticellus*)

<u>Licia Colli</u>¹, Elena Petretto¹, Giulia Riccioni¹, Simone Morabito¹, Daniela Ghia², Gianluca Fea², Antonella Carosi³, Massimo Lorenzoni³, Matteo Capurro⁴, Luca Ciuffardi⁴, Giacomo Actis Dato⁴, Paolo Ajmone-Marsan¹

¹Università Cattolica del Sacro Cuore, Italy, ²University of Pavia, Italy, ³University of Perugia, Italy, ⁴University of Genova, Italy

licia.colli@unicatt.it

The genomic variation of three Italian freshwater fish species, i.e. the Italian chub (*Squalius squalus*), the Italian barbels (*Barbus* spp.) and the vairone (*Telestes muticellus*), is currently being investigated as part of the biodiversity monitoring and conservation activities of the National Biodiversity Future Centre NBFC funded by the PNRR (Piano Nazionale di Ripresa e Resilienza).

Freshwater fish, in fact, play an important role as environmental bioindicators in freshwater ecosystems. To ensure long-term survival of these species, a thorough evaluation of their status is fundamental to monitor the levels of molecular variation and identify populations/species with decreasing variability which might impair their adaptive potential. Furthermore, for some of the investigated taxa, e.g. Italian barbels, additional clarifications regarding their phylogenetic relationships and taxonomic status are needed.

To assess the degree of isolation/interconnection between populations and the distribution of genetic variability for the three species across the country, samples were collected from North-western, Central and Southern Italy. The extent of molecular variation will be estimated by both i) direct sequencing of an informative fragment of the mitochondrial cytochrome oxidase I gene (COXI) and ii) scoring nuclear DNA ddRAD (double digest restriction associated DNA) markers. So far, the sampling encompassed 394 Italian chub samples from 39 populations, 228 Italian barbels from 14 populations and, 222 vairone samples from 14 populations. The data production is in progress for both mitochondrial and nuclear markers. The genetic data will be analysed with multiple approaches to provide useful information consistent with the goals of the NBFC, i.e. the monitoring, conservation, restoration, and valorisation of biodiversity in the Italian and Mediterranean landscapes.

Keywords: Conservation genomics, Biodiversity, Italian chub, Italian barbels, Vairone

From morphological traits to milk: evaluation of Teramana goats for conservation strategies

Costanza Cimini, Marco Florio, Francesca Bennato, Lisa Grotta, Giuseppe Martino

University of Teramo, Italy

ccimini@unite.it

The protection and characterization of indigenous breeds is essential to establishing new breeding policies that are sustainable and adapted to climate change. The aim of this study was to monitor the population and characterize the milk from Teramana goats. We used a multistage strategy, first, we conducted a census of the animals and compared their morphological characteristics. It revealed a total of 188 Teramana goats, which were assessed individually for six qualitative and six quantitative morphological traits. For the quantitative traits, the PCA analysis did not reveal distinct clusters among animals from different breeders. For qualitative attributes the chi-square test did not show differences between groups of animals of different breeders, except for qualitative trait "shape of horns". In the second step, we focused on milk characterization using biochemical techniques (Western blot analysis) to examine β-casein and κ -casein, compared with Saanen goats (chosen as a comparison as a more cosmopolitan breed) followed by in silico methods (STRING and Gene Ontology analysis). The results indicated no significant difference in β -casein levels, while a higher abundance of κ -casein was found in Teramana goat milk. Then, we conducted an enrichment analysis using the STRING database, which identified relevant molecular function and biological pathways associated with κ-casein, including positive regulation of lactation, cytolysis and defense response to bacterium. Additionally, the analysis revealed molecular functions such as lysozyme activity.

In conclusion, this study highlights the importance of monitoring indigenous breeds like the Teramana goat to develop breeding policies for their preservation. The findings emphasize the unique biochemical properties of their milk which might have significant implications for dairy production and breed conservation.

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Keywords: Teramana goat, Milk, Biodiversity, Indigenous breeds, Casein

Genetic characterization of local sheep and goat populations in Apulia within the frame of the regional project L.O.C.A.L.

<u>Maria Gabriela Molina^{1,2}</u>, Silvia Bruno¹, Vincenzo Landi¹, Claudia Pierini¹, Maria Selvaggi¹, Grazia Bramante¹, Valentina Biancardi³, Letizia Temerario¹, Nicola Antonio¹, Davide Monaco¹, Maria Elena Dell'Aquila¹, Giovanni Michele Lacalandra¹, Marzia Albenzio³, Elena Ciani¹

¹University of Bari, Italy, ²Universidad Nacional de Cordoba, Argentina, ³University of Foggia, Italy

mariagabriela.molina@unc.edu.ar

Sheep and goat farming under semi-extensive systems represents a sustainable livestock model, exploiting available natural resources in marginal areas and playing a crucial role in providing income to rural communities. Nevertheless, the sector faces significant challenges, including lowgenerational turnover due to the limited attractiveness and profitability of the profession, thus leading some farmers to favor selected high-yield breeds over local genotypes. While this leads to increased production, it also demands higher input costs, often without proportional market returns.

In this context, local breeds, having adapted over time to specific environmental conditions, assure high-quality animal products at competitive prices, yet their economic potential is often hindered by weak market positioning strategies. As a result, the decline in local populations' farming leads to a significant loss of genetic diversity, a concerning issue in the face of climate change. To contribute to the conservation of local sheep and goat populations at risk of genetic erosion, the Apulia Region funded L.O.C.A.L., a project aimed at surveying and genetically characterizing local genetic resources. The focus is on the Grigia del Subappennino Dauno, Antica della Murgia, and Capestrina goat populations, as well as the Gentile Moretta sheep population, which are integral part of the Apulia's ovi-caprine genetic heritage. Overall, more than 1,600 goat and sheep samples were genotyped using several medium-density SNP arrays (i.e., the Goat Genome Consortium 60K array, the Illumina Ovine SNP50 array and the Axiom Ovine Genotyping Array 50K). Preliminary analyses to assess genetic diversity and genetic originality are currently ongoing. In parallel, *ex-situ* conservation efforts are being conducted at the Apulian Regional Livestock Germplasm Bank to preserve genetic material and secure these valuable breeds for future use.

Keywords: Sheep, Goat, Local breeds, Genetic diversity and SNP genotyping

Interesting insights on wild egg hatchability and chick survival in artificial and seminatural settings: preliminary observations from a rock partridge (*Alectoris graeca*) exsitu conservation program

<u>Pedro Girotti</u>¹, Paolo Viola¹, Pedro Girotti¹, Alessandro Rossetti², Umberto Sergiacomi³, Federico Morandi², Michele Croce³, Fabrizio Marricchi⁴, Riccardo Primi¹

¹University of Tuscia, Italy, ²Sibillini Mountains National Park, Italy, ³Umbria Region, Forestry, Mountain, Natural Systems, and Wildlife-Hunting Service, Perugia, Italy, ⁴La Starniana, Onano-Viterbo, Italy

pedro.girotti@unitus.it

The rock partridge (*Alectoris graeca*) is classified as Near Threatened in Europe and Vulnerable in Italy. In 2017, the Sibillini Mountains National Park, the Umbria Region, and the University of Tuscia initiated an ex situ conservation program through the captive rearing of individuals from wild-collected eggs (ISPRA auth. 28382/T-A31) aimed at reinforcing residual populations in the Apennines. However, standardized protocols for successfully transferring and incubating wild eggs of unknown incubation stage are still lacking.

Between June and July from 2017 to 2022, nine nests were located via VHF telemetry from radio-tagged bird. A total of 78 eggs were collected, stored in thermal bag (36-37 °C) and transferred to two breeding centers (La Starniana and Torre Certalda). Egg candling confirmed the fertility of 72 eggs.

In 2017-2018, 37 eggs were fully incubated under controlled conditions (37.6 °C, 80-83% RH) and hatched artificially. Chicks were reared in a heated room, under a heat lamp, with temperatures gradually reduced from 35 °C to 22 °C over 25 days. They were kept inside a circular fence for the first two weeks and then reared in open pens until 60 days post hatching (dph). In 2021-2022, 35 eggs were incubated artificially for 7 days, then transferred to hens (11-12 eggs/hen) for semi-natural hatching and parental rearing until 60 dph. All juveniles were later moved to outdoor aviaries.

A power surge during artificial incubation caused irreversible damage to 20 eggs. Of the 17 remaining, 6 hatched (35.3%). In contrast, semi-natural incubation yielded 31 chicks from 35 eggs (88.6%). Survival at 90 days post-hatching was 83.3% for those raised without hen and 90.3% for hen-reared chicks.

Preliminary results suggest that semi-natural incubation and rearing represent a more effective and reliable approach, supporting both high hatching success and early chick survival. Further specifically designed studies are recommended to optimize the protocols.

Keywords: Galliformes, Incubation techniques, Rearing methods, Captive breeding, Conservation management

Monitoring and managing of animal genetic resources at risk of extinction in Italy

Roberto Steri, Giacomo Contò, Luca Buttazzoni

Council for Agricultural Research and Economics (CREA) - Research Centre for Animal Production and Aquaculture, Italy

roberto.steri@crea.gov.it

Within the frame of FAO's Global Plan of Action for Animal Genetic Resources (GPA-AnGR), the Italian livestock production system has planned and implemented a powerful intervention in the management and preservation of animal genetic variability. The initiative involved National and Regional Governments, Breeder Associations and Universities and it was co-funded by the European Agricultural Fund for Rural Development (EAFRD), and the National Rural Development Program (NRDP 2014-2022).

The plan strategic objectives were outlined according to the four GPA priority areas (characterization and monitoring; sustainable use and development; conservation; and policies). The ultimate goal of the program was to preserve farm animal biodiversity while improving animal welfare and the environmental impact of animal farming.

Projects covering 9 livestock sectors were funded (Dairy cattle, Beef cattle, Dual purpose cattle, Buffaloes, Horses and donkeys, Sheep and Goats, Swine, Rabbits and Poultry). Overall, 18 Breeder Associations and 8 University worked on 213 animal breeds. A total of over 690,000 phenotypic characterizations and 234,000 genetic/genomic characterizations were carried out on 200 breeds. About 70 indexes were developed and published: 41% related to animal welfare, 29% to reproductive efficiency, 21% to environmental impact and 9% to biodiversity evaluation. Germplasm collections have been established for 112 breeds, which will implement the National Germplasm System to be set up. A total of 113 descriptive sheets of autochthonous breeds were published on the institutional breeder association websites.

The results obtained allowed for a more precise assessment of genetic erosion, for preparing rational mating plans, for estimating genetic distances among breeds, for the identification of genetic variants indicators of disease resistance, development of new welfare indicators, reduction of GHG emissions and the improvement of reproductive and feed efficiency.

Keywords: Characterization, Conservation, Genetic erosion, Policies

Seeds of Resilience: Safeguarding Umbrian Agro-Biodiversity for Future Generations

<u>Marco Caffarelli</u>¹, Francesca Maria Sarti², Alessandro Dal Bosco², Samira Giovannini², Luciano Giacchè³, Alessia Dorillo¹

¹3A Parco Tecnologico Agroalimentare dell'Umbria, Italy, ²Università di Perugia, Italy, ³CEDRAV, Italy

marcocaffarelli@tiscali.it

Umbria boasts a rich heritage of agro-biodiversity, essential for ecosystem resilience and sustainable development. Since 2013, the Regional Commission has safeguarded this genetic wealth by registering 18 animal breeds in the Regional Register of Autochthonous Genetic Resources, each documented with a dedicated descriptive form containing characteristics, distribution, and conservation strategies. The registered breeds include 2 sheep breeds (Appenninica, Sopravissana), 1 goat breed (Facciuta della Valnerina), 3 equine breeds (CAITPR, Del Catria, Maremmano), 3 asinine breeds (Sardo, Amiata, Bianco dell'Asinara), 5 poultry breeds (Livorno Argentata, Livorno Bianca, Livorno Dorata, Livorno Nera, Ancona) along with the Trota Fario, Carpa del Trasimeno, Luccio del Trasimeno, and Ape ligustica. A key conservation effort focuses on reconstituting the ancient Suino Nero Cinghiato breed, known only from historical frescoes. This back-breeding program seeks to restore lost genetic diversity, promote sustainable farming, and enhance traditional Umbrian products. Registration in the Regional Register plays a crucial role in preventing extinction and also enhancing breed value through incentives, short supply chain projects, and agro-food promotion initiatives. Despite the efforts significant challenges persist, including climate change, rural depopulation, and the declining profitability of traditional farming. Recent surveys show population variability among breeds, ranging from a few hundred to several thousand individuals, underscoring the urgency of conservation. Addressing these issues requires integrated strategies and represents an opportunity to develop a sustainable agricultural model that balances environmental conservation, economic growth, and cultural heritage. The future of Umbrian agro-biodiversity depends on a strong synergy between institutions, breeders, and scientific research, ensuring that these genetic resources are preserved for future generations.

Keywords: Animal breed, Regional law, Recovery, Safeguard

Characterization of goat milk from three local breeds in the focus of biodiversity preservation: chemical composition and antioxidant properties

<u>Angela Gabriella D'Alessandro</u>, Nicola Palumbo, Roberta Savina Dibenedetto, Alessio Di Luca, Sara Cifarelli, Giovanni Martemucci

University of Bari Aldo Moro, Italy

angelagabriella.dalessandro@unba.it

In Italy, there are a large number of native breeds well adapted to the territorial realities, which deserve particular attention for their productive valorization and protection in terms of maintaining biodiversity and territorial identity. The consumption of goat milk and its derivatives is taking ever greater interest, due to its peculiar nutritional and biofunctional qualities. Much attention is to be pay to the antioxidant capacity for its potential positive effects on human health by protecting the body against damage caused by oxidative stress and preventing many diseases. Antioxidant properties of milk is affected by different factors. The aim of this study was to determine the chemical composition and antioxidant properties of milk of three local goat breeds reared in Apulia region (southern Italy). Milk samples of Capestrina, Grigia del Sub-Apennino Dauno (Grigia-SAD) and Garganica breeds were collected during the same lactation period (spring, middle lactation) and analyzed for fat, protein, casein and lactose contents, and antioxidant capacity based on total phenol content (TPC), ABTS and DPPH assays. No differences were found among the breeds for the gross composition parameters (P>0.05) while antioxidant properties of milk showed significant differences (P<0.05). Compared to Garganica breed, the highest (P<0.05) total phenol content and DPPH values were found in Capestrina breed, while the highest ABTS value (P<0.05) in Grigia-SAD. In conclusion, these findings give a first knowledge on the antioxidant properties of the local Capestrina, Grigia-SAD and Garganica goat breeds, and provide useful information for their productive valorization, in the focus of biodiversity preservation.

Keywords: Goat milk, Local breeds, Chemical composition, Antioxidant properties, Biodiversity preservation

GreenTraINT - Green Training INTernational Program for agriculture and livestock farming and conservation

<u>Paola Mattarelli</u>¹, Caterina Spiezio², Maria Luisa Dindo¹, Francesco Spinelli¹, Daniel Etongo³, Maryanne Marie⁴, Allen Cedras⁵, Stefen Simm⁶, Matthias Noll⁶, Camillo Sandri⁷

¹University of Bologna, Italy, ²Fondazione Zoom, Natura Viva, Bussolengo, Italy, ³University of Seychelles, ⁴Seychelles Institute Horticulture Agriculture, Seychelles, ⁵Seychelles Parks and Gardens Authority, Seychelles, ⁶University of Couburg, Germany, ⁷Natura Viva - Immersive Parks, Italy

paola.mattarelli@unibo.it

The total land area of Seychelles is 455 km² spread across 115 islands, of which 50% of the land mass is under protection. Seychelles still depends on imported food items, with an estimated 80% of food consumed locally imported into the country. The GreenTraINT, a two-year ERASMUS+ project, aims to improve the educational offerings in agriculture, livestock farming, and conservation in the Seychelles. Started in November 2024, this project, coordinated by the University of Bologna, joins partners from Italy, Germany, and the Seychelles to build a valuable platform for exchanging ideas and perspectives among international partners. Integrating academic knowledge with hands-on expertise is a unique opportunity to bridge academic know-how with practical fieldwork to tackle sustainability challenges effectively through international cooperation in shaping innovative and practical solutions for agricultural and environmental management.

Based on the needs identified in Seychelles through a survey conducted on-site, the key objectives of the project are enhancing educational opportunities in agriculture, livestock farming, and conservation through international cooperation, developing innovative teaching methodologies that integrate field-based experiences with theoretical knowledge and promoting sustainability and biodiversity conservation through interdisciplinary approaches. The first steps of cooperation reinforced the project's commitment to fostering a dynamic and applied learning environment for students and professionals in the field.

The results provided valuable insights into the existing educational gaps and the specific areas where GreenTraINT can make a tangible impact from multiple perspectives -educational, economic, and environmental- highlighting its relevance for agricultural development, biodiversity conservation, and policymaking to ensure its long-term success.

Keywords: Biodiversity, Higher education, Environment, Need analysis, Partnership

The PRO-GRACE (Promoting a Plant Genetic Resource Community for Europe) project

Maria Antonietta Palombi (on behalf of the PRO-GRACE consortium)

CREA – Research Centre of Viticulture and Enology, Velletri, Italy

mariaantonietta.palombi@crea.gov.it

Plants are the basis for all food, feed and renewable bioenergy production. They are essential for the transition from a fossil-based to a bio-based economy. Plant genetic resources (PGR) play a key role in ensuring this transition, as well as food security and climate change mitigation. As reported in the EURISCO database, more than 2 million plant accessions are conserved ex situ in 410 institutions in Europe and associated countries. In addition, even more diversity is found in situ in Europe's farmlands and wild habitats. There, it contributes significantly to agricultural resilience and climate change mitigation. Detailed information on ex situ collections is fragmentary at best and almost non-existent for in situ collections. Due to limitations in ex situ infrastructure and management, climate change, habitat loss and invasive/alien species, a significant proportion of these resources could be lost in the next decade. The 2016 ESFRI (European Strategy Forum on Research Infrastructure) Roadmap identifies a clear gap 'Plant facilities - unlocking green power', namely the lack of dedicated plant genetic resources (PGR) research facilities. The PRO-GRACE project (grace-ri.eu/prograce) coordinated by Italy, involving 31 partners from 17 countries, aims to fill this gap by developing the visionary concept of a European research infrastructure that brings together genebanks and other European institutions working on PGRs, connects them to global genebank organisations and other ESFRI infrastructures, and facilitates their transformation from mere plant or seed repositories into a networked system of dynamic research centres. The ultimate aim of this infrastructure will be to catalogue, describe, conserve and enhance the agrobiodiversity of European plants and to translate the results into conservation practices and agricultural innovation through 7 work packages: WP1 - Plant genetic resources inventory and information systems; WP2 - Quality certified ex situ and in situ management; WP3 - Research infrastructure; WP4 - Plant genetic resources for food; WP5 - Research Infrastructure concept, social and regulatory aspects, governance and financial plan; WP6 - Communication, dissemination, exploitation and training and WP7- Scientific coordination and management.

Keywords: Agrobiodiversity, Research infrastuctures, Conservation, Collections management, Climate change

Promotion of agrobiodiversity: diffused plantation of orchards for biodiversity in urban and nor agricultaral areas for local communities

Isabella Dalla Ragione

Fondazione Archeologia Arborea ets – Umbria, Italy

info@archeologiaarborea.org

The forty-year work of research, conservation and promotion of Archeologia Arborea, created an orchard of old local varieties, as reservoire of genes and culture, to share with the new generations Foundation Archeologia Arborea is created for corservation of memory and knowledge but also for the diffusion of agrobiodiversity.

The proposal of orchards of biodiversity has emerged as a contribution to the maintenance of agrobiodiversity in non-agricultural areas or urban areas, to keep our cultural and cultural roots.

The orchards we propose will be made up of ancient local varieties, so each place will be different and unique. The basic orchard module includes different species and all the measures for a sustainable agro-ecosystem, including intercropping with herbaceous and shrubby plants to enrich the soil with organic matter and to favor beneficial insects as much as possible. They are proposed for different situation and different sizes: municipalities or private companies, therapy areas, historycal gardens.

Collaborations have already been activated with the Umbria Chamber of Commerce, the Municipality of Perugia, and L'Abbondanza Group.

The orchards created could have different functions:

Educational; good nutrition and health passes through knowledge and respect for seasonality; children and adults will be able to see and taste fruits that we are no longer used to eating.

Evocative; fruit trees were strong symbols, present often in art. Furthermore, their beauty in all seasons must be emphasized.

Inclusive; orchards will be a meeting point between different generations; the elderly with their knowledge will be able to communicate to the new generations. The places will be easily accessible to everyone.

Productive; these orchards will be cultivated to encourage community harvests. They will be managed with organic farming systems and will guarantee different fruit in different seasons.

Keywords: Local fruit varieties, urban orchards, Community orchards, Agrobiodiversity

The BIO-MASTER project: development of a standardized protocol for bioaerosol monitoring and classification

<u>Federica D'Alò</u>¹, Olga Gavrichkova¹, Salvatore Romano², Mattia Fragola², Paola Pollegioni¹

¹Research Institute on Terrestrial Ecosystems (IRET), CNR, Italy, ²University of Salento, Italy

federica.dalo@iret.cnr.it

The BIO-MASTER (BIOaerosol Monitoring And classification: development of a Standardized procedure by integrating different data analysis Techniques and Experimental Research methodologies) is a PRIN2022 project aiming to establish a standardized protocol for bioaerosol monitoring and classification, focusing on bacteria, fungi, and pollen. It explores relationships with air pollution levels (PM10 concentrations), seasonality, human health, and environmental factors. This study seeks to address the variability in experimental designs and inefficiencies in current methodologies. Given the low environmental concentration of bioaerosols, obtaining sufficient DNA for molecular characterization is crucial, and the choice of collection substrate influences DNA recovery efficiency. To address this, standardized procedures for collecting both biogenic and non-biogenic particles were developed, starting with tests on commonly used filter types, including quartz and Teflon, whose effects on DNA recovery are not well understood.

Two intensive monitoring campaigns were conducted at the University of Salento in Lecce across two seasons: winter (Dec 2023-Mar 2024) and summer (Jun-Oct 2024). Air samples were collected using a Leland Legacy Personal Sample Pump at a flow rate of 10 L/min for 48 hours on weekdays and weekends with two filter types. DNA was extracted, quantified, and sequenced on the MiSeq platform for species-level resolution of eukaryotic and prokaryotic communities.

The BIO-MASTER project provided guidelines for standardizes bioaerosol monitoring and classification. It improves our understanding of aerosol and bioaerosol characteristics, seasonal variations, and their environmental and health impacts. The comparison of filter efficiency aims to optimize sampling methods for: 1) reconstructing microbial community diversity in relation to pollution levels, and 2) detecting and identifying potential opportunistic human and plant pathogens in particulate matter.

Keywords: Bioaerosol monitoring, Microbial community, Air pollution, Human health, Sampling standardization

Session: Biodiversity in cropping systems

A multi-year study on soil biological quality: key insights for sustainable vineyard management

<u>Isabella Ghiglieno</u>¹, Anna Simonetto¹, Fabio Gatti¹, Pierluigi Donna², Marco Tonni², Leonardo Valenti³, Gilioli Gianni¹

¹University of Brescia, Italy, ²Sata Studio Agronomico Società Benefit, Italy, ³University of Milan, Italy

isabella.ghiglieno@unibs.it

The importance of soil biodiversity in viticulture has received growing attention in recent years. Edaphic arthropod communities, which represent over 85% of soil fauna species richness, play a pivotal role in maintaining the biodiversity and ecosystem functioning of vineyard soils. Their responses to soil characteristics and management practices make them effective bioindicators of soil quality. Understanding the diversity of soil arthropods also contributes to enhancing ecosystem services they provide, offering valuable insights to guide wine producers toward more sustainable vineyard management.

This study presents the findings of a multi-year research investigating the biological quality of Italian vineyard soils and the influence of environmental variables and management practices on soil arthropod communities. Since 2014, a comprehensive survey has been carried out across several important Italian wine regions, resulting in a substantial dataset of 654 records by 2023. To quantify soil biodiversity, the QBS-ar Index (Soil biological quality Index for arthropods) was used. This index serves as a key tool for assessing soil health, which includes physical, chemical, and biological properties. This research specifically explores the relationship between the QBS-ar Index, environmental factors, and vineyard management practices.

This extensive data collection offers a valuable case study demonstrating how biological data can provide insights into ecosystem responses to soil conditions changes. The large dataset and geographical variability of the observations allow to reveal the impacts of soil abiotic conditions and vineyard management practices on soil arthropod communities. This research can help to provide the scientific basis for developing supports for decision in vineyard soil management, promoting ecological transition, and advancing sustainability in viticulture.

Keywords: Biodiversity, Viticulture, Soil biological quality, Soil arthropods, Vineyard management

Session: Biodiversity in cropping systems

Agronomic and qualitative evaluation of four cauliflower landraces in Puglia region (Southern Italy)

<u>Annalisa Somma</u>, Silvia Bitritto, Onofrio Davide Palmitessa, Angelo Signore, Beniamino Leoni, Pietro Santamaria

University of Bari Aldo Moro, Italy

annalisa.somma@uniba.it

Cauliflower (Brassica oleracea var. botrytis) is one of the most widely cultivated brassicaceous crops in the Puglia region (Southern Italy). This region boasts significant agrobiodiversity, including several promising cauliflower landraces. "Cima di Cola" (CDC), "Agostana" (AGO), "Settembrina" (SET), and "San Martino" (MAR) are highly valued at the local level for their distinctive organoleptic properties. To evaluate their agronomic, commercial, and nutritional properties, these landraces were compared to the commercial hybrid variety "Emeraude" (IBR), which is cultivated in the same region. All the varieties produce light-green closed inflorescence (heads). The plants were grown in an open field in Mola di Bari (BA) from late July (transplanting) to mid-February 2024 (30 weeks), at a density of 2.6 plants/m². Drip irrigation was applied during the early growth stages, and cultivation followed local agronomic practices. All aboveground plant organs and heads were described using the morphophysiological standard descriptors of GIBA (Gruppo di lavoro Biodiversità Agricola) and the International Union for the Protection of New Varieties of Plants (UPOV). Yield, firmness, colour and phytochemical composition of the cauliflower heads were also analysed. SET, AGO, and MAR began producing at 13 weeks after transplanting (WAT), followed by IBR at 19 WAT, and CDC at 28 WAT. On average, the landraces produced 1.17 kg/m² of inflorescences, with a dry matter content of 8.3 g/100 g of fresh weight, which were 41.3% and 20.3% lower compared to IBR, respectively. While head height, diameter, and chroma did not differ significantly among the varieties, IBR exhibited the highest firmness, while CDC the highest colour lightness. The ongoing phytochemical analysis will complement these preliminary findings to explore the nutritional potential of the abovementioned landraces.

Keywords: *Brassica oleracea* var. *botrytis*, Agrobiodiversity, Descriptors, Yield, Nutritional profile

Session: Biodiversity in cropping systems

Bambina: a minor Apulian olive cultivar combining nutraceutical value and agroecosystem resilience

Lisa Fiorentino¹, Federica Nevira², Silletti Roccangelo², Cinzia Montemurro², Valeria Scaglione², Volpicella Mariateresa², Francesco Caponio², <u>Wilma Sabetta¹</u>

¹CNR-Institute of Bioscience and BioResources, Italy, ²University of Bari Aldo Moro, Italy

wilma.sabetta@cnr.it

In Italy, the Apulia region is renowned for its extensive olive biodiversity, encompassing a vast array of autochthonous germplasm that plays a crucial role in the regional economy and cultural heritage. The preservation and valorization of this biodiversity are essential for sustaining healthy agro-ecosystems, promoting local olive varieties, and enhancing the marketability of their high-quality food products. This study emphasizes the importance of characterizing minor olive genotypes, such as the cultivar Bambina, which demonstrates rusticity and remarkable adaptability to diverse climatic conditions.

The drupes of cv Bambina were processed using two milling strategies: conventional and nutraceutical. The latter involves the application of low temperatures throughout all stages of drupe processing and oil extraction. Genetic and chemical analyses of the resulting olive pastes and oils revealed a high content of bioactive compounds, such as total phenols and tocopherols, in particular in nutraceutical milling. These compounds contribute to the oxidative stability of the oil and provide significant benefits to human health. The expression levels of genes involved in both vitamin E biosynthesis (VTE1, VTE2, VTE3, etc) and oxidative status regulation (POD and LOX) were significantly higher in cv Bambina compared to cv Coratina.

The qualitative properties of Bambina oil make it comparable to that of the renowned cv. Coratina, underscoring its potential as a valuable resource for nutraceutical applications. By focusing on genetic characterization and the valorization of local cultivars, this research aims to ensure the long-term sustainability of olive cultivation in Apulia while contributing to global efforts to mitigate the impacts of climate change on agriculture.

Keywords: *Olea europaea*, Biodiversity, Nutraceutical milling, Bioactive compounds, Oxidative stability
Biodiversity as a measure of sustainability: impact of agricultural management on soil prokaryotic diversity of rice fields

<u>Paola Quatrini</u>, Giulia Chiommino, Giorgio Schiera, Domenico Schillaci, Angelo Troia, Valentina Catania

University of Palermo, Italy

paola.quatrini@unipa.it

Rice paddies are unique agroecosystems where soil bacterial communities are crucial for nutrient cycling, soil fertility, and ecological balance. However, the effects of agricultural practices on these communities are not fully understood. This study explores the composition, diversity, and functional potential of soil bacterial communities in conventionally and organically managed italian rice fields, with a special focus on methanogenic Archaea and methanotrophic Bacteria due to their impact on climate altering gas emissions.

The study was conducted in three areas of the western Po Valley, where sediments from conventional and organic rice paddies, along with nearby natural wetlands were sampled. Total DNA extracted from sediments was quantified and related to the sediment dry weight, as a proxy of microbial biomass. The sediment microbiota was analyzed by Illumina sequencing of the 16s rRNA gene. The sediment DNAs were probed by PCR to detect the methane oxygenase-encoding gene pmoA.

Wetlands and organic rice fields exhibited higher microbial biomass than conventional rice fields. Greater bacterial diversity was detected in organic rice fields, indicating that organic practices support richer microbial ecosystems. The distribution of methanogenic Archaea is indicative of a clear distinction between cultivated and natural areas, where they are more abundant. In contrast, methanotrophic bacterial genera are more abundant and diverse in organic rice paddy areas although the key gene of methanotrophy was detected in all areas. The study highlights the critical role of agricultural practices in the modeling of soil microbiota and focuses on the search for key taxa as bioindicators. By integrating biotic and environmental parameters, the research offers insights to promote sustainable management of rice fields.

Keywords: Organic rice cultivation, Conventional rice cultivation, Methane cycle, Wetlands

Biodiversity returns. From germplasm banks to cultivated fields, a targeted and participatory use of conserved germplasm

Mauro Gramaccia¹, Valentina Dugo², Ferdinando Desantis¹, Alessia Dorillo¹

¹3A Parco Tecnologico Agroalimentare Dell'Umbria, Italy, ²Consorzio AVO, Italy

mgramaccia@parco3a.org

The Umbria Region has promoted and financed, with PSR/CSR funds, multiple activities aimed at research, conservation, study of Agrobiodiversity, at the same time providing indications through a specific law (L.R. 12/2015, Capo IV). The first project dating back to 2000 led to the creation of a Germplasm Bank of herbaceous species that today collects almost 300 different local accessions. To address the ever-increasing difficulties that farmers encounter in using their own company seeds, 3A-PTA has started an experiment in collaboration with some farmers in 2022 on local legume varieties (Chickpea, Grass Pea, Lentil, Roveja).

The field trials involved the accessions of Lentil and Roveja (2023); Lentil and Chickpea (2024); Lentil, Chickpea and Grass Pea (2025). Together with the company varieties, the other Umbrian accessions available in the regional collection were evaluated and also compared with materials requested outside the region from other Banks or Companies. After the randomized block varietal comparison trials, the accessions were also subjected to field multiplication to increase the stocks and to carry out agronomic evaluations.

At the moment the data have allowed to characterize 24 accessions of Lentil, 6 of Roveja, 16 of Chickpea and 21 of Grass Pea (in progress). From the data collected so far, also discussed together with the farmers, some initial indications have emerged on the most interesting typologies and that, in the case of Lentil, have led to the creation of a population obtained by mixing 9 different local accessions.

Studies are still ongoing and the involvement of professionals in the intentions should contribute to ignite and increase interest in Agrobiodiversity. Paths are also being initiated that allow us to overcome the critical issues encountered and reintroduce, in compliance with the rules, these varieties among farmers.

Keywords: Local varieties, Legumes, Participatory selection

Chemical composition of essential oils from *Smyrnium olusatrum* L. (Apiaceae) ecotypes from Salento

Carmine Negro, Eliana Nutricati, Erika Sabella, Rita Accogli, Luigi De Bellis

University of Salento, Italy

carmine.negro@unisalento.it

Smyrnium olusatrum, well known as wild celery or Alexanders, is a biennial herb belonging to the Apiaceae and used for many centuries as an edible vegetable because of the aromatic flavor of its parts. The entire plant is used for culinary purposes, either raw or cooked. In addition to its traditional culinary uses, Smyrnium has also been utilized for its therapeutic properties for urinary system and prostate disorders, gynecological diseases, gastrointestinal pain, and indigestion. The family Apiaceae is well-known for its ability to produce and store volatile oils in its secretory ducts located in the vegetative and reproductive organs. In the present work the composition of essential oils obtained from different organs of S. olusatrum collected from March to April in five different sites of Salento in Apulia region, was investigated by gas chromatography. The chemical profiles of essential oils of *S. olusatrum* growing in Salento area were similar, although quantitative differences in marker compounds have been highlighted. The results suggest that the wild populations of Smyrnium represent a rich source of isofuranodiene, a furanosesquiterpenoid, a compound found in few other plants. Isofuranodiene has potential applications as hepatoprotective, neuritogenic, anti-inflammatory and anticancer effects. Therefore, the Smyrnium essential oil (EO) may gave interesting pharmaceutical applications. In the framework of the project: Biodiversity of Apulian Non-Fruiting Horticultural Species - BiodiverSO Veg (CUP: B97H22003760009).

Keywords: Smyrnium olusatrum, Apiaceae, Essential oils, Furanosesquiterpenoid

Conserving and enhancing local agrobiodiversity: exchange between Italy and the Sahel region to save local varieties and NUS and promote sustainable food value chains

<u>Maria Gonnella</u>¹, Rosa Anna Siciliano², Francesca Boari¹, El Bilali Hamid³, Filippo Acasto⁴, Jacques Nanema⁵, Romaric Nanema⁵, Lawali Dambo⁶, Reine Fanta Sheirita Tietiambou⁷, Iro Dan Guimbo⁶

¹Istituto di Scienze delle Produzioni Alimentari, CNR, Italy, ²Istituto di Scienze dell'Alimentazione, CNR, Italy, ³International Centre for Advanced Mediterranean Agronomic Studies of Bari (CIHEAM-Bari), Italy, ⁴Italian Agency for Development Cooperation (AICS), Italy, ⁵Joseph Ki-Zerbo University, Ouagadougou, Burkina Faso, ⁶Abdou Moumouni University, Niamey, Niger, ⁷University Centre of Gaoua, Bobo-Dioulasso, Burkina Faso

maria.gonnella@cnr.it

Recovery and enhancement of agrobiodiversity are recognized worldwide as a means to save local varieties and promote food security and sustainable production. BiodiverSO research projects, funded by the Rural Development Program (PSR) in the Apulia region (Italy), support the regional network of farmers and seed savers to recover and enhance local agrobiodiversity. The expertise gained in BiodiverSO projects is the basis of the exchange of knowledge between Italy and the Sahel region within the internship organized in the framework of the project "SUSTLIVES: SUSTaining and improving local crop patrimony in Burkina Faso and Niger for better LIVes and EcoSystems" (EU DeSIRA program). The main objective of the internship is to undertake training on agrobiodiversity management towards more sustainable and resilient food systems in the two countries.

BiodiverSO VEG and Karpos projects, while spreading sustainable and agroecological cultivation techniques and strengthening informal community biodiversity management systems, have in common with SUSTLIVES their focus on niche crops or neglected and underutilized species (NUS). During the last edition of the internship all the activities developed in BiodiverSO were discussed. The program will be implemented again in 2025 for eight interns from Burkina Faso and Niger.

Nutritional and functional valorisation of NUS, agroecological criteria for the agrobiodiversity management, creation of local supply chains and related income, and increase in the use of vegetables for healthier diets were central topics of the last year's exchange program, animating the discussion on several points. The new edition is expected to be more in-depth and livelier since various points of view and knowledge needs will be on the table.

Keywords: Agrobiodiversity, Neglected and Underutilized Species (NUS), BiodiverSO VEG, BiodiverSO Karpos, Sustlives

Defining soil quality indicators in vineyards under conventional and organic practices

Oussama Bouaicha¹, Nadine Praeg², Alexander Schönafinger³, Georg Niedrist³, Tanja Mimmo¹, Paul Illmer², <u>Luigimaria Borruso¹</u>

¹Free University of Bolzano, Italy, ²Universität Innsbruck, Austria, ³Institute for Alpine environment, Eurac research, Bolzano, Italy

luigimaria.borruso@unibz.it

Intensive grape production has dramatically impacted chemical, physical, and biological soil fertility due to the significant inputs of agrochemicals and fertilizers. This work aims to identify the biotic and abiotic drivers of soil quality and the keystone species influencing it, applying an innovative agroecological network analysis in vineyards based on their management and geographic location. The sampling area is in South Tyrol (Italy), one of the highest-quality viticultural regions in Italy. One thousand eight soil samples associated with *Vitis vinifera* cv. Pinot Noir were collected from 42 vineyards (22 organic and 20 conventional) distributed along a geographic gradient from south to north over two seasons (spring and summer). The soil was analyzed to determine its chemical properties, including carbon (C), nitrogen (N), phosphorus (P), and pH. Agrochemicals were extracted using the QuEChERS method and quantified using LC-MS. Furthermore, the soil will be examined for its enzymatic activity and biodiversity, encompassing bacterial, fungal, and faunal diversity.

Preliminary results showed that conventional vineyards had significantly higher total organic C (TOC), inorganic C (IC), total C (TC), and total N (TN) compared to organic vineyards (P < 0.03), while the pH was significantly lower in conventional vineyards (-7.15%). However, there was variability among sampling areas and seasons. In the northern area, pH, TOC, TC, IC, and TN were significantly higher in organic vineyards (p < 0.001), while they were lower in the other areas. The phosphorus content did not significantly differ between management practices and geographic areas.

Finally, agrochemical residues were found to accumulate significantly more in conventional vineyards compared to organic, while seasonal variation and geographic location had minimal effects. Together with enzymatic and microbial results, the networks will provide a potential monitoring approach for sustainable agriculture.

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Keywords: Vineyards, Biological, Conventional, Soil quality, Sustainability

Dominance Vulnerability Index (DVI): a biodiversity index for early prediction of weedinduced yield losses

<u>Valerio Cirillo</u>, Ottavia Puma, Claudio Russo, Nausicaa Pollaro, Antonio Marciano, Marco Cepparulo, Fabrizio Cartenì, Albino Maggio

University of Napoli Federico II, Italy

valerio.cirillo@unina.it

Chemical weeding causes the over-simplification of the agroecosystems, leading to the establishment of dominant species that are the main cause of crop yield losses. The ability to selectively remove only these species, thus rebalancing the species equilibrium, can be an effective strategy to contextually preserve yield and biodiversity. The aim of this study was to identify a biodiversity index calculated at the early stage of weed infestation, able to predict which areas in the field would be more susceptible to weed overgrowth (i.e., high biomass), and thus where and how the weed removal is necessary to contain yield losses.

Triticum aestivum var. Rebelde was cultivated in Portici (NA) and Bellizzi (SA). Two treatments, namely weed-free and weedy, have been randomly assigned to different plots. Weed number and biomass have been measured per species at the tillering and heading stage. Wheat biomass and yield have been measured at kernels maturity. On the datasets obtained, we developed a novel biodiversity index, named Dominance Vulnerability Index (DVI).

DVI shows high and significant correlation with total weed biomass at the heading stage of wheat, and with wheat yield losses at harvest both in Portici and Bellizzi fields. Moreover, DVI allowed the identification of the dominant species, and the amount to be removed to maximize the equitability of the production. The linear equation obtained allowed us to calculate that, once the maximum equitability was reached (DVI = 0), the impact of weeds on yield was significantly reduced compared to conditions where dominant species were present.

DVI can be a functional approach to guide weeder robots to remove only dominant weeds, while leaving non-competitive species in the field. Restoring species balance will preserve crop yields while maintaining high levels of biodiversity in the fields for the maximization of the ecosystem services provided by agriculture.

Keywords: Dominant species, Wheat, SSWM, Ecology

Effect of cytokinin and inductive treatments on the regrowth and rooting of encapsulated microcuttings for olive conservation

Maurizio Micheli¹, Luca Regni¹, Mara Rondolini¹, Daniel Fernande da Silva², Cristian Silvestri³,

¹University of Perugia, Italy, ²Universidade Federal do Paraná, Jardim das Américas, Brazil, ³University of Tuscia, Italy

maurizio.micheli@unipg.it

Germplasm preservation could be considered as one of the most significant applications of encapsulation. Synthetic seeds, which are the end product of this technology, can effectively support the conservation of plant material over short, medium, and long-term periods under various temperature conditions, ranging from frigoconservation to cryopreservation systems. Suitable protocols were already identified in several fruit species, but not in olive (Olea europaea L.). Unsatisfactory levels of regrowth and conversion of encapsulated unipolar propagules (microcuttings) seem to limit the application in this species, depending on genotype traits, different rooting ability or effectiveness of inductive treatments for the differentiation of the root primordia. This work was conducted with the aim to identify a suitable protocol for the production of synthetic seeds of "Moraiolo", widespread in Central Italy and collected in our laboratory as a pilot olive cultivar. Compared to previous studies, these experiments allowed for highlighting the influence of the nutritive conditions prior the collection of the olive microcuttings on their sprouting (regrowth) after the encapsulation in a calcium alginate matrix and sowing in aseptic conditions. A less expensive formulation of zeatin (a natural cytokinin) added to the medium during the multiplication phase allowed the improvement of the sprouting of encapsulated propagules of olive (from 30 to 67%). In addition, the effect of two different root inductive treatments (classic and innovative) positively influenced the rhizogenic ability of synthetic seeds of olive, showing the effectiveness of the innovative protocol in terms of conversion and average length of roots. In the overall evaluation of the experiment, the well-known "genotype-dependence" should not be neglected, which may at least partly account for the reduced conversion capacity (limited to 47%) influenced by the reduced rhizogenic aptitude of the "Moraiolo" cv..

Keywords: Olea europaea L., Synthetic seed, Zeatin, Sprouting, Conversion

Glucosinolates profiles and antioxidant activity of *Brassica rapa* subsp. *sylvestris* from Salento area

Eliana Nutricati, Alessandro Frontini, Carmine Negro, Rita Accogli, Luigi De Bellis

University of Salento, Italy

eliana.nutricati@unisalento.it

Brassica rapa subsp. *sylvestris* is a vegetable crop widely distributed in Southern Italy, their consumption has been related to human health due to their phytochemicals, such as glucosinolates and phenolic compounds that influence different physiological functions including antioxidant activity, enzymes regulation and apoptosis control and the cell cycle. In Apulia region many cultivated landraces are characterized by wide phenotypic variability and named according to length of time between sowing and inflorescence appearance as "cima di rapa cinquantina and sessantina" and "rapacula". Many cultivars of this species and the resulting large metabolic variation have been obstacles for systematic research of the plant. Metabolomic analysis of different landraces of *Brassica rapa* L. subsp. *sylvestris* (L.) Janch. var. *esculenta* was performed. Inflorescences from six landraces growing in three areas of Salento were collected in April and May 2024.

The profile of glucosinolates and phenolic compounds in relation to the antioxidant activity of six *Brassica rapa* landraces were determinate and compared. The qualitative and quantitative compositions of metabolites were determined by HPLC/MS (high performance liquid chromatography/mass spectroscopy) technique.

We found 11 different glucosinolates and two main phenolics, kaempferol and quercetin in each extract analyzed.

This study provides a starting point for subsequent genetic characterization with the aim to preserve genotypes with relevant biological activities.

In the framework of the project Biodiversity of Apulian Non-Fruiting Horticultural Species - BiodiverSO Veg (CUP: B97H22003760009).

Keywords: Brassica rapa subsp. sylvestris, Glucosinolates, Phenolics, HPLC/MS

Impact of cover crops on belowground microbial diversity in a Mediterranean olive grove

<u>Cristiana Sbrana</u>¹, Maria Grazia Caruso¹, Claudio Porqueddu², Rita Melis², Giovanni Altana², Maria Ventimiglia¹

¹Institute of Agricultural Biology and Biotechnology (IBBA), CNR, Pisa, Italy, ²Institute for Animal Production System in Mediterranean Environment (ISPAAM), CNR, Sassari, Italy

cristiana.sbrana@cnr.it

Cover crops (CCs) are temporary plants grown between main crops to improve soil health, biodiversity, and nutrient cycling while reducing erosion. In Mediterranean olive groves, where erratic rainfall limits fertility, CCs of self-reseeding annual legumes can fix nitrogen, suppress weeds, and reduce fertilizer use.

This study, performed within the project Agritech National Research Center, funded by the European Union Next-Generation EU (PNRR, MISSION 4 COMPONENT 2, INVESTIMENT 1.4, D.D. 1032 17/06/2022, CN0000022), assessed the impact of different CC mixtures on soil microbial communities and on mycorrhizal root colonization in a traditional olive grove in northern Sardinia. Two CC treatments, Commercial Mixture (CM) and Innovative Mixture (IM), were compared with natural herbaceous cover and conventional tillage. Soil and plant community root samples collected in 2023 and 2024 were analysed using targeted metagenomics to study bacterial and fungal communities and evaluate CCs' influence on soil health and beneficial symbionts.

Results showed that seasonal variations had a stronger effect on soil microbial communities than CC treatment, with shifts in dominant bacterial and fungal groups between years. However, CC treatments influenced microbial composition of plant community roots, as 16S sequencing showed differences between CC treatments and natural cover, while ITS sequencing indicated no significant alpha-diversity differences. Multivariate analyses confirmed treatment-dependent microbial variations, suggesting that CCs may shape belowground biodiversity.

The ability of CCs to foster beneficial microbial associations suggests the need for further analyses, aimed at integrating molecular and physiological data, allowing the selection of CCs able to enhance soil fertility with limited water/nutrient competition with trees, to optimize olive grove management in Mediterranean agroecosystems, under varying climatic conditions.

Keywords: Soil microbial communities, Mycorrhizal symbiosis, Soil fertility, Cover crop plants

Innovative management for organic ornamental crops in nurseries

<u>Antonio Ferrante¹</u>, Daniela Romani², Alice Trivellini³, Daniele Massa⁴

¹Scuola Superiore Sant'Anna di Pisa, Italy, ²University of Catania, Italy, ³University of Pisa, Italy, ⁴CREA Research Centre for Vegetable and Ornamental Crops, Italy

antonio.ferrante@santannapisa.it

The ornamental sector of organic outdoor ornamental plants needs innovative technical means that can improve the sustainability and competitiveness of production companies.

There are numerous difficulties that stand in the way of adopting organic production protocols and the most limiting are the poor availability of certified organic technical means. Pot cultivation is very difficult to manage in an organic regime. Another problematic phase in ornamental nursery is propagation, usually carried out by cutting with the aid of synthetic products with hormone-like action. Last, but not least, is the challenge of controlling biotic and abiotic stress with remedies permitted in organic farming, which implies a holistic approach to the problem with respect to the use of synthetic chemical products, possible above all thanks to a conscious use of bioactive substances. Of particular importance are the control of weed flora and the defense against soil-borne pathogens. In this context, the BIOVIVO project aims to analyze with a multidisciplinary approach, also thanks to the direct support of horticultural companies, the critical points of the production process - propagation, growing substrates, fertilization, defense - with the aim of outlining a cognitive framework that can support the organic cultivation process for ornamental shrub plants in pots to be used in green spaces. The project will use technical means of natural origin such as biostimulants to improve the production process of ornamental plants in nurseries.

This research was funded by the Ministry of Agriculture, Food Sovereignty and Forests (MASAF, Italy), project "Dal green deal al vivaio: innovazioni al servizio delle coltivazioni biologiche nel vivaismo ornamentale – BIOVIVO", D.D. 0576439 - 31st October 2024.

Keywords: Substrates, Propagation, Weeds, Nutrition, Bioactive substances

Investigation of local Italian varieties of *Ficus carica* L.: morphological, physicochemical and aromatic characterization

<u>Raffaella Petruccelli</u>¹, Francesca Ieri², Deborah Beghè³, Margherita Ridolfi³, Tommaso Ganino³, Cristiana Giordano⁴

¹IBE-CNR, Italy ²Institute of Biosciences and BioResources, CNR, Sesto Fiorentino, Italy, ³University of Parma, Italy, ⁴Institute of BioEconomy, CNR, Sesto Fiorentino, Italy

raffaella.petruccelli@ibe.cnr.it

Mediterranean fig (*Ficus carica*), is one of the earliest cultivated fruit trees, it is a classical fruit tree of Mediterranean region, where is concentrated more than 80 % of production. The fruit is an important resource of the MD and it is consumed fresh, dried, and processed. In recent years, fig has been gaining increasing attention, for the fruit's nutritional properties and exceptional resilience to climate change. Among fruit trees, the fig is recognised as an extremely polymorphous species with a rich varietal platform. The Italian fig germplasm consists of a large number of cultivars, more than 300. This number is approximate; there are many genotypes that are still poorly known and studied that may possess interesting agronomic traits, especially in terms of response to climate change. Therefore, it is necessary to characterize the local germplasm to identify genotypes with desirable traits. Aim of this study was to describe Italian fig cultivars through fruit morphological parameters, physicochemical characteristics, and aromatic profiles.

11 pomological parameters, physicochemical characteristics (TSS, pH, and TA), and flavor profiles (HS-SPME/GC-MS analysis) of the pulp and peel were evaluated on fruits of 15 varieties of Ficus

Significant differences were observed in fruit pomological traits, as well as in the physicochemical paremeters and the aroma profiles. Volatile compounds detected in flesh and skin being distributed by distinct chemical classes: aldehydes, alcohols, ketones, esters, monoterpenes and sesquiterpenes. All varieties presented a similar volatile profile, although with different intensities between the varieties. Peels exhibited a greater number of volatile compounds, especially for sesquiterpenes, compared to the pulps.

The results obtained highlight that among the fig varieties studied, some exhibit superior morpho-chemical characteristics; these could be used in breeding programs and in the establishment of commercial orchards.

Keywords: Fig tree, Local varieties, Morphological parameters, Qualitative analysis, Volatile profile

Metabolites and nutritional value of different local varieties of tomato (*Lycopersicon* esculentum Mill.) cultivated in Salento

<u>Rita Accogli</u>, Eliana Nutricati, Carmine Negro, Luigi De Bellis

University of Salento, Italy

rita.accogli@unisalento.it

Tomato (*Lycopersicon esculentum* L.) is one of the world's most consumed vegetables, known as nutritional and healthy food. Thus, various cultivars have been developed to attract more consumers. The beneficial effects of tomatoes such as antioxidant, anti-inflammatory, anti-cancer and anti-atherogenic properties, reducing risk of cardiovascular diseases, have been widely studied. Therefore, it is interesting analyze metabolic differences and nutrient content of different cultivars. We carried out a metabolomic analysis and an evaluation of nutritional properties of four different tomato local accessions from Salento area, named pomodoro di Morciano, pomodoro leccese, pomodoro racalino, pomodoro di Salve.

Results show that cultivars have a lower level of lycopene, but the same content of α -carotene and β -carotene than commercial tomato varieties. Moreover, the four cultivars were characterized by their high content of all-trans lutein, a carotenoid used for protecting retinal damages.

In addition, total phenolic and flavonoid contents were evaluated.

The data obtained provide valuable information of different characteristic in various tomatoes, which can be considered for improving tomato cultivars.

Funded by BiodiverSO KARPOS CUP B97H22003670009.

Keywords: Lycopersicon esculentum, Local varieties, Phenolic compounds, Carotenoid

New insights into the diversity of Apulian wheat landraces known as Saragolla

Angela Rosa Piergiovanni, Giacomo Mangini, Benedetta Margiotta, Paolo Direnzo

Istituto Bioscienze Biorisorse, CNR, Bari, Italy

angelarosa.piergiovanni@ibbr.cnr.it

Durum wheat (*Triticum turgidum* L. subsp. *durum* (Desf.) Husn.) has been cultivated in Southern Italy since ancient times. Historically, farmers cultivated landraces that evolved in response to environmental conditions in which they were traditionally grown. Among the Italian durum landraces, the "Saragolla group" played a significant role in Southern Italy until the mid-20th century. This group included landraces such as "Saragolla o duro di Puglia" "Saragolla Lucanica", and "Saragolla Siciliana", all characterized by long grains and semolina used for pasta production.

The release of improved durum cultivars led to the progressive decline of the landraces, including the "Saragolla group" which now survives in small marginal areas of Southern Italy. Recently, through the Rural Development Program, seven durum landraces were recovered in Apulia region, one of which named "Saragolletta" while the others were collectively referred to as "Saragolla".

In this study, the genetic variation within and among these landraces was assessed using biochemical markers. The gliadin profiles revealed considerable genetic diversity within the "Saragolletta" which appeared to be a mixture of three genotypes. The main distinguishing feature in the gliadin profiles of the six "Saragolla" landraces was the presence/absence of components in the slow-moving ω -gliadin region. This result allowed us to split the Apulian "Saragolla" into two subgroups. Two of the "Saragolla" landraces, polymorphic for ω -gliadin, were further genotyped using Single Nucleotide Polymorphism (SNP) markers, alongside a panel of durum (landraces and cultivars) and Khorasan (*Triticum turgidum* L. subsp. *turanicum* (Jakubz.) Á. Löve & D. Löve) accessions. Phylogenetic analysis confirmed the genetic diversity among the Apulian "Saragolla", suggesting that the term "Saragolla" includes landraces consisting of a mixture of genotypes from different *T. turgidum* subspecies.

Keywords: Durum wheat, Genetic diversity, Landraces

Old and new paths for seeds of European vegetable landraces

<u>Adriano Didonna</u>¹, Massimiliano Renna¹, Angelo Giordano¹, Riccardo Bocci², Pietro Santamaria¹ ¹University of Bari Aldo Moro, Italy, ²Rete Semi Rurali, Scandicci, Italy

adriano.didonna@uniba.it

In Europe, the commercialization of vegetable seeds is only permitted for varieties registered in the Common Catalogue of Varieties of Vegetable Species, after satisfying the distinctness, uniformity and stability (DUS) requirements. This regulation therefore totally excludes the possibility of marketing landraces or participatory varieties which, due to their high variability, do not meet the DUS requirements. To overcome this limitation, Directive 98/95/EC introduced two derogation regimes: Conservation Varieties (CV) and varieties with no intrinsic value (or amateur varieties, AV). This paper analyses: (i) the effectiveness of these regimes with respect to the European seed market and (ii) the dissemination channels - formal and informal - used for European vegetable seeds. In 2024, in the Common Catalogue, 1,133 AV and 235 CV were registered out of a total of 22,821 varieties, equal to 5% and 1.1% respectively of marketable vegetable varieties. The diffusion of landraces and, more generally, of farmer's varieties, takes place mainly through informal channels, such as custodian farmers, seed savers, associations or Community Seed Banks. The European seed system therefore needs to be renewed in order to offer more formal distribution channels for landraces, especially in light of their increasingly common use in non-conventional agricultural systems, and to protect agrobiodiversity. In this sense, with Regulation (EU) 818/2018 and with the Implementing Directive (EU) 2022/1648, the European seed system has adopted two additional regimes: the Organic Heterogeneous Material (OHM) and the Organic Varieties of vegetable species suitable for organic production (OV). These, together with new regulations that will be discussed in the European Union in the coming months, could open up new and unexpected scenarios for the seeds of European vegetable landraces.

Keywords: Conservation varieties, Amateur varieties, Landraces, Seed regulation, in situ conservation

The garlic landrace of Resia, Eastern Italian Alps. The plant genetic resource managing in a Slavic enclave, twenty years later

Fabiano Miceli¹, Luisa Dalla Costa¹, Riccardo De Infanti¹, Stefano Santi²

¹University of Udine, Italy, ²Parco Naturale Prealpi Giulie, Italy

fabiano.miceli@uniud.it

At the crossroad of Latin, Slavic and Germanic culture, Friuli - Venezia Giulia region (FVG) is a true land of differences. Despite being reasonably small, it includes 3 out of the 5 European biogeographical regions. A few languages, dialects and idioms are spoken here. The Alpine valley of Resia stretches 21 km W-E and is closed towards the Slovenian border by the Canin massif (2580 m). A group of alpine Slavic shepherds settled in the valley, between the 7th and 9th centuries AD. A high level of genetic insulation for Resia people has been recently assessed. The landrace (strok in Resian idiom) is a hardneck (bolting) garlic, putatively assigned to the Ophioscorodon group. Through reproductive stages, a long and curving scape is developed, then the scape uncoils and the lumping shape of the umbel capsule become evident, with a white spathe that includes sterile flowers and topset.

Since 2003, the garlic was included in the FVG Repertoire of Landraces and by 2005 it entered among the Slow Food Presidia of FVG. This casted light at national level, so the garlic prices rose dramatically. Phenotype characterization was performed by standard IPGRI descriptors as well as agronomic evaluation in comparison to other bolting materials.

Intrinsic biological and agronomic difficulties interacted to limit the crop area enlargement and some frictions among local horticulturists arose, so in recent years the number of farmers involved with the Presidium dropped significantly. After 20 years, the Municipality of Resia, the Prealpi Giulie Natural Park and the University of Udine are being striving to foster the garlic landrace: agronomic evaluation, on farm management practices and communication measures have been put in place, in order to safeguard the Allium genetic resource: an identity flag for the Resia community.

Keywords: Allium sativum ophioscorodon, Landrace, Resia, SlowFood Presidium

The potential use of Sicilian chili pepper accessions for ornamental purposes

<u>Gaetano Giuseppe La Placa</u>, Lorena Vultaggio, Beppe Benedetto Consentino, Pietro Bellitto, Fabiana Mancuso, Salvatore La Bella, Leo Sabatino

University of Palermo, Italy

gaetanogiuseppe.laplaca@unipa.it

Chili pepper (*Capsicum* spp.) in recent decades has been rediscovered as an ornamental plant mainly due to its efficient sexual propagation, short crop cycle, high temperature tolerance, and variability in fruit color and plant height. In the genera Capsicum, Capsicum annum is the most widely cultivated species for ornamental purposes. Although ornamental chili pepper plants are self-pollinators, entomophilous pollination may occur with cross-pollination which can varies from 2% to 90%. Nurseries do not always provide adequate isolation among plants to promote self-pollination, so hybridization among cultivars may occur. Our preliminary observations suggest that there is considerable variation among Sicilian genotypes, perhaps due to cross-pollination. Consequently, a specific study to characterize Sicilian chili pepper accessions for ornamental purposes is needed. In our research, the germplasm was established in an experimental field of the Department of Agricultural, Food and Forestry Sciences of the University of Palermo for 2 consecutive years. Nineteen chili pepper accessions were grown. The characterization of the genotypes was accomplished using the IPGR (International Plant Genetic Resources Institute) descriptors. Results pointed out that chili pepper accessions A33, A27, G1 and A1 attained good attitudes for ornamental purposes since they revealed high visual quality traits. Our findings also showed different yield traits among the accessions evaluated. This suggests a greater degree of variability among genotypes. Remarkably, the study indicated that the visual quality scores of the plants increased as the number of fruits per plant decreased. Thus, the variability detected could suggest an overtime selection pressure for yield or ornamental purposes.

Keywords: Capsicum, Sicilian biodiversity, IPGR descriptors, Visual quality

Valorizing Apulian chickpea (*Cicer arietinum* L.) biodiversity: a multidisciplinary approach

Wilma Sabetta, Lisa Fiorentino, Nicoletta Rapanà, Angela Rosa Piergiovanni, <u>Mariella Matilde</u> <u>Finetti Sialer</u>

Institute of Bioscience and BioResources, CNR, Italy

mariella.finetti@cnr.it

Legumes have been cultivated in Italy since ancient times. Each Italian region has its own group of landraces, belonging to different legume species. They are deeply embedded in the traditional agricultural practices, as well as in the local landscape, dishes and cultural heritage. In the Apulia region, chickpea exhibits considerable unexplored variability, particularly in seed traits. In the PSR project SavegrainPugliaLeg, nine landraces were characterized using a multidisciplinary approach to uncover their potential for more sustainable farming systems.

A sample of seeds representative of each landrace was acquired from farmers who traditionally cultivated it. The genetic variation within and among the landraces was assessed through biochemical and genetic analyses, including the evaluation of some genes involved in drought stress tolerance.

An unequivocal genetic fingerprint was obtained for each landrace. The genetic diversity indices revealed a moderate level of polymorphism. As expected, due to the strictly self-pollinating nature of chickpea, the observed heterozygosity (Ho) was lower than the expected one (He), resulting in positive inbreeding coefficients. The analysis of the mRNA accumulation of two genes encoding for Kunitz-type trypsin inhibitor, which are responsive to water deficit, revealed a higher expression of CaTPI-1 transcript in roots of the "black chickpea from Murgia dei Trulli" in the presence of the stress. In addition, this black chickpea showed also the highest CaKPI transcript expression. In terms of seed nutritional quality, all the landraces showed protein contents within the typical range for chickpea. Higher levels of some nutraceutical compounds, such as carotenoids and total phenolic compounds, were recorded for the "black chickpea from Murgia dei Trulli". Collectively, these findings suggest that this landrace is a promising genetic resource for chickpea crop improvement.

Keywords: Drought, Chickpea, Landraces, Apulia

Virtual fencing as a tool for biodiversity-oriented pasture management in alpine grasslands

<u>Luca de Guttry</u>¹, Annarita Balingit¹, Andrea Confessore¹, Aquilani Chiara¹, Nicolina Staglianò¹, Giovanni Argenti¹, Camilla Dibari¹, Simona Rainis², Carolina Pugliese¹

¹University of Florence, Italy ²ERSA - Regional Agency for Rural Development, Tolmezzo, Italy

luca.deguttry@unifi.it

While fulfilling a valuable productive role, pastoral systems based on extensive grazing provide and maintain numerous ecosystem services, such as high levels of plant and habitat diversity. These functions become even more relevant in the alpine environment, where the complexity of the landscape is often associated with high levels of biodiversity. However, inappropriate stocking rates and deficient pasture management can lead to environmental degradation and a loss of ecosystem functionality due to overgrazing or pastures' abandonment. A rational and adaptive management of livestock distribution is therefore essential to preserve the ecological integrity of these grassland systems, though difficult to apply in extensive mountain grazing environments. In this context, the use of Virtual Fencing (VF) GPS collars, a precision livestock technique that consists of defining the grazing areas from remote and confining the animals through an acoustic and electric stimulus, allows for an almost real-time and spatially explicit regulation of livestock movement without the need to set physical fences. This technology was tested during the 2023 grazing season in an alpine dairy farm in the Eastern Italian Alps (Mount Zoncolan, UD, 1700 m a.s.l.). The animals (35 Bruna dairy cows) reacted well to the coupled stimuli and grazed inside the imposed virtual boundaries for most of the time. Such a fine-scale control enabled the implementation of adaptive and rational grazing patterns. Under a biodiversity conservation approach, a rotational grazing scheme can be used to enhance a differentiated use of the pasture and maintain habitat heterogeneity or, on the other hand, to protect sensitive ecological areas by excluding them from animal grazing during specific periods. As such, VF may represent a powerful tool to align productive livestock farming with biodiversity conservation through an intelligent and adaptive pasture management.

Keywords: Grasslands, Pastures, Adaptive Grazing, Virtual Fencing

Crop Wild Relatives (CWRs): a promise for the future of the European farming systems

<u>Riccardo Bocci</u>¹, Arena Donata², Branca Ferdinando²

¹Rete Semi Rurali ETS, Italy, ²University of Catania, Italy

riccardo.bocci@semirurali.net

Crop Wild Relatives (CWRs) are the COUSINs of crops, which can have an important role for broadening the genetic basis of European farming systems. They can contribute to enhancing crop resilience to biotic and abiotic stresses, promoting the agroecological transition, in alignment with the EU Green Deal and the United Nations Sustainable Development Goals.

Currently, 75% of the world's food is generated from only twelve plant species and since the 1900s, plant diversity has been lost as farmers worldwide have left their diverse set of local varieties for genetically uniform, high-yielding varieties. In this frame, 26 partners from 12 European countries joined their effort to set up the European Union-funded project "Crop Wild Relatives Utilization and Conservation for Sustainable Agriculture" (COUSIN - Project: 101135314 - HORIZON-CL6-2023-BIODIV-01). Working on five flagship crops (barley, brassica, lettuce, pea, wheat), the COUSIN main objectives are to: i) identify pathways to use CWRs to strengthen sustainable agriculture; ii) recognize in situ genetic reserves; iii) determine stakeholder-demanded characteristics of CWRs; iv) implement CWRs into breeding and farming activities; v) provide information about CWRs in an accessible format to stakeholders and potential users; vi) train and raise awareness about the value of CWRs in the society. COUSIN will provide new organic heterogeneous materials (OHMs) to use in organic farming to increase the resistance to biotic and abiotic stress and the organoleptic and nutraceutical traits of the produce. CWRs need to be included into national strategies on Plant Genetic Resources for Food and Agriculture, but they are hardly considered. In Italy, for example, the National Biodiversity Strategy to 2030, approved in 2023, doesn't not include any action to protect and conserve CWRs. It is important to raise awareness on the importance of CWRs starting from the scientific community.

Keywords: Crop wild relatives, Organic breeding, Organic heterogeneous materials, National biodiversity strategy

The European funded project pro-wild: protect and promote crop wild relatives

Lorenzo Raggi¹, Valeria Negri¹ & the PRO-WILD consortium

¹University of Perugia, Italy

lorenzo.raggi@unipg.it

Crop wild relatives (CWR) are wild plant species genetically related to cultivated crops. Their untapped diversity can enhance resilience to biotic and abiotic stress and the nutritional quality of modern crops. Wheat, sugar beet, and oilseed rape were selected by Pro-wild because of their importance to food security and EU farmers and because some of their wild relatives are endemic to Europe. Moreover, these CWRs constitute a rich and under-exploited resource needed to face challenges linked to climate change and the transition to lowinput agriculture. The genetic diversity and vulnerability of these CWRs must be better characterized to optimize their conservation and utilization. The objectives of Pro-Wild are to identify priorities for insitu conservation of the selected CWR gene pools, to survey and complement CWR genebanks collections, and to increase the use of CWRs in crop improvement.

Coordinated by the National Research Institute for Agriculture, Food and Environment (INRAE, France), Pro-Wild associates 18 partners from 11 EU and associated countries with expertise in ecology, conservation, genomics, pathology, microbiology, plant breeding, agriculture, and sociology. Pro-Wild will compile and analyse CWR occurrence maps and perform new in-situ collections. It will predict the vulnerability of several CWR species and populations to ongoing climate changes. Ex-situ collections will be complemented with endangered CWRs accessions. Pro-Wild will investigate the resilience of CWR collections for relevant biotic and abiotic stresses. The identification of CWRderived desired traits and their transfer into elite backgrounds will be done to promote CWR use. Overall, Pro-Wild specific goals will be coordinated with input from breeders, farmers, and consumers. Pro-Wild outcomes will contribute to European Green Deal initiatives through research, education, and training. It will serve the EU biodiversity and the Farm to Fork strategies by preserving, characterizing, and utilising wild species that have unique importance for the resilience of our food systems.

Keywords: Agrobiodiversity, Plant breeding, Plant genetic resources, Biodiversity, Conservation biology, Conservation genetics, Beet, Brassica, Wheat, Genebank, Microbiota, Tolerance to biotic and abiotic stress

Session: Insect biodiversity in the modern era

Exploring biodiversity with molecular and morphological analyses to define species boundaries of the ectoparasitoid *Sclerodermus cereicollis* Kieffer

Paolo Masini¹, Manuela Rebora¹, Wesley Colombo², Celso Azevedo¹, Gianandrea Salerno¹

¹University of Perugia, Italy, ²Universidade Federal do Espirito Santo, Brazil

gianandrea.salerno@unipg.it

The genus *Sclerodermus* comprises over 80 cosmopolitan species of idiobiont ectoparasitoids of many insect taxa, among which many xylophagous or stored product insect pest associated to anthropized environments are present. This genus exhibits high biodiversity, including various morphotypes and pronounced sexual dimorphism. Its role as a biological control agent of pest species and a cause of sting dermatitis in humans makes it a key genus in Bethylidae family. Understanding *Sclerodermus* biodiversity is challenging due to simplified morphology, limited diagnostic traits, outdated descriptions, difficult access to type specimens, and a lack of identification keys. Sclerodermus cereicollis Kieffer, includes syntypes from Annobón Island (Afrotropical) and Giglio Island (European). According to the concept of allopatric speciation, these sites - separated by the Atlantic Ocean and the Sahara Desert - suggest that the two syntype groups likely represent different species. The syntypes of *S. cereicollis* are deposited in the Nat. Hist. Museum of Genoa and were redescribed following Lanes et al. (2020). Two Italian field specimen groups were compared with the type series and used for molecular analysis. We analyzed the mitochondrial Cytochrome Oxidase I gene and reconstructed a Maximum Likelihood phylogeny with seven S. cereicollis specimens and 11 outgroups, including other Sclerodermus species and bethylids. Molecular analyses showed intraspecific genetic distances of 0-3%, and, together with morphological analyses, confirmed that all analyzed specimens belong to the species *S. cereicollis*. To stabilize taxonomy, we designated a lectotype. Although the syntypes belong to populations found in such distant geographical areas, their morphological differences do not justify classifying the Afrotropical syntypes as a new species. These bethylids often spread through infested furniture, which could explain the presence of two distinct populations in distant geographical areas.

Keywords: Bethylidae, Sclerodermus, Xylophagous insect pest, Stored product insect pest

A 50-year evolutionary history of *Lactobacillus helveticus* associated with the natural whey starters (NWS) of the traditional dairy environment

<u>Martina Filippini</u>¹, Ida Mercurio¹, Chiara Montanari¹, Federica Barbieri¹, Monica Gatti², Erasmo Neviani², Alessia Levante², Fausto Gardini¹, Giulia Tabanelli¹

¹University of Bologna, Italy, ²University of Parma, Italy

martina.filippini4@unibo.it

This research investigates the genotypic and phenotypic variability between and within *Lactobacillus helveticus* strains isolated in two different periods to explore potential changes that have been undergone over the past 50 years. This approach can reveal species' evolutionary adaptation, aiding the identification of strains with technological and functional traits.

The study leverages a unique collection from the Department of Agricultural and Food Sciences (University of Bologna) of *L. helveticus* strains isolated in 1970 from natural whey starters used in traditional cheese-making. These 20 never-before-revived strains were compared to recent isolates (2023) from the same area, representing the current biodiversity of the species in this environment. Molecular genotyping has been performed by Amplified Fragment Length Polymorphism (AFLP). Safety features were assessed, including antibiotic resistance to EFSA-recommended antibiotics (2012). Phenotypic growth performances and metabolic features were studied by monitoring bacterial growth in culture media and using GENIII microplates on an OMNILOG instrument (Biolog, Inc.).

Preliminary AFLP results of the molecular genotyping suggested significant genetic diversity between the strains from the 1970s and modern strains. Historical strains exhibit lower antibiotic resistance, potentially offering a sustainable approach to mitigate the spread of resistant genes within the dairy sector. Data revealed different growth performances among the tested strains, not only depending on the time of isolation but also highlighting notable biodiversity among the present biotypes.

Understanding the genotypic and phenotypic traits that *L. helveticus* strains have adapted over time is crucial for valorising a unique 1970 microbial collection, harnessing phenotypic reservoirs for innovative applications and fostering the sustainable utilization of microbial diversity in dairy production.

Keywords: *Lactobacillus helveticus*, Microbial biodiversity, Dairy application, Natural whey starters

Citizen Salad: investigating plant leaf microbiota with a citizen science approach

<u>Emma Tedeschini</u>¹, Alessandro Ciampanelli², Valentina Fiorilli², Lara Reale¹, Marco Giovannetti², Matteo Chialva²

¹University of Perugia, Italy, ²University of Torino, Italy

emma.tedeschini@unipg.it

Lettuce is a widely consumed raw vegetable, making it essential to understand and predict its leaf-associated microbial communities for both plant and human health. While environmental factors strongly influence plant microbiomes, the role of plant-specific traits and the origins of microbial diversity remain unclear.

To bridge these knowledge gaps, we launched a citizen science experiment partially funded through crowdfunding. The campaign attracted 144 donors and recruited 100 participants from across Italy to grow two lettuce varieties and collect soil, environmental, and leaf samples. The project involves diverse contributors, including primary and secondary schools, ecomuseums, urban gardens, and botanical gardens.

We will analyze bacterial communities using 16S rRNA amplicon sequencing to disentangle the contributions of plant morphology, soil, and environmental microbial communities.

By integrating public engagement with rigorous, hypothesis-driven research, Citizen Salad aims to advance our understanding of plant microbiomes while fostering scientific literacy and community involvement.

Keywords: Leaf microbiota, Environment, Human health, Citizen science

EPS-producing microbial communities from water kefir in gluten-free sourdough production

Federica Spaziani¹, Maria De Angelis², Leonardo Caputo¹

¹Institute of Sciences of Food Production (CNR-ISPA), Italy, ²University of Bari Aldo Moro, Italy

leonardo.caputo@cnr.it

Kefir water is valued for its stable microbial communities associated with kefir grains, which produce exopolysaccharides (EPS) with significant technological potential. These compounds, along with the microorganisms responsible for their synthesis, can enhance food texture and stability. Their application in gluten-free bakery production may introduce variations in microbial communities, leading to new functional attributes. This study aimed to screen and select microbial communities based on their EPS production. Commercial kefir grains were used to ferment kefir water, which was then applied as a starter for rice-flour-based sourdough, routinely back-slopped. The different microbial communities, including lactic acid bacteria (LAB) and yeasts, were characterized using MRS agar with 0.0005% aniline blue and 5% sucrose for LAB and PDA agar with 0.008% ruthenium red and 5% sucrose for yeasts. A total of 70 isolates were analysed, with the vast majority from kefir water demonstrating EPS production. Moreover, 80% of the isolates from sourdough retained EPS production. These findings confirm that kefir-related microbial communities can adapt to the sourdough habitat, unveiling bio-functional properties in terms of EPS production and fermentation.

Gluten-free sourdough produced from water kefir could improve the structural and sensory properties of gluten-free leavened products improving their clean label.

Keywords: EPS, LABs, Yeasts, Sourdough

Food-derived *Levilactobacillus brevis* M3R3 as an emerging probiotic: genomic and functional study of Bile Salt Hydrolase activity

<u>Marianna Cristofolini</u>¹, Gianluigi Agolino², Maria Anna Ronsivalle¹, Alice Cattivelli¹, Davide Tagliazucchi¹, Alessandra Pino², Cinzia Caggia², Lisa Solieri¹, Cinzia Lucia Randazzo²

¹University of Modena and Reggio Emilia, Italy, ²University of Catania, Italy

287012@studenti.unimore.it

Bile salt hydrolase (BSH) deconjugates bile acids (BA), regulating lipid and glucose metabolism, and microbial homeostasis. BSH, a probiotic trait, is widespread among Lactobacillaceae gut bacteria. *Levilactobacillus brevis*, a probiotic species with QPS status, is found in fermented foods, with many strains exhibiting cholesterol-lowering effect linked to BSH. However, the characterization of bsh genes in *L. brevis* remain unclear. Here we studied the BSH activity in *L. brevis* strain M3R3.

M3R3 genome was sequenced with Illumina platform. bsh genes were identified and kinetic growth response to BA was analyzed. bsh gene expression was determined by RT-qPCR in presence of BA compared to MRS medium. BA profiling was carried out by UHPLC/HR-MS.

78 available *L. brevis* bsh proteins were phylogenetically clustered into three groups (bsh1, bsh2, and bsh3), with several strains with more than one protein. Strain M3R3 had a 2.30 Mbp long genome, with 2375 CDS. Neither AMR genes nor virulence factors were found. M3R3 possessed bsh2 and bsh3 genes, expressed both in control and in presence of BA. BAs exposure decreased kinetic parameters A and λ . M3R3 completely deconjugated glycine-conjugated BAs and app. half of the tauro-conjugated BA, respectively.

By combining genomics and metabolomics, we identified *L. brevis* M3R3 as promising BAsmodulating probiotic with two bsh proteins.

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Keywords: *Levilactobacillus brevis*, Probiotic candidate, Sourdoughs, Bile salt hydrolase activity

Galactose utilization profiles in *Streptococcus thermophilus* strains

Carlo Perla¹, Antonio Francioso², Remo Ferri¹, Alessio Pio Rossetti², Grazia Di Campli¹, Giorgia Perpetuini², Nunzio Lobefaro¹, Antonio Spinosi¹, <u>Rosanna Tofalo²</u>

¹Dalton Biotecnologie s.r.l., Italy, ²University of Teramo, Italy

rtofalo@unite.it

Streptococcus thermophilus is widely in the dairy industry. While glucose is rapidly consumed, many S. thermophilus strains lack efficient galactose (GAL) uptake or catabolism, leading to its accumulation in the final product. High residual galactose is undesirable due to potential implications for product quality; in fact, its occurrence is correlated with browning of Mozzarella cheese upon heating. In this study, the galactose phenotype of 100 presumptive S. thermophilus strains from dairy origin has been studied. The strains were identified through a species-specific PCR. Moreover, strains were typed by RAPD-PCR using GTG₅ primer. The content of lactose, glucose, and galactose was determined by UPLC. All strains were identified as S. thermophilus. The analysis of galactose residues among S. thermophilus strains revealed substantial variability in galactose utilization efficiency, suggesting the presence of distinct fermentation phenotypes. Residual galactose concentrations ranged from 0.65 to 4.16 g/L, with the majority of strains (92 out of 100) falling between 1 and 2 g/L. In 4 samples, the content of residual galactose was <1 g/L. Based on these values, strains were categorized into three phenotypic groups: low-GAL (≤ 1.3 g/L), intermediate-GAL (1.31–2 g/L), and high-GAL (>2 g/L) users. Approximately one-third of the strains exhibited low residual galactose levels, indicating efficient uptake and metabolism of galactose. Conversely, several strains-most notably those with GAL values exceeding 3 g/L—demonstrated limited galactose utilization, potentially reflecting a gal⁻ phenotype. The glucose was depleted by all strains, suggesting a preferential glucose consumption consistent with carbon catabolite repression. These results showed a galactose fermentation diversity among S. thermophilus strains, which could be exploited to develop tailored starter cultures.

Keywords: Streptococcus thermophilus, Galactose metabolism, Mozzarella cheese

Gempipe: a computational tool for exploring strain-level bacterial metabolic diversity and screening strains for desired metabolic traits

Gioele Lazzari, Giovanna E. Felis, Matteo Calgaro, Francesca Di Cesare, Nicola Vitulo

University of Verona, Italy

gioele.lazzari@univr.it

Strains of the same species may have phenotypic differences due to mutations, gene losses and horizontal gene transfers, sometimes related to niche adaptation. This diversity is relevant in biotechnology industry: the ability to synthesize specific metabolites varies between strains and can be harnessed for applications in health, food, and bioprocessing.

Genome-scale metabolic models (GSMMs) are in silico tools describing a cell's metabolic potential. They are built on a genome by annotating enzyme-encoding genes, which are translated into a network of metabolic reactions. Assuming a steady state and providing a biomass composition, the flux-balance analysis of a GSMM allows growth simulations on a specified nutritive input and predicts specific abilities for each sequenced strain.

Given the increased availability of genomes, we present Gempipe, a tool that enables the simultaneous reconstruction of hundreds of GSMMs, providing a comprehensive view of strain-specific characteristics and offering valuable insights for comparative and applied studies in biotechnology. Building upon large genome datasets and an optional reference GSMM, it rapidly constructs a pan-GSMM, which is then leveraged to derive and analyze strain-specific GSMMs, enabling the identification of auxotrophies, preferred growth substrates, and potential for target metabolite production.

Gempipe was validated on public datasets and outperformed other state-of-the-art tools in strain-specificity studies, thanks to its hybrid reconstruction mode. A case study on 1000+ *Limosilactobacillus reuteri* genomes demonstrated its ability to cluster strains by metabolic potential, highlighting phenotypic variability beyond the six subspecies proposed in the literature.

Gempipe predicts strains' metabolic potential, helping microbial collections unlock bioresources. Per-strain GSMM availability enables rapid, cost-effective analysis, improving selection beyond trial-and-error screening.

Keywords: Genome-scale metabolic models, Strain-level metabolic diversity, Rational screening, Phenotype predictions

Polyphasic characterisation of lactic acid bacteria diversity associated with sheep milk from "Gentile di Puglia": starter culture design for Pecorino cheese and for cereal-based fermented beverage

<u>Mariagiovanna Fragasso</u>¹, Hülya Cunedioğlu¹, Ghofrane Omri¹, Giuseppe Spano¹, Vittorio Capozzi²

¹University of Foggia, Italy, ²Institute of Sciences of Food Production, CNR, Italy

mariagiovanna.fragasso@unifg.it

Preserving and valorising Apulian agrobiodiversity is a key strategy to promote the innovation of agro-food systems associated with regional Marginal Areas (MAs), including a diverse range of animals, plants, and micro-organisms. Fermented foods, in particular, are defined as "those foods or beverages made through controlled microbial growth and enzymatic conversions of major and minor food components". Fermentation and fermented products represent interesting elements to ensure the transition of food systems toward greater environmental, economic, and social sustainability. "Gentile di Puglia", literally "Gentle Apulian" in reason of the fine wool, is an autochthonous sheep breed of millenary origins typical of the South of Italy, particularly associated with Foggia province (i.e. Subappennino Dauno and Tavoliere areas). "Gentile di Puglia", genetically adapted and resilient to the environmental conditions of marginal areas, is also recognised for cheese production. Cross-over fermentation has been defined by Dank et al. as "processes in which a microorganism from one traditional fermentation process is introduced onto a new substrate and/or to a new partner". Here, we report a case study related to the marginal area of the Subappennino Dauno/Monti Dauni, in the north of Apulian Region, i) isolating lactic acid bacteria (LAB) from sheep milk (breed "Gentile di Puglia") and ii) performing a polyphasic characterisation of LAB for the design of multi-strains starter culture for Pecorino cheese and the design of a cross-over cereal-based fermented beverage ("Senatore Cappelli" durum wheat variety).

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Keywords: Microbial diversity, Innovation, Plant-based, Fermentative cross-over, Lactic Acid Bacteria

Production of a "fermented lactic beverage" with health and probiotic properties from "Almond milk" of almond Apulian varieties

<u>Francesco Loperfido</u>¹, Valentina Petrelli¹, Sabrina Pupillo¹, Aronne Galeotti¹, Andrea Turco², Pasquale Venerito², Giuseppe Maggi¹, Giuseppe Romano³, Francesco Tedesco³, Carmela Gerardi³, Maria Tuffariello³, Francesco Grieco³

¹Fondazione ITS Academy AgriPuglia, Italy, ²CRSFA Centro di Ricerca, Sperimentazione e Formazione in Agricoltura Basile-Caramia, Italy, ³Institute of Sciences of Food Production (ISPA), CNR, Italy

lope.francesco@gmail.com

The almond represents one of the most common fruit crops in Puglia and is a food rich in unsaturated fats, protein, vitamins and flavonoids. Some of the Apulian most deserving varieties, processed into almond milk, can be used to obtain a highly digestible novel food product that is a vehicle for useful and potentially probiotic microorganisms.

This study involved the production and comparison of two fermented almond milk products one to a mixture of three microorganisms (one yeast and two bacteria) isolated from kefir granules, and a second product obtained using the combination of three strains of lactic acid bacteria (WCFS1, probiotic; B2, riboflavin producer; Lp90, exopolysaccharide producer).

The microbial consortium and the three strains of lactic acid bacteria were separately used for the production of different fermented lactic beverages using three almond milk preparations of the Apulian almond varieties "Montrone", "Ferrara", and "Calia", prepared using a homogenizer and ultrasonic treatment.

The fermented products showed a difference in the final structure of the obtained product. In fact, the one obtained by the microbial consortium from the Eastern European kefir granules exhibits greater homogeneity, the product obtained with the three strains of lactic acid bacteria has two phases, a whey and a clot, both of which are organoleptically sound.

Results from the analysis of fresh almonds and fermented products, obtained by HPLC, gas chromatography coupled with mass spectrometers, GC-FID E-Nose and sensory analysis evaluation will be discussed.

Keywords: Almond, Fermented, almond milk, Probiotic, Microorganisms

Unraveling *Lactobacillus helveticus* species inhabiting cultivable fraction of natural whey starter: a genotype and phenotype-based study

<u>Maria Anna Ronsivalle</u>¹, Marianna Cristofolini¹, Valentina De Martino¹, Valentina Pizzamiglio², Lisa Solieri¹

¹University of Modena and Reggio Emilia, Italy, ²Consorzio del Formaggio Parmigiano Reggiano, Reggio Emilia, Italy

maria.ronsivalle@studenti.unimore.it

The lactic acid bacterium (LAB) *Lactobacillus helveticus* is a key player in thermophilic dairy fermentation. LAB also inhabit the human gut, which has often been exploited as a reservoir of potential novel probiotics. We analyzed the cultivable fraction of 12 natural whey starters (NWS) sampled in 2 different sampling times through a DNA barcoding e genotypic approach. Twenty-five candidates were evaluated for tolerance to bile acids (BA), low pH, and lysozyme as probiotic traits.

Pentaplex-PCR and 16S-ARDRA analyses were used as DNA barcoding techniques. (GTG)5 REP-PCR was carried out to estimate the intra-species diversity (Simpson's index) and dereplicate the clones library. BA tolerance and pH tolerance were assessed by cultivating strains in the presence bile salt mixture (0.05%, 0.3%, 0.6%, and 1%), and at pH of 3.5, 4.5, and 5.4, respectively. Lysozyme (0.1 mg/mL) was used to test lysozyme tolerance.

Inter-species diversity was >0.9 Simpson's index for NWS enriched in *L. helveticus* (type-H), while was slightly lower in NWS enriched in *L. delbrueckii* (type-H). Huge phenotypic diversity was found within a pool of 25 genotypically unique strains. Two candidates showed the best growth response to all three stresses tested.

Two *L. helveticus* strains were found as good probiotic candidates.

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Keywords: Bile salts tolerance, pH tolerance, Lactic acid bacteria, *Lactobacillus helveticus*, Natural whey starter

Biotechnological approaches of OMIBREED project for sustaining olive genetic resources: micropropagation and in vitro conservation

Anna De Carlo, Waed Tarraf

Institute of BioEconomy (IBE), CNR, Italy

anna.decarlo@cnr.it

The conservation of plant biodiversity has gained worldwide attention, not only for endangered species but also for those with important cultural and economic values, such as Olea europaea L. In this context, the Italian Ministry of Agriculture, Food Sovereignty and Forests (MASAF) has funded the project "OMIBREED - Characterization and Valorization of Agrobiodiversity through Multiomic and Next-Generation Breeding Approaches for Resistance to *Xylella fastidiosa*". The main objective of this research is to identify genetic traits that confer resistance to Xylella fastidiosa (Xf) and to adopt advanced techniques such as micropropagation, slow-growth storage, and cryopreservation for the sustainable management of olive tree genetic resources. To achieve this goal, micropropagation in vitro was initiated with explants collected from various varieties. These explants were disinfected and placed on Rugini Olive medium (OM) supplemented with zeatin, mannitol, and Gelrite. For conservation at low temperatures, healthy and high-quality micropropagated shoots were cultured on OM medium containing different concentrations of zeatin, both in the presence and absence of light. Preliminary results have shown the effectiveness of micropropagation protocols and in vitro storage at low temperatures for short periods only for some varieties of olive. This finding will enable rapid clonal propagation, conservation, and enhancement of valuable olive biodiversity, including the genotypes selected by the project and centuries-old plants threatened by Xf in olive groves in the Apulia region. Since cryopreservation protocols are not yet optimised, studies are being conducted to verify how olive genotypes respond to the cryogenic process. Finally, the outcomes of OMIBREED could suggest a strategy to protect and propagate this vital genetic material through clonal methods, ensuring maximum diversity and phytosanitary safety.

Keywords: *Olea europaea*, in vitro culture, Slow-growth storage, Cryopreservation, *Xylella fastidiosa*

Characterisation of ancient citrus cultivars from Florentine Medici Villas by the use of Machine Learning techniques

<u>Elena Buonafede</u>¹, Cristiana Giordano¹, Deborah Beghè², Tommaso Ganino², Lorenzo Arcidiaco¹, Raffaella Petruccelli¹

¹Institute of BioEconomy (IBE), CNR, Italy, ²University of Parma, Italy

elena.buonafede@ibe.cnr.it

Originated in the Eastern world, citrus plants now include countless varieties and have been used for centuries for pharmaceutical, cosmetic, food, and ornamental aims, which have made them very desirable among collectors.

In the 16th century, the Medici family gathered and hybridised many citrus varieties, which are now hosted in the Florentine Medici Villas and taken care of following strict techniques, being placed outdoors from April to October while protected in citrus greenhouses during winter. These ancient varieties represent a great potential for the future of agriculture, holding unique morphological characteristics which reflect the historic agronomic practices and the adaptation to specific agricultural techniques.

The aim of this study was to perform a morphological characterisation of the citruses belonging to Medici's ancient collections hosted in Boboli Gardens and Villa Castello - both located in Florence -, using a mapping which dates back to the 1980s.

The dataset was digitised and the variability among varieties was evaluated considering morphological characters of fruit, seed, flower, and leaf, including both quantitative and qualitative variables. Analysis of variance was accompanied with: clustering, to identify homogeneous groups; feature importance, using models based on decision trees (random forest) to examine the contribution of every characteristic to the definition of the groups; PCA, to explore the overall variability.

The preliminary results reveal that some of the ancient varieties show strong morphological similarities, suggesting possible genetic correlations or convergences due to cultivation techniques. In addition, the feature analysis states that fruit weight, seed shape and leaf dimension are among the most discerning variables.

In conclusion, this study represents a substantial step towards the valorisation of the historic agronomic heritage of the Medici Villas, providing useful, objective data for conservation programs.

Keywords: Citrus cultivars, Medici Villas, Machine Learning, Morphology, Digitisation

Evaluating biostimulant effects on aromatic and medicinal plants cultivation within sustainable Mediterranean agroecosystem

<u>Paschalina Chatzopoulou</u>¹, Helen Lalidou¹, Maria Irakli¹, Kyriakos Giannoulis², Nektaria Tsivelika¹

¹Hellenic Agricultural Organization "Dimitra" - Institute of Plant Breeding and Genetic Resources, Greece, ²University of Thessaly, Greece

pchatzopoulou@elgo.gr

Mediterranean agro-ecosystems are increasingly vulnerable to climate change with challenges such as soil degradation and biodiversity loss impacting the farming practices. However, the region's dry climatic conditions, limited water resources and rich biodiversity offer unique opportunities for cultivating crops, resilient to both abiotic and biotic stresses. Aromatic and Medicinal plants (MAPs) are well-suited to organic farming, due to low pest susceptibility and reduced input requirements. Greek oregano is a high-value crop with growing global demand and holds a prominent position among MAPs in the Mediterranean. Sustainable fertilization practices can improve oregano's yield and overall product quality. Biostimulants emerged as a promising solution, promoting plant development and improving nutrient use efficiency. This study investigates the effect of various biostimulant treatments on Greek oregano, focusing on agronomic performance and essential oil yield and composition.

Four fertilization treatments were applied to experimental oregano fields using a randomized block design:

- 1. Control (no treatment)
- 2. Growers standard fertilization scheme
- 3. Basic fertilization + Biostimulant 1 + nitrogen fertilization
- 4. Basic fertilization + Biostimulant 1 + Biostimulant 2.

The essential oils were obtained by using hydrodistillation and the chemical composition was analyzed by GC/MS.

The results indicated that Treatment 4 was the most effective in enhancing essential oil yield, reaching 6.4%. Carvacrol was identified as the main essential oil compound, with the highest content observed in Treatment 3 (72.3%), followed by Treatment 4 (70.8%). Treatments 3 and 4 demonstrated the potential of biostimulants to enhance both essential oil yield and quality as indicated by high carvacrol content. In conclusion, the use of biostimulant-based fertilization schemes can reduce chemical inputs in oregano cultivation and improve the quality.

Keywords: MAPs, Greek oregano, Biostimulants, Sustainable agriculture, Mediterranean agroecosystems

From genetic diversity to phenotypic diversity: characterization and potential of a Historical Lemnoideae Collection

<u>Cristian Perna</u>, Luca Braglia, Maria Adelaide Iannelli, Silvia Gianì, Chiara Forti, Laura Emma Maria Morello

Institute of Agricultural Biology and Biotechnology (IBBA), CNR, Italy

cristian.perna@cnr.it

The Lemnoideae, an aquatic subfamily of the Araceae, diverged from their terrestrial ancestors \sim 40-50 Mya. Fossil evidence suggests a common pre-clade in North America, followed by rapid global dispersal. This enabled morpho-physiological adaptation to a floating lifestyle in eutrophic freshwater bodies across different climate zones.

The renewed interest in Lemnoideae, long known for water remediation, is currently driven by their remarkably high growth rate and valuable biomass, rich in proteins and starch, making them suitable for both animal and human consumption. Four species have been recently approved by EFSA as novel food, making them an emerging crop.

To study their genetic diversity and evolution, we started the molecular characterization of about 600 accessions from the historical Landolt collection, now at IBBA. The principal method employed was the Tubulin-Based Polymorphism (TBP), based on length polymorphisms in intron regions of β -tubulin genes, which provided a reliable clustering of accessions at species level. Plastid marker sequencing, genome size measurement and chromosome counting integrated this nuclear marker. Despite similar morphologies, results revealed high genetic diversity and phylogenetic complexity, including the existence of cryptic interspecific hybrids and variable ploidy in *Lemna*. Morphology-based classifications often proved inaccurate.

To assess ecophysiological diversity, we compared clones of representative species for their growth performance on dairy effluents, converting nutrients into valuable biomass. Results showed both inter- and intra-specific variation, with a triploid clone of L. × *mediterranea* exhibiting superior biomass increase and a specific *L. minor* accession displaying higher stress tolerance.

Such diversity supports duckweed exploration in agrifood systems, their role as bioindicators in ecotoxicological assays, and their use in nutrient recovery within a circular economy framework.

Keywords: Lemnaceae, Molecular Phylogeny, Emerging crop, Phytoremediation, Ecotoxicological assays

Genetic analysis of Sicilian forest trees as a tool to improve the management and conservation of local resources in face of global changes

<u>Claudia Mattioni</u>¹, Salvatore Pasta², Luca Leonardi¹, Giuseppe Clementi³, Marcello Cherubini¹, Giuseppe Traina³, Tommaso La Mantia³

¹IRET-Consiglio Nazionale delle Ricerche, Italy, ²IBBR-Consiglio Nazionale delle Ricerche, Italy, ³University of Palermo, Italy

claudia.mattioni@cnr.it

Several surveys have highlighted the enormous value of the genetic heritage of Sicilian forests, which, despite covering less than 10% of the island, host the richest tree floras in Italy. Many species live here at the southernmost edge of their distribution range; hence may have developed particular adaptations to extreme environmental conditions, which make them of high interest for reforestation in an increasing alarming scenario of global warming. In this context, the study of the genetic diversity of local trees is of fundamental importance to implement management and conservation measures for the island's forest. Our research (financed by the Sicilian Regional dept. of Rural and Territorial Development) focused on studying the intra- and interpopulation diversity of several forest trees as Acer (platanoides, pseudoplatanus, obtusatum, monspessulanum), Alnus glutinosa, Quercus petraea, Fraxinus excelsior, Ostrya carpinifolia, Malus sylvestris and Prunus mahaleb. Indices of genetic diversity within population as expected and observed heterozygosity (He, Ho), inbreeding coefficient (Fis) and differentiation among populations (Fst) were calculated. A Bayesian approach was performed, using the software STRUCTURE v.2.3.4, to identify the different gene pools. The results highlight a low genetic variability of A. *platanoides* stands and the presence of complex introgression processes between *A. pseudoplatanus* and the other two maple species. As for *O. carpinifolia* and *M. sylvestris*, the presence of the same gene pool was recorded in all stands on the island, while a clear genetic divergence emerged between the stands of *P. mahaleb*. We provide indications on the biogeographical history, the natural dispersal capacity and the possible impact of human activities on the current genetic pattern of the species. Moreover, we underline the importance of studying genetic diversity in order to implement conservation and management programs.

Keywords: Genetic diversity, Conservation, Global change, Forest Trees

Genetic and functional traits variability of Sardinian populations of strawberry tree (*Arbutus unedo* L.)

<u>Matteo Busconi</u>¹, Giuseppe Brundu², Elena Petretto¹, Alessandra Lanubile¹, Lorenzo Stagnati¹, Alessandra Lezzi¹, Pierpaolo Zara³, Tony Chahine², Donatella Spano², Simone Mereu³

¹Università Cattolica del Sacro Cuore, Italy, ²University of Sassari, Italy, ³CNR IBE Sassari, Italy

matteo.busconi@unicatt.it

Strawberry tree (Arbutus unedo L) is an evergreen shrub belonging to the Ericaceae family and a common element of the flora and vegetation of the Mediterranean basin. It is a highly vigorous resprouting species that can form forests, particularly in wildfire prone regions. At the genetic level, the species is diploid (2n = 26) with an estimated genome size of 450 Mb approximately. Only few papers dealing with the genetic characterisation and the determination of the population structure of strawberry tree (ST) are available, usually based on medium throughput approaches or on a defined number of markers, and no in-depth research have been carried out so far in Italy. In this study, 116 single plants belonging to 8 wild populations of ST from different sites in Sardinia (Italy) were sampled and analysed by using the Genotyping by Sequencing approach. Sampling sites were selected in areas, where STs grow spontaneously, characterised by different altitude, climate and geography in terms of sun exposition, temperature, water availability, soil types and composition. One of the sites was subject to a major fire a few years ago. Further, plant materials from all the individuals, fully expanded leaves, shoots of the year and leaves of different size, were sampled to assess functional traits: Huber Value, Leaf Mass per Area, Leaf Dry Matter Content, Leaf Size. A high level of genetic variability was observed, with each plant being unique and different from the others. Concerning the 8 populations, two of them were clearly different, while all the others present a very high level of intra-population variability, higher than the inter-population variability, preventing them to be clearly separated. Removing the two most different populations from the analyses, plants from other populations appeared to be more dispersed and other intermediate clusters could be defined. At the phenotypic level it is possible to see that all four traits vary between sites, but only moderately.

Keywords: Strawberry tree, Genotyping by sequencing, SNPs, Functional traits, Genetic variability
Micropropagation and in vitro conservation of "Patata dei Cortigli" germplasm

Anna Tagarelli, Giuseppe Natale Basile, Claudia Ruta

University of Bari, Italy

anna.tagarelli@uniba.it

Patata dei Cortigli, also known as patata del bosco, is a local Apulian variety of Solanum tuberosum L., found in clearings and forest edges on the Gargano promontory, between San Giovanni Rotondo and San Marco in Lamis. It represents a significant example of native agrobiodiversity, the result of both natural and human selection processes, which have enabled the variety to adapt to the specific soil and climate conditions of the area. As part of the project "Biodiversity of non-fruit vegetable species of Puglia - BiodiverSO VEG" (Rural Development Programme Puglia 2014-2020, action 10.2.1), a study was initiated on the potential application of micropropagation protocols to this genotype. Tubers provided by the Department of Agricultural Sciences, Food, Natural Resources and Engineering of the University of Foggia were conserved at 4 °C in the laboratory of micropropagation and microscopy at the Department of Soil, Plant and Food Sciences (UniBa). Subsequently, they were placed in a mixture of blond peat, brown peat, and perlite to induce sprouting. Axillary buds of approximately 0.2 cm were collected from the resulting sprouts and sterilized for in vitro introduction. The buds were then placed on a nutrient substrate (base medium - MB), solidified with agar and enriched with different concentrations of 6-Benzylaminopurine (BAP). After about three weeks, the shoots that had developed at least 6 nodes were multiplied using binodal cuttings and transferred to a renewed hormone-free nutrient medium. From that point on, the culture was subcultured every 25 days, showing a tendency toward tillering, resulting in an average multiplication index higher than 8. Rooting was observed without the need to add auxinic plant growth regulators. The plantlets obtained will soon be transferred to appropriate conditions for slow-growth conservation.

Keywords: Solanum tuberosum L., Local variety, Tuber, Shoots, 6-benzilaminopurine

Morphological traits of Olea europaea leaves in Italian Germplasm Collections

<u>Cristiana Giordano</u>¹, Elena Buonafede¹, Federico Stefani¹, Deborah Beghe¹², Tommaso Ganino², Cecilia Faraloni¹, Raffaella Petruccelli¹

¹IBE-CNR, Italy, ²University of Palermo, Italy

cristiana.giordano@cnr.it

The olive tree (*Olea europaea* L.) is a crop of global importance, with worldwide olive oil production exceeding 3 million tonnes in the 2024/2025 season (ISMEA, 2024), marking a 23% increase compared to 2023/2024. In contrast, Italy's production declined to 224 thousand tonnes, reflecting a 32% reduction from the previous season. Unfavorable conditions linked to the pathogen *Xylella fastidiosa*, responsible for the death of thousands of plants, and climate change have severely impacted southern Italy's production. Thus, the recovery, study, and conservation of olive agrobiodiversity are essential to maintain a genetic pool for breeding programs. This study aimed to morphologically characterize twenty-four olive cultivars from the Italian germplasm.

Twenty-four olive cultivars grown in CNR (Florence, Italy) collection field under uniform agroenvironmental conditions were analyzed. Mature leaves were subjected to:

- Color analysis (Konica Minolta CR-400),
- Macro- and micro-morphological measurements (Leica DM LB2 microscope; TESCAN GAIA3),
- Chlorophyll a fluorescence transient and JIP-test (Handy-PEA, Hansatech Instruments).
- Statistical analyses included ANOVA and multivariate methods (Cluster Analysis, PCA).

All examined traits exhibited significant variability among cultivars, highlighting distinct leaf characteristics. Two leaf color groups were identified: Light green (L* > 40, e.g., "Sant'Agostino", "Picholine") and Dark green (L* \approx 34, e.g., "Leccio Maremmano"). Anatomical analysis revealed statistically significant differences in total leaf thickness, ranging from 330.6 µm ("Maurino") to 488.6 µm ("Nocellara del Belice"), indicating structural diversity. The *Fv/Fm* index (about 0.8) suggested good photosynthetic efficiency.

The parameters evaluated in this study could facilitate the screening of cultivars resilient to adverse climatic conditions (e.g., drought, high temperatures).

Keywords: Olive cultivar, Trichomes, Leaf anatomy, Color, *Fv/Fm*

Nutritional profile of edible wild species from "Laguna del Re" Oasis

Anna Bonasia, Lucia Botticella, Corrado Lazzizera, Antonio Elia, Giulia Conversa

University of Foggia, Italy

anna.bonasia@unifg.it

This study aims to determine the key nutritional and anti-nutritional compounds and the antioxidant capacity of four spontaneous edible species (sea beet, bristly-ox-tongue, soft thistle, golden thistle). These obligate/facultative halophytes were collected during the spring period from "Laguna del Re" Oasis (Siponto, Manfredonia, Foggia province), a coastal wetland along the Adriatic Sea with high ecological and agricultural significance for the conservation and valorisation of edible wild species. Sea beet (along bristly-ox-tongue) exhibited the highest concentration of cations as well as carotenoids, phenolic compounds, and vitamin C. Sea beet also proved the highest antioxidant capacity. Sea beet showed the highest nitrate and oxalate levels, though both remained within safe limits for human consumption. Bristly-ox-tongue stood out for its high anthocyanin and flavonoid content. In contrast, soft thistle exhibited the lowest concentration of cations, antioxidant compounds and antioxidant capacity. Both softthistle and golden thistle were distinguished by their highest iodine content (129 µg 100 g f.w., on average), indicating that a 120 g serving portion could meet the Recommended Dietary Allowance for an adult. The examined species had an average Na content of 3.6 g kg-1 f.w. and a relatively high Na/K ratio (1.5), attributed to the saline conditions of their habitat. To avoid exceeding the recommended daily Na intake (2 g day-1), consumption should be limited to 500 g per day.

This study highlights the nutritional potential of spontaneous species from bio-saline environments; in particular, sea beet and bristly-ox-tongue stand out for their antioxidant and mineral content, while soft thistle and golden thistle stand out for their iodine content.

Keywords: Antioxidants, Iodine, Sea-beet, Bristly-ox-tongue, Soft- and golden-thistle

Propagation of *Achillea maritima* for its re-introduction in the Marine Protected Area of Torre Cerrano (TE), Italy

<u>Loretta Giuseppina Pace</u>¹, Maria Carla de Francesco^{2,3}, Beatrice Farda¹, Jordan Parmegiani¹, Francesca Tantalo¹, Angela Stanisci¹

¹University of L'Aquila, Italy, ²University of Molise, Italy, ³National Biodiversity Future Center (NBFC), Palermo, Italy

loretta.pace@univaq.it

The Marine Protected Area (AMP) "Torre del Cerrano" (Abruzzo, Italy), recognized as a Special Area of Conservation (SAC IT7120215) by the EU, hosts dune ecosystems with highly valuable species of psammophilous vascular flora. The SEED (Spread and Store Coastal Biodiversity) project, funded by Spoke 8 NBFC, involved the creation of a Germplasm Bank for ex-situ plant conservation and propagation used for rehabilitation of degraded dune sites. Particular attention was paid to an Asteraceae, which has disappeared from much of the Abruzzo coastline, with the aim of reintroducing it into the AMP: *Achillea maritima* (L.) Ehrend. & Y.P. Guo ssp. *maritima*. Antibacterial, antifungal, anti-inflammatory, and anticancer effects have also been ascribed to this plant.

Collection, cleaning and preservation of germplasm of native psammophilous plant species, including this species. On the latter: assays of in vivo and in vitro propagation protocols in controlled growth chambers; morphological study at M.O. Axio Zoom V16; analysis of chlorophyll and carotenoid content and antioxidant activity.

In vivo seed germination at 9 weeks reached about 20% while in vitro propagation required several trials to achieve sterility and a longer germination period. Physiological analyses performed on the aerial part of the plants showed a fair content of carotenoids (44.06 μ g/g FW) and chlorophylls (average content 406.48 μ g/g FW). Differences emerged between early germination stages and adult plants, particularly in chlorophyll content, 620.93 μ g/g FW and 458.40 μ g/g FW respectively. Antioxidant activity showed values of 30-31 IC50, indicative of strong antioxidant capacity.

The preliminary results obtained on *A. maritima* are being used for its propagation and reintroduction into the wild. An ecological characterization of the optimal germination conditions (salinity level and seed dormancy period) will be the next step in the research.

Keywords: Psammophilous flora, Germoplasm bank, Antioxidant activity, Seed germination, Plant conservation

The "ancient apple" varieties of "Central Italy" an inexhaustible source of biodiversity and health

Roberto Luneia¹, Alessio Luneia¹, Elena Luneia,¹, Francesca Moretti¹, Emanuele Scocchera²

¹Analysis Sarel srl, Italy, ²Melise srl, Italy

analysis@analysisgroup.it

The varieties of ancient apples from Central Italy are very numerous, highlighting how "fortunately" the biodiversity of these fruits is still wide. Furthermore, in many cases they also have high contents of phenolic compounds and anthocyanins with antioxidant and antiinflammatory properties, which increase their "health" value. In this work, the content of these bioactive molecules of some varieties of apples were studied: Sanguinella and Limoncella from Molise, Roggia and Rossa di Todi from Umbria.

The apples were cooled, homogenized and then extracted with a 70-30 water/ethanol solution. The extracts were stained with Folin-Ciocalteù reagent and read spectrophotometrically against a standard calibration curve of gallic acid at 765 nm to determine the total phenolic compounds. For total anthocyanins, the extracts were read directly spectrophotometrically at 518 nm. The antioxidant capacity was also determined with the ORAC degree by measuring the ability to protect fluorescein from degradation induced by radical activity, then expressing the results as TE (Trolox Equivalents), according to the method (Cao et al., Free Radic. Biol. Med., 1993, 14, 303-311).

Sanguinella and Limoncella apples showed a total phelolic compound content of 2248±67 and 2346±72 mg/Kg respectively referred to the dry substance, while Roggia and Rossa di Todi apples showed a content of 2985±87 and 2588±82 mg/Kg respectively. For the Roggia apple, the ORAC degree was then determined which gave a result of 4570±275 mmol TE/100g.

These preliminary results are very interesting and deserve a molecular investigation by evaluating the LC-MS profile of both phenolic compounds and anthocyanins to obtain an antioxidant and anti-inflammatory "Finger Print" of these very interesting ancient apples from Central Italy.

Keywords: Ancient apple, Central Italy, Phenolic compounds, Orac, anthocyanins

The "Traditional" varieties of grains, an inexhaustible repository of biodiversity: the "Saragolletta Rossa Molisana"

<u>Stefano Ripert</u>¹, Bruno Lasserre¹, Davide Marino¹, Luigi Mastronardi¹, Roberto Luneia², Alessio Luneia², Elena Luneia², Francesca Moretti²

¹Università degli Studi del Molise, Italy, ²Analysis Sarel Srl, Italy

stefano.ripert@gmail.com

The "Saragolletta Rossa Molisana" has been almost abandoned and it is very difficult to find data, there are only studies on the characterization of the Saragolle (*Triticum turgidum* subsp. *durum* of Abruzzo) that have shown how these varieties are a precious repository of biodiversity. Previous studies have identified genetic differences between *Triticum aestivum* and Saragolletta del Sannio. In this study we want to verify whether the population of seeds currently found in Molise, is a distinct variety or overlapping with the Saragolle that insist in the same area.

Three different plots were sown in the municipality of Castel del Giudice (IS) and the sowing will then be repeated for two consecutive years in the same conditions, with a basic technique. We expect significant differences in production due to different slopes and shading and for this purpose, we have geolocalized the plots by creating a grid with five square meter meshes. In each sector, surveys were carried out and then cross-referenced the data with those of the nearest meteorological station, to verify the existence of correlations with temperature and precipitation.

At the moment, data are available for the primary phenological phases developed so far, as the three plots were sown at an altitude of over 800 meters. In fact, the cultivation is still in the tillering phase, so in addition to the soil horizons, only the germination times, dry matter and the formation of culms for the tillering potential were evaluated. The protein content $(14.1\pm0.4 \text{ g/100g of dry matter})$ and total phenolic compounds (65 mg/Kg as gallic acid) were also determined on a small portion of unsown grain.

Obviously, it will be necessary to wait for the first definitive results in June to evaluate the effect of the particular area and the sowing altitude on the characteristics of the grain which, especially in terms of proteins, appear to be already good.

Keywords: Saragoletta Rossa Molisana, Repository of biodiversity, Saragolle, Protein, Phenolic compounds

Uncovering the genetic diversity of Tunisian monumental olive trees to promote the olive sector

<u>Monica Marilena Miazzi¹, Sameh Mnasri Rahmani², Olfa Saddoud Debbabi³, Cinzia Montemurro¹</u>

¹University of Bari Aldo Moro, Italy, ²University of Sfax, Tunisia, ³Banque Nationale de Gènes, Boulevard du Leader Yesser Arafet, Charguia, Tunisia

monicamarilena.miazzi@uniba.it

Centenary olive trees in Tunisia have a great symbolic cultural value of resilience. Neither the genetic diversity of these historical trees nor their commercial potential have been studied so far. Our study represents the first molecular analysis of historical olive trees in Tunisia.

The genomes of twenty-eight ancient olive trees from archaeological sites of Tunisia were analysed using nine highly polymorphic microsatellite markers. The genetic profiles were then compared with those of local varieties and other regions of the Mediterranean basin.

The study revealed the remarkable polymorphism of these ancient trees, which showed a high degree of observed heterozygosity and a remarkable allelic richness. Relatedness and structural analyses have shown that the centenary trees share a common genetic background with some Tunisian cultivars but also with varieties from Italy, Spain and Greece. These results indicate that the Tunisian germplasm has a common ancestry and that there has been a significant genetic exchange between olive plants in the Mediterranean region. The conservation of these unique trees is crucial and requires the implementation of effective conservation measures and strategies to ensure ecological benefits for future generations.

Keywords: Olive, Microsatellites, Genetic exchange, in situ conservation

Agroecological innovation through green mulch transplanting: enhancing soil health and biodiversity in mediterranean organic horticulture

<u>Gianmarco Mugnai</u>¹, Lorenzo Favaro¹, Cristina Micheloni², Stefano Bortolussi², Raffaela Petris³, Marina Basaglia¹

¹University of Padova, Italy, ²Associazione Italiana Agricoltura Biologica (AIAB) Friuli Venezia Giulia, Italy, ³Agenzia Regionale per lo Sviluppo Rurale del Friuli Venezia Giulia (ERSA FVG), Italy

gianmarco.mugnai@unipd.it

SOrBioTraP (Development of an Organic Horticultural System Based on Transplanting into Green Mulch) is a multi-stakeholder project financed by the Italian Ministry of Agriculture, Food Sovereignty, and Forests (MASAF), supporting agroecological transition and biodiversity conservation in Mediterranean horticultural systems. It addresses the critical challenge of weed management in organic farming by applying an innovative transplanting technique into green mulch (living or terminated cover crops). This strategy aims to improve soil fertility, reduce mechanical inputs and irrigation needs, and enhance crop resilience.

The project operates across different environments (open field and greenhouse), seasons, and mulch compositions (e.g., rye-vetch, Sudan grass), employing a sod transplanting machine adapted from Northern Europe. The project is focused on a microbiology-based evaluation of soil health. A dual analytical strategy integrates microscopic methods for assessing viable and metabolically active microorganisms, with metabarcoding (NGS) to characterize the taxonomic diversity and functional traits of bacterial and fungal communities. This approach will provide insights into microbiome composition, diversity, and ecological responses under the different soil management treatments highlighting their impact on microbial composition and activity.

Complementary assessments will include soil mesofauna, weed flora, crop productivity, water use efficiency, and socio-economic impacts. The involvement of farmers in shaping project strategies ensures both contextual applicability and scalability of the proposed practices.

SOrBioTraP will contribute to enhance Mediterranean biodiversity through soil conservation, reduced external inputs, and agrobiodiversity valorization. These outcomes align with EU Farm to Fork and Soil Health and Food strategies, offering a replicable model for sustainable organic horticulture.

Keywords: Agroecology, Green mulch, Soil microbiome, Organic horticulture, Sustainable farming

Exploiting yeast isolates from pear cv. Abbé Fétel carposphere as biocontrol candidates against *Stemphylium vesicarium*, the causal agent of the brown spot disease

<u>Viola Ceramelli Papiani</u>¹, Chiara Nasuti¹, Viola Ceramelli¹, Sara Zanetti¹, Alessandro Montorsi¹, Massimiliano Menghini², Marina Collina², Davide Giovanardi¹, Lisa Solieri¹

¹University of Modena and Reggio Emilia, Italy, ²University of Bologna, Italy

viola.ceramellipapiani@unimore.it

Microbial biodiversity is essential for plant health. The EU Farm to Fork Strategy restricted pesticide use in agriculture. This study explored the potential of yeasts inhabiting pear cv. Abbé Fétel carposphere as candidate biocontrol agents (BCA) against *Stemphylium vesicarium*, causal agent of brown spot of pear (BSP).

In 2024, pear fruits were collected from thirteen Emilia-Romagna orchards conducted with organic and integrated pest management, respectively. Yeasts were isolated on YPDA medium, morphologically characterized, and in vitro screened for their antimicrobial activity against *S. vesicarium*. Then, a selection of 25 yeast isolates were molecularly identified by sequencing the rDNA ITS region.

A biobank of 260 isolates was established, displaying a mycelia growth inhibition of *S. vesicarium* ranking from -15.71% to 42.48%. The yeasts were attributed to *Aureobasidium pullulans, Metschnikowia* spp., *Rhodotorula babjevae, Pichia kluyveri,* and *Hanseniaspora uvarum*. One isolate belonged to *Papiliotrema horticola*, an endophytic yeast previously associated with apple fruits. Sequencing of ITS amplicons failed for *Metschnikowia* spp. isolates, according to the well-documented rDNA heterogeneity within this clade. When yeast BCA candidates were tested against different *S. vesicarium* strains, their antagonistic activities were slightly variable, depending on the *S. vesicarium* strain used.

The presence of diverse yeast species with antagonistic activity against *S. vesicarium* highlights the pear carposphere as a reservoir of potential novel BCAs for effective and sustainable pathogen management. In planta experiments will investigate their ecological role and potential in controlling BSP.

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Keywords: Epiphytic yeasts, *Pyrus communis*, Biocontrol, Agro-environmental microbiology, Sustainable agriculture.

Fermented milk fortified with polyphenols extracted from olive leaves and functional strains: preliminary data

<u>Sofia Cosentino</u>¹, Roberta Comunian², Margherita Addis², Massimo Pes², Antonio Paba², Carlo Piga², Angela Carboni², Federica Mereu¹, Maria Barbara Pisano¹

¹University of Cagliari, Italy, ²Agris Sardegna, Servizio Ricerca Prodotti di Origine Animale, Italy

scosenti@unica.it

Consuming foods enriched with functional ingredients could reduce the risk of chronic diseases and improve physical and mental well-being. The project FUNDAIRIES (granted by PNRR, NextGenerationEU - PE_00000003) aims to develop new functional dairy products by adding probiotic strains and bioactive polyphenols recovered from olive leaves (PE). This study was carried out to assess the effect of PE on the growth of two probiotic strains, Bifidobacterium animalis subsp. lactis BB12 and Lactiplantibacillus plantarum UNICA B26, in fermented sheep's milk (FM).

A preliminary screening was conducted using the broth microdilution method to analyze the antibacterial activity of PE and establish the MIC towards the two probiotic strains. The ability of the strains to tolerate PE concentrations of 20 and 10 mg GAE 100 g-1 was then assessed. The FM was produced using either the BB12 or the UNICA B26 strain with and without PE at 20 mg GAE 100 g-1. FM samples underwent microbiological analyses to evaluate the impact of PE on probiotic growth and viability, as well as sensory analyses to assess the influence of probiotics on the sensory profile of the final product.

Both strains were not affected by PE concentrations tested under the experimental conditions applied. The acidification curves of FM showed a similar pH decrease for samples added with probiotics only and with PE, suggesting that polyphenols do not affect the starter activity. FM added with BB12 and UNICA B26 plus PE showed similar microbial counts during the whole shelf-life. Differences in sensory characteristics were only observed for the samples fortified with PE.

Overall, data suggests that the addition of PE to FM did not negatively affect the acidification process or the viability of both probiotic strains during refrigerated storage. This supports the potential use of polyphenols to enhance the functionality of probiotic fermented dairy products.

Keywords: Functional food, Probiotic, Polyphenols, Dairy products

Isolation and characterization of yeast diversity in nectar of Onosma spp.

<u>Ciro Sannino</u>¹, Samuele Pignedoli², Daniele Calabrese², Massimo Nepi², Pietro Buzzini¹, Benedetta Turchetti¹

¹University of Perugia, Italy, ²University of Siena, Italy

ciro.sannino@unipg.it

Over the last ten years, significant research has been conducted on the microorganisms present in floral nectar and how they affect nectar composition. These microorganisms transform sugars, amino acids, and various compounds, leading to alterations in the chemical profile of nectar. Due to its high sugar concentration, along with proteins and secondary metabolites (NSCs), nectar acts as a selective barrier against microbial colonization. NSCs not only possess antimicrobial properties but also potentially affect interactions with other organisms. Some yeast species are specifically adapted to flourish under the high osmotic pressures found in nectar, yet their diversity and ecological significance remain largely neglected. Investigating the connection between yeast diversity in nectar and other plant-related microhabitats could provide valuable insights into their ecological functions. It is essential to establish a standardized method for collecting and characterizing yeasts from nectar to facilitate further research. The genus Onosma (Boraginaceae: Lithospermeae) includes plants that are particularly suitable for such investigations because of their abundant nectar production, as well as their floral morphology and orientation, which minimize dilution from rainfall. These characteristics may reduce random variability and mitigate potential errors associated with limited nectar availability volumes.

This study aims to investigate yeast diversity in floral nectar, their ecological roles, and their interactions with secondary metabolites, using the genus *Onosma* as a model system.

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Keywords: Microhabitat, Antimicrobial properties, Ecological functions

Multispecies bioinoculant enhances sugarloaf chicory (*Cichorium intybus* L.) performance while modulating rhizosphere microbial diversity and functionality

Lorenzo Pin¹, Giulio Testone¹, Salvatore Gaglione², Flavia Pinzari¹, Donato Giannino¹

¹Institute for Biological Systems, CNR, Monterotondo, Italy, ²Enza Zaden Italia, Tarquinia, Italy

lorenzopin@cnr.it

The use of bioinoculants in organic farming is increasing due to their ability to enhance crop yields, boost immunity, and suppress soil-borne pathogens. They offer a sustainable alternative to chemical fertilizers, which harm soil health and the environment. However, the large-scale introduction of microorganisms raises concerns about potential disruptions to native microbial communities, which are crucial for soil resilience. Understanding these effects is key to sustainable bioinoculant use.

This study evaluated Micosat F® UNO-a bioinoculant based on a mixture of mycorrhizae (*Rhizophagus* spp.), beneficial fungi (*Trichoderma harzianum*), and other microbes-on sugarloaf chicory (*Cichorium intybus* L. var. *foliosum*) cultivated in an organic farming system. Bioinoculated plants had higher post-transplant survival (99.8% vs. 97.2%), reduced disease incidence (88.7% vs. 72.7%), and greater net yield (397 vs. 320 q/ha) than controls. Illumina shotgun metagenomic sequencing was performed to evaluate shifts in rhizosphere microbiota. Alpha diversity measurements showed significantly higher evenness in bioinoculated soils (t(17) = 2.35, p = 0.0312). Moreover, bioinoculation altered the beta diversity of microbial assemblages, as supported by PERMANOVA of Bray-Curtis dissimilarity (p = 0.0091, R² = 0.10687). Functional gene characterization showed no significant difference in total gene abundances, though treated samples had lower overall functional gene abundances. These findings suggest that bioinoculant-induced microbiota variations enhance plant growth and may sustain long-term fertility, paving the way for further research on plant-microbiome interactions.

Keywords: Bioinoculant, Soil biodiversity, Metagenomics, rhizosphere, Sugarloaf-chichory

Surviving the cold: unraveling molecular strategies of *Mrakia gelida*'s resilience in freezing conditions

Daniele Andreani, Benedetta Turchetti, Gianpiero Marconi, Emidio Albertini, Pietro Buzzini

University of Perugia, Italy

daniele.andreani@dottorandi.unipg.it

Cold-adapted yeasts, such as *Mrakia gelida*, not only play a critical role in organic matter turnover in cold habitats but are also considered valuable biotechnological resources, thanks to their ability to thrive in very low-temperature environments. However, further genetic investigation is required to comprehensively elucidate the mechanisms underlying their coldstress responses. In this study, three strains of *M. gelida* were grown in YPD liquid media at their optimal temperature (15°C), then exposed to cold stress (4°C), and subsequently returned to 15°C. Biomass from each phase was processed for RNA extraction and RNA-seq analysis to characterize transcriptomic changes associated with cold adaptation and recovery. Preliminary findings indicate that, when comparing cold stress to the control, there is an overexpression of CDSs related to membrane transporters, detoxification-related proteins, and enzymes involved in expanding the range of utilizable carbon substrates under cold stress conditions. Additionally, in the comparison between stress and restored conditions, these CDSs show expression levels similar to the control, suggesting a return to baseline transcription after cold stress. These findings suggest that *M. gelida* utilizes diverse strategies to preserve cellular homeostasis and metabolic flexibility during cold stress. The results enhance our knowledge of psychrophilic yeast biology and may contribute to future biotechnological advancements, including the development of enzymes and other products tailored for cold environments.

Keywords: *Mrakia gelida*, Psychrophilic yeasts, Cold stress response, Transcriptomic analysis, RNA-seq

Synthetic microbial communities assembly for bacterial cellulose synthesis optimization

<u>Federico Lasagni</u>¹, Robab Ezazi¹, Marilisa Giavalisco², Emanuela Lavanga², Alessandro Ulrici¹, Teresa Zotta², Maria Gullo¹

¹University of Modena and Reggio Emilia, Italy, ²University of Basilicata, Italy

federico.lasagni@unimore.it

Bacterial cellulose (BC) is a biopolymer with many industrial uses. Within PRIN 2022-SynBioCell project (code: 20228Z34PF), to enhance BC production, Synthetic Microbial Communities (SMCs) consisting of acetic acid bacteria (AAB) as core microbial components, lactic acid bacteria (LAB), and yeasts (Y) were developed and studied.

Komagataeibacter xylinus K1G4, K2G30, K2G30 Δgdh, *K. rhaeticus* K2G14 (AAB), *Lacticaseibacillus casei* N87, *Lactiplantibacillus pentosus* O17, *Levilactobacillus brevis* LB12 (LAB), *Brettanomyces bruxellensis* KCO149, *Kluyveromyces lactis* UMCC701, *Saccharomyces cerevisiae* UMCC165 (Y) strains were used for SMC assembly. A Plackett-Burman design (PBD) was used to screen strain significance in BC production (static growth system, HS medium, 28°C). Top SMCs were reassembled to study AAB, LAB, and Y interactions during BC production, and the best SMC was tested for LAB's stimulatory effect on BC production. Single AAB strains served as control. Finally, a second PBD was used to select top SMCs by modelling key factors affecting BC yield.

SMC2 (K2G30, K1G4, O17, N87, LB12), SMC9 (K2G30, K2G30 Δgdh, O17, KCO149, UMCC701) and SMC11 (K2G30 Δgdh, K1G4, K2G14, N87, UMCC701) were top BC-producing while SMC7 (K2G30 Δgdh, N87, O17, UMCC165, KCO149) was the worst. Unlike Y, LAB actively moved to BC layer. O17 and LB12 were the most stimulant LAB, while K2G30 and K1G4 were the most performing AAB strains. AAB and LAB settled in BC layers. PBD revealed incubation temperature and carbon source amount as the key factors affecting BC yield, identifying SMC9 as the highest BC-producing SMC during the process.

A selected SMC optimized BC production, unravelling interactions among AAB, LAB and Y. Lactic acid and ethanol exchange likely boosted BC production by AAB, highlighting LAB and Y as effective helpers. Further metabolic and transcriptomic studies will be performed to clarify SMC members interactions and roles.

Keywords: Synthetic microbial communities, Acetic Acid Bacteria, Bacterial cellulose, Microbial interactions, Microbial communities

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