XXX SIPaV
CONGRESS 2025
CATANIA • SEPTEMBER 15-17

XXX CONGRESS
OF THE ITALIAN PHYTOPATHOLOGICAL SOCIETY

PLANT HEALTH: CONTRIBUTIONS OF PLANT PATHOLOGY TO A SUSTAINABLE FUTURE

CATANIA, SEPTEMBER 15-17, 2025
MONASTERO DEI BENEDETTINI

BOOK OF ABSTRACTS

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PLATINUM

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CONGRESS PROGRAM

Monday, September 15

8:00-9:30 **Registration & Poster Setup**
Welcome Coffee

9:30-10:00 **Opening of the XXX Congress of the Italian Phytopathological Society**
Francesco Priolo, *Rector of the University of Catania*
Mario D'Amico, *Director of the Department of Agriculture, Food and Environment*
Paola Battilani, *President of the Italian Phytopathological Society (SIPaV)*

10:00–10:30 *Invited talk*
Crop Health: a multidisciplinary system approach to reduce the use of agrochemicals
Alessandra Gentile**,** *UNICT Coordinator for AGRITECH project, Department of Agriculture, Food and Environment, University of Catania*

10:30 – 12:30 Session 1: **Sustainable Strategies for Plant Disease Management**
Chairs: Roberta Marra, Giorgio Gusella

Oral Presentations (OP): Agritech Contributions

OP1 Capacity of yeast-derived products to enhance grapevine immunity and tolerance to combined drought and *Botrytis cinerea* infection
A.G. Ilesanmi, C. Gonzalez-Dehennault, M. Lucchetta, I. Busato, F. Meggio, M. Marangon, M. Perazzolli, R. Musetti, L. Sella, F. Favaron, S. Tundo

OP2 Environmentally friendly RNAi-based control of grapevine powdery mildew
M. Karas, F. Negrini, R. Baroncelli, X. Chen, F. Pacini, E.G. Kabeto, L. Capriotti, S. Sabbadini, B. Mezzetti, E. Baraldi

OP3 Mitigating the impact of soil salinity on tomato crops: unveiling the role of soil microorganisms
M.I. Prigigallo, S. Pirra, G. Bubici

OP4 The effect of biological control agents on peach fruit infected by *Monilinia laxa*: biochemical and molecular analyses
A. Lizzio, V. Battaglia, E. Lahoz, M. Reverberi, M. Petriccione

OP5 Application of antimicrobial peptides for the control of grapevine flavescence dorée phytoplasma
E.G. Kabeto, M. Karas, F. Pacini, X.Q. Chen, T.Q. Gao, F. Pizzuti, C. Lanzoni, C. Marzachì, L. Galetto, D. Bosco, B. Mezzetti, S. Sabbadini, L. Capriotti, L. Landi, P. De Angeli, R. Musetti, S. Favia, M. De Zotti, E. Baraldi, C. Ratti

OP6 Exploring *Hermetia illucens* frass as a new source of bacteria with potential antifungal and plant growth promoting activity
L. Coviello, M. Nuzzaci, J. De Smet, J. Ceusters, C. Scieuzo, P. Falabella, D. Ronga, A. Vitti

OP7 Genetic variability within *Diaporthe amygdali* populations in almond orchards in Apulia (Southern Italy)
A. Agnusdei, F. Dalena, P.G. Lucchese, P. Tancredi, F. Faretra, S. Pollastro, D. Gerin

OP8 Microbial biocontrol agents reprogram tomato response to pests and pathogens: a multi-omics perspective
M. Sinno, I. Di Lelio, G. Manganiello, M. Ranesi, G.S. Falconieri, A. Pascale, A. Becchimanzi, M. Sulli, G. Diretto, F. Pennacchio, M. Lorito, S. Proietti, S.L. Woo

OP9 A MultiOmics approach for better understanding and comprehensive management of durum and soft wheat kernels quality and safety in the Italian Peninsula
L. Lascala, M. Beccaccioli, S. Frasca, M. Kratter, V. Cecchetti, C. Manetti, M. Reverberi

12:30-13:30 **Light lunch**

13:30-14:30 **Poster Session I** – In-person discussion of Posters 1-60

14:30-16:30 Session 2: **Sustainable Strategies for Plant Disease Management**
Chairs: Stefania Somma, Daniele Schiavi

Flash Talks (FT) from "Young Researchers in Training"

FT1 Improved tolerance to grey mold of tomato plants fertigated with micronutrient amounts of zinc
V. Artico, I. Battisti, L. Sella, S. Tundo, G. Dal Corso, B. Molesini, T. Pandolfini, G. Arrigoni, R. Musetti, A. Furini, F. Favaron

FT2 Sustainable control of *Plasmopara viticola* in grapevines via SafeWax: a bioinspired passive coating strategy
A. Brannetti, M.A. Ibanez Revert, N. Ben-Arie, I. Polishchuk, B. Pokroy, S. Fermani, I. Filippetti, C. Ratti, E. Baraldi

FT3 Unveiling the antibacterial potential of eucalyptus-based nanoparticles: a game-changer in crop bacterial disease management
M. Pinto, C. Soares, A. Ribeiro, T. Andreani, F. Fidalgo, F. Tavares

FT4 Varietal susceptibility and biological approaches for the management of *Albugo occidentalis* in Spinach cultivated in the Capitanata Area
P. Marino, A. Carlucci, M.L. Raimondo, F. Lops

FT5 Plant products as putative botanical fungicides assayed *in vitro* and *in vivo* conditions against fungal soilborne pathogens on fennel seedlings
M.G. Morea, T. Conte, G. Ricciardi, D. Paulicelli, P. Morea, A. Carlucci

FT6 Salvia spp. extracts contain bioactive terpenoids against grapevine downy mildew
A. Smaldone, O. Giovannini, M. Oberhuber, P. Robatscher, M. Perazzolli

Oral Presentations

OP10 Italian peanuts: an integrated approach to ensure safety and sustainability
M. Crosta, M. Camardo Leggieri, P. Battilani

OP11 Metabolomics-guided optimization of *Trichoderma*-based bioformulates for sustainable crop improvement in grapevine and sorghum
A. Staropoli, D. Lotito, L. Izzo, V. Battaglia, E. Lahoz, S.L. Woo, M. Lorito, F. Vinale

OP12 *Diaporthe amygdali* inside out: leveraging genetic insights for sustainable and precision control strategies
S. Turco, F. Brugneti, A. Cardacino, M. Cirilli, A. Mazzaglia

OP13 Antifungal factors or resistance elicitors? Role of polycyclic tetramate macrolactams in the biological control of *Peronospora belbahrii* and *Plasmopara viticola* by *Lysobacter capsici* AZ78
A. Dinesh Kothari, S. Nadalini, M. Masi, A. Cimmino, I. Pertot, G. Puopolo

OP14 Circular plant protection measures against Xanthomonadaceae plant pathogens: antibacterial potential of pomegranate peel extract and cellulose nanocrystals
M.A. Muawiya, D. Schiavi, L. Felici, C. Miccoli, D. Rongai, M.R. Ecija, L. Moll, B.B. Landa, G.M. Balestra

OP15 Combined *Trichoderma-Clonostachys* reduce Fusarium head blight infection and mycotoxin content of wheat under greenhouse conditions
A. Petrucci, S. Conlan, S. Sarrocco, D.B. Collinge, B. Jensen

OP16 Integrated control strategies for managing crown and fruit rot of pomegranate caused by *Coniella granati* in Southern Italy
M.L. Raimondo, G. Ricciardi, T. Conte, A. Carlucci, F. Lops

16:30-17:00 **Coffee Break**

17:00-19:00 **Italian Phytopathological Society and Journal of Plant Pathology**
Chairs: Paola Battilani - *President of SIPaV*, Laura Mugnai - *Vice President of* SIPaV

"Giovanni Scaramuzzi" SIPaV Award 2025
Journal of Plant Pathology & SIPaV Awards: "Fresh Ideas in plant health: the latest research from young plant pathologists"
Sabrina Sarrocco, *Editor of JPP special issue*
Thirty Years of Science and Passion: Tracing the History of SIPaV and its Congresses
Giovanni Vannacci, *Former President of SIPaV*

Agritech Challenges in Research and Education
Matteo Lorito, *Rector of the University of Naples Federico II*, *President of National Agritech Center*

19:00 **Welcome Cocktail**
Chiostro di Levante, Monastero dei Benedettini

Tuesday, September 16

08:30-10:00 **Session 3: Diagnosis and Characterization of Plant-Associated Pathogens**
Chairs: Alessandra Di Francesco, Dario Gaudioso

Flash Talks from "Young Researchers in Training"

FT7 A new molecular seed detection method to quantify *Ustilago nuda* and reduce prophylactic seed treatments
C. Panzetti, E. Jenny, I. Bänziger, A. Kägi, S. Vogelgsang, T. Hebeisen, P. Büttner, D. Croll, F. Widmer, K. E. Sullam

FT8 Exploiting actinomycete biodiversity in Arctic soils to find new biocontrol agents of fungal pathogens
L. Pisoni, S. Viganò, C. Pizzatti, A. Kunova, P. Cortesi, M. Pasquali, M. Saracchi, L. Bertini, C. Caruso, D. Bulgari

FT9 Image-based time series analysis for the early evaluation of the biocontrol efficacy of *Trichoderma gamsii* T6085 on Fusarium head blight disease progression in wheat
D. Mencarini, A. Petrucci, G. Del Cioppo, S. Poque, K. Himanen, K. Mäkinen, S. Sarrocco

FT10 Strains of *Aureobasidium pullulans* from extreme environments: new potential biocontrol agents?
M. Lucci, N. Khomutovska, G. Firrao, A. Di Francesco

FT11 Genetic insights of *Aspergillus flavus* population in Azerbaijan and perspectives on the use of aflatoxin biocontrol products
A. Casu, K.A. Callicott, H.L. Mehl, P. Battilani

Oral Presentations

OP17 Botryosphaeriaceae and *Phytophthora* species involved in the decline and mortality of ornamental trees on Albarella Island (Italy)
C. Bregant, M. Piccioni, C. Antonelli, L. Montecchio, M. Narduzzi, A.M. Vettraino, B.T. Linaldeddu

OP18 Advancing plant health monitoring: nanopore sequencing for quarantine pathogen diagnostics
V. Crosara, V. Scala, M. Reverberi, N. Pucci, L. Faino, S. Loreti

OP19 Invisible foes: cutting-edge non-destructive diagnostics for quarantine pathogens in legume seeds in a globalized market
D. Gaudioso, L. Calamai, C. Pastacaldi, C. Beltrami, L. Cavigli, G. Agati, S. Tegli

OP20 Assessing the spread and impact of candidate priority pests to support risk management in the EU: EFSA's method and results
A. Nougadère, M. Scala, S. Tramontini, E. de la Peña, G. Gilioli, D. Makowski, A. Mastin, S. Parnell, S. Vos

OP21 Innovative e-probe detection of 11 viruses infecting tomato using e-probes diagnostic nucleic-acid analysis and microbe finder (EDNA-MiFi)
A. Ragona, D. Ramos-Lopez, A.S. Espindola, E. Yahyaoui, S. Davino, F. Ochoa-Corona

10:00-11:00 **Poster session II & Coffee break -** In-person discussion of Posters 61-120

11:00-11:30 *Invited talk*
Koch's postulates in a microbiome era
Carolee T. Bull, *Department of Plant Pathology and Environmental Microbiology, Pennsylvania State University, University Park, USA*

11:30-13:00 **Session 4: Molecular Interactions and the Plant Microbiome**
Chairs: Elodie Vandelle, Donato Gerin

Flash Talks from "Young Researchers in Training"

FT12 Seed treatment with bacterial and fungal endophytes modulates transcriptional and phenotypic responses of rice to *Fusarium fujikuroi*
S. Bosco, G. Mannino, M. Mezzalama, C. Bertea, D. Spadaro

FT13 Characterization of the MAT1 locus involved in the sexual behaviour in isolates of *Podosphaera xanthii* from south Italy
M. Crudele, P.R. Rotondo, P. Loizzo, S. Laera, C. Laguardia, S. Pollastro, R.M. De Miccolis Angelini, F. Faretra

FT14 Early insights into spore germination and compatibility between *Trichoderma gamsii* and *Clonostachys rosea* under stress conditions: toward dual biocontrol of Fusarium head blight
A. Dalli, A. Petrucci, S. Sarrocco, B. Jensen, D.B. Collinge

FT15 RNAi-based control of *Stemphylium vesicarium* in pear: genomic insights into host specificity
X.Q. Chen, T.Q. Gao, M. Karas, F. Pacini, E.G. Kabeto, R. Baroncelli, E. Baraldi

FT16 Sieve element cell wall composition and sugar transport are strictly interconnected and affect Micro-Tom tomato plant response to 'Candidatus Phytoplasma solani'
S. Favia, O.C. Viscardo, K. Konate, S. Tundo, L. Sella, F. Favaron, R. Musetti

Oral Presentations

OP22 Deciphering the impact of different belowground pathogens on the aboveground bacterial microbiome in tomato plants
E. Francomano, M.M. Aci, M. Casuscelli, L. Schena, A. Malacrinò

OP23 What happened to the grapevine microbiome? Spontaneous grapevines as reference standard
G. Del Frari, F. Marroni, M. Guazzini, F. Marcolin, S. Ponte, R. Boavida Ferreira, G. Zdunic, G. Di Gaspero, M. Morgante

OP24 Deciphering FHB infection: the metabolomics-driven quest for sustainable wheat protection
S. Risoli, T. Rypar, M. Doppler, C. Bueschl, B. Seidl, A. Parich, G. Adam, L. Cotrozzi, C. Nali, P. García-Pérez, S. Sarrocco, E. Pellegrini, L. Lucini, R. Schuhmacher

OP25 A dual-function metabolite from *Beauveria bassiana* shapes plant-pathogen interactions
M. Ranesi, S. Vitale, A. Staropoli, L. Di Costanzo, M. Lorito, S.L. Woo, F. Vinale, D. Turrà

OP26 Streptomycetes as biocontrol agents against *Fusarium oxysporum* f.sp. *lycopersici* and *Fusarium graminearum* in tomato and wheat crops
V. Mattei, G. Franzoni, C. Muratore, K. Sergeant, C. Pizzatti, D. Bulgari, A. Kunova, M. Saracchi, P. Cortesi, G. Cocetta, L. Espen, J. Renaut, A. Ferrante, B. Prinsi, M. Pasquali

13:00-14:00 **Light lunch**

14:00-14:30 *Invited talk*
Building resilience to insect-vectored plant pathogens
Saskia A. Hogenhout, *John Innes Centre, Norwich Research Park, Norwich, UK*

14:30-15:30 **Session 5: Molecular Interactions and the Plant Microbiome**
Chairs: Valeria Scala, Lorenzo Cotrozzi

Oral Presentations

OP27 Investigations on resistance to agents of grapevine yellows in different pathosystems
M. Schillaci, D. Danzi, G. Gambino, L. Galetto, F. Cavagna, S. Palmano, A. Polverari, C. Marzachì

OP28 Decoding the Regulatory Role of PsaR3, a LuxR Solo, in *Pseudomonas syringae* pv. *actinidiae* virulence
I. Lucato, A. Regaiolo, D. Danzi, R. Heermann, A. Polverari, E. Vandelle

OP29 Sophisticated Sabotage: how phytoplasma effectors manipulate their host plant's cell fate and metabolism
C. Malfertheiner, S. Egger, M. Raffeiner, C. Mittelberger, B. Hause, T. Letschka, S. Üstün, K. Janik

OP30 Deciphering molecular mechanisms in the interactions of '*Candidatus* Phytoplasma solani' with its experimental herbaceous hosts
W. Acosta Morel, A. Moussa, P. Bianco, C. Bernardini, P. Ermacora, F. Quaglino, M. Martini

OP31 Interkingdom interactions: transcriptional reprogramming of tomato by beneficial and harmful organisms
F. Palomba, M.M. Monti, M. Novero, V. Bianciotto, S. Ghignone, E. Lumini, D. D'Esposito, A. Salvioli, P. Bonfante, M. Ruocco

15:30-18:30 **Poster session III & Coffee break -** In-person discussion of Posters 121-198

16:30-18:30 **General Assembly of SIPaV Members**

20:30 Social dinner at the 'RADICEPURA – Horticultural Park' Via Fogazzaro 19, Giarre (Catania)

Wednesday, September 17
8:45-10:00 Open coffee

9:00-09:30 *Invited talk*
Making sense of the NLR immune receptor alphabet soup
Sophien Kamoun, *The Sainsbury Laboratory, UK*

09:30-12:00 **Session 6: Emerging Plant Pathogens and Epidemiological Trends**
Chairs: Marco Camardo Leggieri, Guglielmo Gianni Lione

Flash Talks from "Young Researchers in Training"

FT17 From observations to forecast: advancing aflatoxin risk prediction with seasonal climate projections
D. Balkova, R. Raj, H. Rieder, M. Camardo Leggieri, P. Battilani

FT18 Twig canker and shoot blight of peach in Italy: the role of *Diaporthe amygdali* and a cultivars tolerance screening
F. Brugneti, L. Rossini, M. Cirilli, A. Cardacino, A. Mazzaglia, S. Turco

FT19 The role of EFSA commodity risk assessments in identifying high-risk plant pathogens
M.F. Lombardo, C. Gardi, G. Stancanelli

FT20 Unraveling the pathogenicity of *Pseudomonas syringae* pv. *syringae* Italian strains causing severe wilting in eggplants
M. Paglialunga, B. Orfei, A. Scian, T.H.M Smits, C. Ramos, G. Carannante, V. Stravato, R. Buonaurio, C. Moretti

Oral Presentations

OP32 *Trichoderma afroharzianum*, an emerging pathogen of maize in Europe: identification and early diagnosis
M. Sanna, V. Guarnaccia, D. Spadaro, M. Mezzalama

OP33 Survey of *Neofabraea vagabunda* in Friuli Venezia Giulia Region: causal agent of apple bull's eye rot
A. Di Francesco, M. Camardo Leggieri, M. Lucci, R. Cignola, A. Francavilla, A. Malacrinò, S. Mosca, V. Guarnaccia, P. Battilani

OP34 Several *Phytophthora* species are associated with chestnut ink disease in Tuscany, central Italy
A. Benigno, V. Papini, D. Rizzo, S. Moricca

OP35 Emergence of acute oak decline in Mediterranean holm and kermes oaks: detection of bacterial pathogens and ecological considerations
A. Bene, G. Carluccio, M. Vergine, E. Sabella, A. Delle Donne, L. De Bellis, A. Luvisi

OP36 Advances in understanding genomic diversity and adaptive evolution of the plant pathogenic model system *Colletotrichum*
J. Sunmoon, M. Ramos, I. Martino, P. Talhinhas, V. Guarnaccia, R. Baroncelli

OP37 Apple bitter rot and Glomerella leaf spot: diversity and tissue-specific behavior of *Colletotrichum* spp. in Northern Italian orchards
M. Calì, E. Cappelletti, S. Iacono, R. Bugiani, P. Talhinhas, R. Baroncelli, A. Prodi

OP38 Drought is a key factor exacerbating the virulence of emerging pathogens of London plane trees (*Platanus* x *hispanica*)
G. Lione, V. Guarnaccia, G. Costa, P.M. Travaglia, P. Gonthier

OP39 New insights on the role of oospores in primary infections and seasonal dynamics of downy mildew
G. Fedele, M. Furiosi, S.L. Toffolatti, V. Rossi, G. Maddalena, T. Caffi

OP40 New insights on mycotoxigenic *Aspergillus* species on peach fruits in Southern Italy
M. Masiello, S. Somma, A. De Girolamo, L. Gambacorta, L. Catalano, L. Laghezza, A. Carella, S. Iandiorio, C. Telser, A. Moretti, G. Cozzi

12:00-13:00 SIPaV Awards and initiatives – Closing ceremony

INVITED TALKS

Crop Health: a multidisciplinary system approach to reduce the use of agrochemicals

Alessandra Gentile

Università degli studi di Catania, via Santa Sofia 100, 95124, Catania, Italy; email: alessandra.gentile@unict.it

The development of novel varieties showing increased tolerance toward biotic stress is becoming one of the most important challenges for humanity. Agriculture is called upon to feed a growing population and to reduce its environmental impact. These achievements are made even more complex by climate change and its effect on temperatures and rainfall, especially in the Mediterranean area.

In this context, plant breeding plays a pivotal role in developing novel selections coupling increased tolerance to biotic stress with superior fruit quality. This achievement relies also on the precise characterization of local varieties, enabling the set-up of controlled crosses and/or the identification of candidate genes and the development of edited plants.

To achieve this goal, it is fundamental to integrate, to plant pathology, other expertise such as: bioinformatic, *in vitro* culture, molecular biology and agronomy. The recent results related to the plant-host interactions of three Mediterranean tree crops (almond, grape and lemon) are here discussed and challenges and future perspectives are outlined.

Almond: One of the main pathogens affecting almond cultivation in the Mediterranean is *Diaporthe amygdali*, the causal agent of almond constriction canker. Symptomatology consists of cankers centered around the shoot nodes, gummosis and shoot blight. To decipher the genetic determinism of the tolerance to almond constriction canker, a germplasm collection of 123 accessions (mostly local varieties) was genotyped using 47,946 SNPs. The same individuals were subjected to a detached-twig inoculation test and the area of the necrotic lesion was employed as phenotypic data for a genome-wide association study (GWAS). GWAS enabled the identification of 9 SNP significantly associated to tolerance/susceptibility to *D. amygdali* and the detection of four genes related to the response to biotic stress, showing differential expression between susceptible and tolerant genotypes. Grape: Powdery mildew represents one of the major threats affecting grape cultivation worldwide. In the last years, the MLO genes were identified as major genes involved in the susceptibility to the disease. Genome editing represents an unprecedented tool for the introgression of genes in elite cultivars, in this context, the local grape varieties 'Nero d'Avola' e 'Frappato' were employed for a targeted CRISPR/Cas9-mediated knock-out for the development of new edited selection coupling high fruit quality with a higher tolerance to the disease.

Lemon: One of the main limiting factors for lemon cultivation in the Mediterranean basin is represented by mal secco disease, a tracheomycosis caused by the mitosporic fungus *Plenodomus trachiphilus*. To detect candidate genes linked to tolerance to mal secco, a pedigree-based analysis (PBA) was carried out employing two segregating families connected through a pedigree encompassing the known ancestors of lemon. Phenotyping was performed through both *in vitro* inoculation and observation of the symptoms in plants held in open fields in an area characterized by high pathogen pressure. All accessions were genotyped with 30,008 robust SNPs. QTL analysis highlighted significant marker trait associations on LG 2, 4 and 6 highlighting the Pumelo as the main source of tolerance to the disease.

Koch's Postulates in a Microbiome Era

Carolee T. Bull

Department of Plant Pathology and Environmental Microbiology, Pennsylvania State University, University Park, USA. Email: ctb14@psu.edu

Plant pathologists have long investigated microbiomes, particularly the phytobiome, to better understand the microbial components that influence plant disease. As new technologies have emerged, our discipline has consistently adapted, embracing innovative tools to explore the complex and dynamic interactions between microbial communities and plant health. At the core of the practice of plant pathology lies Koch's postulates, a foundational framework for establishing causal relationships between pathogens and disease. These postulates involve isolating a suspected pathogen from symptomatic tissue, reproducing the disease phenotype in a healthy host, and then re-isolating the same pathogen from the experimentally infected host. Building on this framework, Stanley Falkow introduced Molecular Koch's Postulates, which extend the concept of causality to the genetic level. These postulates demonstrate that disrupting a specific gene in a pathogen leads to the loss or alteration of its associated phenotype, and that restoring the gene restores the original pathogenic trait. This molecular approach has significantly advanced our understanding of microbial virulence and host-pathogen interactions. Today, plant pathologists and microbiome researchers are working to extend these principles to the study of complex microbial communities through the development of *Microbiome Koch's Postulates*. These emerging frameworks aim to establish causal links between entire microbial assemblages, or specific components within them, and host or ecosystem-level phenotypes. Unlike traditional approaches that focus on individual pathogens, microbiome-based methods consider the collective influence of microbial consortia on plant health and disease outcomes. Experimental strategies within this framework include additive, subtractive, and evolutionary or enrichment approaches to manipulate microbial communities. Subtractive methods often involve the use of group-specific antimicrobial compounds or microbial predators to selectively remove portions of the microbiome. These interventions help identify functional groups or taxa that contribute to specific phenotypes. Additive approaches involve the application of synthetic communities, probiotics, or prebiotics to recreate desired system-level traits. The combination of subtractive followed by additive approaches most closely resemble traditional Koch's postulates. A particularly promising strategy is *microbiome passaging*, a set of practices that promote adaptation and intensify host-microbiome interactions. By repeatedly exposing microbial communities to the same environmental conditions and selective pressures, microbiome passaging encourages the evolution of traits that enhance system-level phenotypes. Trait enhancement is the goal of passaging approaches, but causality in the relationships between microbiome composition and plant outcomes could be strengthened by combining this approach with additive or subtractive methods. In this presentation, we will review key literature supporting the formulation of Microbiome Koch's Postulates and discuss their implications for advancing our understanding of plant-microbiome interactions. These evolving tools not only deepen our insight into the microbial ecology of plant systems but also open new avenues for disease management and crop improvement through microbiome manipulation.

Building resilience to insect-vectored plant pathogens

Saskia A. Hogenhout

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Sap-feeding insects, including aphids, psyllids, leafhoppers, and froghoppers, are among the most important vectors of bacterial plant pathogens, such as *Candidatus Phytoplasma*, *Liberibacter* species, and *Xylella fastidiosa*. These vector–pathogen complexes are highly invasive and have been linked to the collapse of fruit and crop production systems, as well as the decline of native plant communities across the globe. Their impact on agricultural productivity and ecosystem stability is profound, yet the biological mechanisms underpinning their success remain poorly understood.

Our research addresses this gap by investigating how these pathogens, and the effector proteins they secrete, manipulate plant physiology and alter interactions with their insect vectors. These manipulations can change host plant traits in ways that improve vector performance, enhance their attraction to infected plants, and ultimately facilitate pathogen transmission.

To support this work, we have generated comprehensive genomic and transcriptomic resources for more than 40 hemipteran species, providing a platform to explore the evolution and adaptation of vector species. We have also resolved the global population structure and reconstructed dispersal pathways of several key invasive vectors, offering insight into their routes of introduction and spread.

Our findings reveal that the success of these pathogens is closely linked to their ability to boost insect vector fitness and long-distance migratory capacity, traits that are actively promoted through pathogen-mediated changes in plant physiology. These interactions create a positive feedback loop in which plant manipulation drives increased pathogen dissemination.

Importantly, our work highlights that the strict dependence of these pathogens on their insect vectors presents a potential vulnerability. By understanding the mechanisms of vector attraction, feeding, and reproduction, we can identify opportunities to disrupt these processes. This knowledge can be applied to the development of crops with enhanced resistance to vector colonization, potentially breaking the transmission cycle.

Taken together, these results underscore the urgent need to deepen our understanding of sap-feeding insect biology, ecology, and evolution. A more complete grasp of the factors driving vector and pathogen success will be essential for designing sustainable strategies to mitigate the spread of vector-borne plant diseases, safeguard agricultural production, and protect biodiversity in natural ecosystems.

Making sense of the NLR immune receptor alphabet soup

Sophien Kamoun

The Sainsbury Laboratory, Norwich Research Park, Norwich, United Kingdom. Email: sophien.kamoun@tsl.ac.uk

Plants possess a sophisticated innate immune system that enables them to defend against a vast array of microbial pathogens. A central component of this defense is a large family of intracellular immune receptors known as nucleotide-binding domain and leucine-rich repeat-containing receptors (NLRs). These proteins act as intracellular sentinels that detect pathogen-secreted effector molecules and, upon recognition, trigger a cascade of immune responses often culminating in the hypersensitive response (HR)—a localized programmed cell death that effectively restricts pathogen proliferation. Remarkably, NLRs account for approximately 1% of all plant proteins, underscoring their central role in plant immunity and the evolutionary pressure exerted by host–pathogen interactions.

Despite being grouped under one class, NLRs exhibit striking diversity in function and organization. Some act as singleton receptors, combining pathogen detection and immune signaling within a single molecule. Others operate as specialized sensors and helpers in higher-order pairs and networks, forming interconnected systems that provide robustness and adaptability against rapidly evolving pathogens. These networks, sometimes encompassing dozens of NLRs, illustrate how modularity and redundancy are embedded into the plant immune system to ensure durability in the face of pathogen attack.

In this talk, I will review the basic principles of plant NLR biology, emphasizing how these receptors perceive effectors and orchestrate immune responses. I will highlight the most recent structural and functional insights, including cryo-electron microscopy studies that are unraveling the molecular mechanisms of NLR activation.

An exciting frontier is the integration of artificial intelligence to better classify and functionally annotate NLRs. We showed that AI-driven protein structure prediction systems such as AlphaFold 3 can categorize NLRs into functional classes based on their predicted oligomeric configurations. In our analyses, helper NLRs consistently showed higher AlphaFold 3 confidence scores when modeled in oligomeric states, and their structures revealed funnel-shaped assemblies essential for immune activation. By contrast, sensor NLRs lacked these features. Applying this method to uncharacterized NLRs, AlphaFold 3 reliably distinguished putative sensors from helpers even when both lacked non-canonical domains. These findings suggest that AI-guided structural prediction offers a powerful new approach to classify NLRs, providing functional insights even in the absence of sequence-based annotations.

Pathogens, in turn, have evolved effectors that target and suppress NLR-mediated immunity, revealing critical nodes in these networks and illustrating the relentless co-evolutionary arms race. Understanding these suppression mechanisms not only illuminates fundamental biology but also informs strategies to engineer more resilient immune systems in crops.

To make sense of the expanding "alphabet soup" of NLRs, a multidisciplinary approach is essential, integrating genetics, genomics, structural biology, computational modeling, and synthetic biology. By decoding the logic of NLR networks and leveraging AI tools, we are poised to unlock new opportunities in durable disease resistance breeding and to usher in an era of rational design of plant immunity.

SIPAV "GIOVANNI SCARAMUZZI"2025 AWARD

Cold plasma as an innovative technology in integrated crop and plant protection strategies.

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Low-temperature plasma (LTP) is proposed as a green technology for sustainable agriculture. It consists of electrons, ions, radicals, stable and short-living radicals, such as reactive oxygen and nitrogen species (RONS), and ultraviolet radiation. The PhD thesis explores the effects of both direct and indirect applications of LTP for microbial inactivation.
The effectiveness of Volume Dielectric Barrier Discharge (VDBD) was evaluated by *in vitro* conidial germination assays in five different species of phytopathogenic fungi, various discharge conditions, and medium composition. The inhibitory effect was influenced by the applied voltage, increased with treatment duration, and decreased with fungal spore complexity. Differences among different fungal species could be related to the cell wall thickness, structure, and composition. In this work, albino mutants of *Botrytis cinerea* and *Aspergillus carbonarius* were used to explore the protective role of fungal melanin on sensitivity to plasma exposure, with mutants showing higher sensitivity to treatments compared to the melanized wild-type strains. The decontaminant activity of VDBD was also tested on barley seeds artificially inoculated with three different *Fusarium* species. Inoculated seeds were exposed to a barrier discharge in synthetic air, humid air, and pure oxygen, at different exposure times, in the attempt to investigate the better requisite for seed decontamination while preserving seed germinability.
Plasma Activated Water (PAW) generated through Surface Dielectric Barrier Discharge (SDBD) was tested as a decontaminating medium against fungi and bacteria. The concentration of reactive species and acidity of water and oxidation-reduction potential increased with the treatment time, with higher levels of reactive species and low pH associated with higher efficacy against microorganisms. Furthermore, PAW was tested as an innovative irrigation medium to enhance growth and trigger defence responses in tomato seedlings. PAW-irrigated seedlings exhibited significant growth enhancement compared to those receiving conventional fertilization. Gene expression analysis showed up-regulation of defence genes in PAW-treated plants post-infection with *Tomato mottle mosaic virus*.
Plasma Activated Fog (PAF), composed of small droplets of plasma-activated water could be a more efficient medium. PAF, generated using the plasma afterglow of a VDBD in a jet-like configuration to nebulize water through the Venturi effect, was evaluated for fruit decontamination against postharvest fungal pathogens and pesticide residues in fruits. In i*n vitro* experiments, the almost complete inhibition of conidial germination of major fungal postharvest pathogens was achieved after 3-5 min of exposure. The efficacy of PAF against fungal rots was assessed on table grapes and strawberries, revealing a significant reduction in the percentage of symptomatic fruits exposed to 10-min treatments, as well as the reduction of pesticide residues. In addition, the activation of defence responses in strawberry fruits exposed to PAF was revealed by whole transcriptome analysis.
The results gained in the PhD project allowed to demonstrate the potential of plasma applications as a tool for decontamination, promoting plant growth, inducing defence response in plants and fruits, potentially contributing to an increase of shelf-life of fresh products.
Overall, these studies enable us to identify the main critical factors for applying plasma technology and to optimize treatment parameters based on specific objectives.

SESSION 1

Sustainable Strategies for Plant Disease Management

ORAL PRESENTATIONS

OP1 Capacity of yeast-derived products to enhance grapevine immunity and tolerance to combined drought and *Botrytis cinerea* infection

A.G. Ilesanmi[1], C. Gonzalez-Dehennault[2], M. Lucchetta[1], I. Busato[1], F. Meggio[2,3], M. Marangon[2,3], M. Perazzolli[4,5], R. Musetti[1,3], L. Sella[1,3], F. Favaron[1,3], S. Tundo[1,2]

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Viticulture is affected by abiotic and biotic stresses causing yield losses and deterioration of berry quality. Climate change, characterized by alternating periods of increased water supply and drought, poses threats to grapevine production. Among biotic stresses, *Botrytis cinerea,* the causal agent of grey mold, is a major concern for grapevine cultivation. Romeo®, a yeast-derived product whose active ingredient is cerevisane, is registered against grapevine diseases. While cerevisane has been shown to induce defense responses in grapevine, its efficacy varies depending on the pathogen. To broaden our understanding of the protective potential against grapevine pathogens and the mechanism of action of *Saccharomyces cerevisiae*-derived products, Romeo® and another yeast-derived product, Cultus Lievito™, were compared for their capacity to prevent *B. cinerea* infections. Additionally, the study aimed to investigate whether these products could mitigate the stress determined by different watering conditions and to ascertain possible interactions between biotic and abiotic stress factors. Cultus Lievito™ and Romeo® treatments determined a positive impact on stomatal conductance after water deprivation during the recovery phase. Cultus Lievito™ proved effective in reducing *B. cinerea* symptoms on grapevine leaves both in regular watered and in drought stressed plants. Cultus Lievito™ treatment induced higher expression of molecular markers related to water stress and pathogenesis such as *NCED*, *STS* and *PR2*. Finally, to investigate the mechanisms underlying the differing efficacy of the two yeast-derived products, we used HPLC to quantify cell wall polysaccharides, separated by molecular mass. The analysis revealed that Cultus Lievito™ contained a higher concentration of oligosaccharides than Romeo®.

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). This manuscript reflects only the authors' views and opinions, neither the European Union nor the European Commission can be considered responsible for them.

OP2 Environmentally Friendly RNAi-Based Control of Grapevine Powdery Mildew

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Powdery mildew caused by *Erysiphe necator* is one of the most widespread and economically severe grapevine diseases worldwide. To keep vineyards marketable, growers commonly apply 8–15 fungicide sprays per season, making powdery-mildew control a major driver of chemical use in viticulture. This heavy reliance on synthetic fungicides raises production costs, accelerates pathogen resistance and creates significant environmental impacts and public concern.
Spray-Induced Gene Silencing (SIGS), a RNAi-based controkl strategy, offers an environmentally friendly alternative that can suppress *E. necator* without chemical residues. We designed and tested three double-stranded RNA (dsRNA) constructs directed against fungal genes with unknown function that are strongly expressed during infection. dsRNA targeting *CYP51*, a well-established fungicide locus, and a unspecific dsRNA were used as controls to check for non-target effects. Greenhouse experiments showed that two of the three novel constructs, together with the *CYP51* control, produced a clear and statistically significant reduction in pathogen biomass during grapevine leaf infection, whereas the unspecific dsRNA had no measurable influence.
These results validate two new SIGS targets for controlling *E. necator* and demonstrate that RNAi sprays can deliver substantial disease suppression while avoiding the environmental costs of conventional fungicides. Future work will test these constructs under field conditions and explore nanoparticle formulations to enhance dsRNA stability, uptake and longevity.

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 the PRIN PROJECTCross-Kingdom RNAi for enhancing plant resistance-Bando 2022-Prot. 2022LBK9R4. This work reflects only the authors' views and opinions, neither the European Union nor the European Commission can be considered responsible for them.

OP3 Mitigating the impact of soil salinity on tomato crops: unveiling the role of soil microorganisms

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Soil salinization poses a significant threat to modern agriculture, particularly in southern Italy, where climate change exacerbates the challenges faced by crops. This research aims to investigate the soil microbiome of three Apulian locations, including coastal (Fasano and Margherita di Savoia) and inland areas (Foggia), to identify salt-adapted microorganisms that may lead to the discovery of novel plant-beneficial taxa for sustainable tomato cultivation. Soil of the three locations differed in macro- and micronutrients content, including sodium, with the highest and lowest salinity in Fasano and Foggia, respectively. No remarkable difference occurred in texture. By a metagenomic analysis (Illumina platform), differential operational taxonomic units (OTUs) were identified in the Bacteria-, Archaea-, and Fungi-specific amplicons among locations and through three stages of the tomato cropping cycle. β-diversity indices were significantly different among locations for bacteria and fungi, and over the season for archaea. α-diversity indices indicated greater variation among the locations than among the sampling time points. Microbial isolates from some soil samples, specifically *Bacillus* spp., *Aspergillus* spp., and *Penicillium* spp., were evaluated *in vitro* for their resistance to salinity and plant growth-promoting traits. Isolates from the saline soil (Fasano) showed Effective Concentration 50 (EC_{50}) values higher than the isolates from Foggia, suggesting that the saline environment (Fasano) selected more resistant microbial populations. Overall, fungi exhibited greater resistance to salinity than bacteria. *In planta* experiments are underway to assess the ability of microbial isolates to improve tomato plants' salinity tolerance.

This work was funded by the research project "Deciphering microbiomes from extreme environments for the improvement of crop resilience to climate change, food security and safety (MiCroResi)" (framework "4th EU-LAC Multi-thematic Joint Call for collaborative projects from Europe, Latin-America and the Caribbean Countries"), by "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 17/6/2022,CN00000022) and by the PNRR project SUS-MIRRI.IT "Strengthening the MIRRI Italian Research Infrastructure for Sustainable Bioscience and Bioeconomy" (code n. IR0000005). This manuscript reflects only the authors' views and opinions, neither the EU nor the European Commission can be considered responsible for them.

OP4 The effect of biological control agents on peach fruit infected by *Monilinia laxa*: biochemical and molecular analyses

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Monilinia laxa, responsible for brown rot in peaches, causes significant economic losses. Biological control agents (BCAs) represent a sustainable alternative for managing fungal disease. This study investigated the effect of three commercial formulations, 3Logy® (three essential oils), Serenade® Aso (*Bacillus subtilis* strain QST 713), and Biorestore flow (*Bacillus* spp.), on the antioxidant system (total phenolic and flavonoid content, antioxidant activity) and enzymatic activities (catalase, polyphenol oxidase, phenylalanine ammonia lyase) of peaches inoculated with *M. laxa*. Five days after inoculation, analyses were performed using biochemical assays and RT-qPCR. Tissue samples were collected at 1 cm from the wound and inoculation site. All three formulations reduced disease severity compared to the untreated inoculated control. Serenade® Aso significantly increased total phenolic and flavonoid contents, as well as antioxidant activity. In contrast, the effects of Biorestore flow and 3Logy® were comparable to those observed in the inoculated control sample. These findings were supported by the expression levels of the phenylalanine ammonia lyase gene. Catalase activity increased in fruits treated with Biorestore Flow and 3Logy®, while it was lower in those treated with Serenade® Aso. Considering the expression level of the catalase gene, results suggested the involvement of post-transcriptional regulation mechanisms. The downregulation of the polyphenol oxidase gene observed in all treatments was associated with a corresponding reduction in enzymatic activity in the treated samples compared to the untreated. These findings highlight the potential of BCAs to enhance peach defense responses against *M. laxa*, supporting their use as a sustainable alternative to chemical inputs.

This work was supported by PNRR Project "National Research Centre for Agricultural Technologies (Agritech) - SPOKE 2 Crop Health: a multidisciplinary system approach to reduce the use of agrochemicals" CUP C23C22000450006 funded by the Italian Ministry for Universities and Research (MUR).

OP5 Application of Antimicrobial Peptides for the Control of Grapevine Flavescence Dorée Phytoplasma

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Grapevine flavescence dorée phytoplasma (GFDp) is associated to a grapevine disease that has significant consequences for the wine industry in terms of economic losses and it is classified as a quarantine pest by the European Union. GFDp is a systemic, phloem-limited and wall-less pathogen, primarily transmitted by the sap-sucking insect vector *Scaphoideus titanus*. Current management strategies are limited as effective compounds like tetracyclines are not allowed in agriculture due to health risk, and resistant varieties are not yet available for breeding. Therefore, there is a need for discovering advanced pathogen management approaches. Among the emerging alternatives, antimicrobial peptides (AMPs) have emerged as a promising alternative as they are naturally present in almost all living organisms and can be synthesized based on natural analogs. Their antimicrobial action can be displayed directly either through membrane disruption or interfere with cellular functions, and indirectly through mechanisms involving activation of the plant immune response. Another promising application of AMPs is their expression in transgenic plants to protect the host from multiple pathogens. Availability of optimized synthetic AMPs with improved stability, low toxicity, and broad-spectrum efficacy against economically important plant pathogens is making significant progress. The aim of our research is to develop novel protocols and tools using optimized AMPs to manage GFD phytoplasma through different approaches.

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SIPaV Società Italiana di Patologia Vegetale Italian Phytopathological Society — XXX SIPaV CONGRESS 2025 CATANIA · SEPTEMBER 15-17 — Università di Catania — Uni ct AGRICOLTURA, ALIMENTAZIONE E AMBIENTE

OP6 Exploring *Hermetia illucens* frass as a new source of bacteria with potential antifungal and plant growth promoting activity

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With the aim to develop new and sustainable strategies to control phytopathogenic fungi, thermal-treated frass (70°C, 1-2h, according to EU regulation), a by-product of the non-pest fly *Hermetia illucens* breeding, as such or as aqueous extract (TT-FE), and its microbiome, were assessed. We focused on their effects on plant growth, fungal disease suppression, and substances and genes implicated in the plant defense pathway including enzymatic and non-enzymatic antioxidant system and defense-related genes. Frass, added in the soil, was able to control *Fusarium oxysporum* f.sp *lycopersici* on tomato while was not able to reduce the lesion diameter caused by *Alternaria brassicicola* (AB) and *Botrytis cinerea* (BC) on Arabidopsis. When used as TT-FE for seed priming, frass determined a reduction of damping-off caused by *F. sporotrichioides* on durum wheat. With both techniques frass improved growth performance in all tested plant species, induced changes in the antioxidant system in tomato and wheat, and reduced the expression of the chitinase *CHI9* gene in tomato. *Bacillus licheniformis*, *B. velezensis* and *Paenibacillus polymyxa,* isolated and molecularly identified from frass extract, could be responsible of the disease suppression caused by phytopathogenic fungi, being known their biocontrol activity. Indeed, all three strains were positively tested *in vivo* on Arabidopsis leaves for their ability to reduce lesion diameter caused by BC and AB, and also to improve germination and root development of seedlings. In conclusion, frass can ameliorate plant resilience, also thanks to its content of microorganisms, thus representing a valuable alternative to agro-chemicals in plant biostimulation/biocontrol.

This research was carried out within the Agritech National Research Center and was funded by 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).

OP7 Genetic variability within *Diaporthe amygdali* populations in almond orchards in Apulia (Southern Italy)

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Twig canker and shoot blight, caused by *Diaporthe* complex including *Diaporthe amygdali* seriously compromising the productivity of almond orchards. Quick desiccation of buds, flowers, and leaves after early spring infections, followed by the appearance of brown lesions around buds that further develop into annual sunken cankers, sometimes with gummy exudate and withering twigs are the main disease symptoms. Recent studies on local and international cultivars in Apulia (Southern Italy) showed a greater susceptibility of cvs Ferragnes and Guara/Tuono than Filippo Ceo. On 'Guara' (Casamassima, Apulia) a broad population of *Diaporthe* was obtained and preliminary grouped in a Vegetative Compatibility Group Assays. A phylogenetic study was then conducted on 16 different isolates of *D. amygdali*, selected as representative of different VCGs. Molecular identification was conducted using the primer couples ITS1/ITS4 and EF-728F/EF-986R, targeting the partial region of ITS1-5.8S-ITS2 and translation elongation factor 1-alpha (TEF1), respectively. The retrieved sequences were aligned by MUSCLE and maximum-likelihood trees for both *loci* were constructed using bootstrap method on 1000 trees. The hierarchical depth of both ITS and TEF trees suggested divergence into multiple groups, with at least 4 major clusters discriminable. Furthermore, to better understand fungal diversity, the determination of mating types was conducted by PCR using primers couples MAT1-1-1F/ MAT1-1-1R and MAT1-2-1F/MAT1-2-1R. All the isolates were heterothallic and carried MAT 1-2-1 *locus*. The occurrence of only one mating type would prevent the sexual process. The extension of investigations to other almond orchards is ongoing to better understand the origin of intraspecific variability.

This research was partially carried on within the Agritech National Research Center and received funding from the European Union Next-Generation EU (PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR) –MISSIONE 4 COMPONENTE 2, INVESTIMENTO 1.4 – D.D. 1032 17/06/2022, CN00000022). This manuscript reflects only the authors' views and opinions, neither the European Union nor the European Commission can be considered responsible for them.

OP8 Microbial biocontrol agents reprogram tomato response to pests and pathogens: a multi-omics perspective

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Microbial biocontrol agents (mBCAs) represent a valuable strategy in sustainable agriculture to control pest and pathogen damage while promoting plant growth. In this study, tomato plants were inoculated with *Trichoderma afroharzianum* and/or *Beauveria bassiana*, either singly or as a consortium. Treated plants were subsequently subjected to biotic stress induced by the fungal pathogen *Botrytis cinerea* or the aphid *Macrosiphum euphorbiae*, while unstressed plants served as controls. Bioassays demonstrated that mBCA applications significantly reduced disease incidence and severity, as well as decreased aphid infestation and reproduction rates, compared to untreated controls. To explore the underlying mechanisms, metabolomic, proteomic, and hormonomic analyses were employed. The multi-omics profiling revealed marked shifts between stressed and non-stressed plants, and among treatments. In *B. cinerea*-infected samples, untreated plants displayed a metabolic signature consistent with oxidative stress and programmed cell death. Conversely, mBCA-treated plants accumulated defensive secondary metabolites—including oxylipins, phenols, phenylpropanoids, and alkaloids—along with an accumulation of defense-related hormones, suggesting the activation of targeted defense pathways. Furthermore, aphid infestation induced degradation pathways in untreated plants, whereas microbial treatments promoted growth recovery and defense activation. Interestingly, *B. bassiana* primarily triggered jasmonate signaling, while *T. afroharzianum* enhanced abscisic acid levels, indicating the activation of distinct defence pathways, but when applied in combination both responses were preserved.
Overall, these findings demonstrate the dual role of mBCAs in enhancing plant resistance and modulating metabolic responses to stress. The observed biochemical reprogramming supports the application of microbial consortia as effective and sustainable tools in integrated crop protection strategies.

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OP9 A MultiOmics approach for better understanding and comprehensive management of durum and soft wheat kernels quality and safety in the Italian Peninsula

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Wheat is one of the most cultivated cereal crops in the Mediterranean basin area, with both durum and soft wheat representing strategic resources for food security. Climate and environmental changes endanger the cultivation of key crops by influencing their growth and yield. This is related also to changes in the microbiome composition and the plant metabolome. By examining the kernel's metabolome and microbiome composition, it is possible to assess sample quality before planting or food processing. As plant microbiome influences the host's performance, it is crucial to gain a comprehensive understanding of its composition. Identification of the presence of species that produce toxins, or, of beneficial microbials that can limit pathogen growth may lead to the development of new strategies to protect the agricultural market and consumer health. To conduct this research, a multi-omics approach was applied to study several durum and soft wheat varieties harvested in Italian peninsula in 2023. Untargeted metabolomics (LC-Orbitrap) analyses were performed to explore chemical signatures linked to wheat variety, quality and traceability and to find possible correlations with metagenomic and agronomic data. Metabolic fingerprints tend to cluster samples according to their eco-geographical origin, suggesting that environmental conditions have a stronger influence on the metabolome than the wheat genotype. A metagenomic analysis through metabarcoding sequencing using Oxford Nanopore Technology was performed in parallel with *in vitro* isolation of fungal endophytes, revealing both emerging pathogens and promising biocontrol agents, which are being investigated in co-culture assays against wheat pathogens, supporting future applications in sustainable disease management.

This work has been supported by PNRR MUR project CN_00000022 "Agritech" and IR0000033 "Metrofood"

POSTER SESSION I

Poster list from 1 to 60

1. **Soil-derived *Pseudomonas* spp. suppress *Armillaria mellea* and promote plant growth modulating underground microbiomes.**
M. M. Aci, G. Pelle, G. E. Agosteo, A. Malacrinò, L. Schena

2. **Monitoring Dothistroma needle blight in protection forests of the Eastern Alps**
C. Aglietti, L. Stazione, D. Andreis, N. Luchi, A. Santini, L. Ghelardini, G. Maresi

3. **Non-invasive early detection of ToBRFV using near-infrared (NIR) spectroscopy**
G. Agrò, G. Masoero, M. M. Barone, S. Davino, S. Matic

4. **Screening of seven citrus viroids incidence in commercial orchards of the main Sicilian citrus areas**
G. Agrò, M. M. Barone, E. Yahyaoui, A. G. Caruso, S. Panno, S. Matic, G. Scuderi, G. Licciardello, A.F. Catara, S. Davino

5. **Survey on *Xanthomonas campestris* pv. *campestris* strains from *Brassica* spp. in Latium Region**
L. Albanese, M. A. Muawiya, G.M. Balestra, D. Schiavi

6. **Pathotype diversity of *Plasmopara halstedii* in Central Italy: preliminary data and establishment of a monitoring system**
I. Alberti, M. Dal Prà, N. Pecchioni, A. Del Gatto

7. **Preliminary results on the control of *Fusarium* wilt on lettuce by insect frass and exuviae from *Hermetia illucens***
L. Alfarano, S. Bellezza Oddon, L. Gasco, M. Pugliese

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P1 Soil-derived *Pseudomonas* spp. suppress *Armillaria mellea* and promote plant growth modulating underground microbiomes.

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The soilborne pathogen *Armillaria mellea* poses a significant threat to a wide range of host plants, and its control presents considerable challenges. In this study we explore soil microbiomes hunting for potential biocontrol agents against *A. mellea*, focusing on their antifungal efficacy and plant growth promotion in controlled conditions. Through an *in vitro* mass screening method followed by dual culture assays, we isolated four *Pseudomonas* species with *in vitro* biocontrol efficacy against *A. mellea*: three isolates inhibited almost completely fungal growth, while one isolate prevented rhizomorph development. The sequencing of their whole genomes confirmed their biocontrol potential, evidentiating the presence of biosynthetic gene clusters related to antifungal compounds and siderophores, crucial not only for suppressing fungal pathogens but also for plant growth promotion. The inoculation of olive plant with biocontrol agents caused a significant increase in plants biomass and clear alterations in the bacterial diversity and community structure of roots and in rhizosphere soil. The results of a Structural Equation Model suggested that the inoculation of the biocontrol agents influenced plant biomass directly but also indirectly by modulating root and rhizosphere microbiomes, indicating a holistic approach to plant health and soil ecosystem balance. These findings underscore the significant potential of the selected bacterial isolates as sustainable solutions for managing soilborne fungal pathogens such as *A. mellea* by promoting plant health and growth and diminishing the need for synthetic fungicides.

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P2 Monitoring Dothistroma needle blight in protection forests of the Eastern Alps

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Dothistroma needle blight (DNB) is regarded as one of the most harmful diseases of conifers affecting over 100 species in the family Pinaceae. For much of the 20th century, the greatest damage by DNB was to pine plantations in the Southern Hemisphere, whereas the disease is currently a global concern due to increasing outbreaks worldwide. In the Italian Eastern Alps, DNB caused by *Dothistroma septosporum* (Dorogin) M. Morelet was confirmed at a few sites in Trentino-South Tyrol in 2020. As further spread and increased disease severity may be expected especially in the mountains due to climate change, we monitored DNB and assessed damage at one hundred fifteen sites in the region, at altitudes from 1000 to over 2000 m a.s.l.. Symptomatic needles, with or without Dothistroma-like acervuli, were collected from each area and tested by species-specific LAMP diagnostics. *Dothistroma pini* Hulbary was not detected, while *D. septosporum* was confirmed at all the sites, on *Pinus cembra* L., *Pinus mugo* Turra, *Pinus sylvestris* L., *Pinus nigra* J.F.Arnold or more than one of the aforementioned species in each area. Defoliation of both adult and juvenile trees was severe at many sites, including protection forests above 2000 m altitude. The results warn that DNB may contribute to increase geo-hydrological hazards in the Eastern Alps by limiting the buffer service of protection forests, jeopardise habitat conservation, and deplete the genetic resources of native pine species.

P3 Non-invasive early detection of ToBRFV using near-infrared (NIR) spectroscopy

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Tomato brown rugose fruit virus (ToBRFV) is one of the most aggressive viruses infecting tomato, causing severe economic losses in commercial cultivars. Surveillance systems to monitor the sanitary status of the plants are an important strategy for avoiding ToBRFV infection. However, conventional molecular or serological analyses are expensive, require specialized personnel and the shipment of samples to testing facilities. Near-infrared (NIR) spectroscopy is a technique that has been recently tested for the detection of some plant diseases in the early stages. Therefore, in this work, a portable, pocket-sized NIR spectrometer was used to assess if ToBRFV-induced infection in tomato plants could be detected before the appearance of symptoms. Five tomato seeds were grown under greenhouse conditions, and the resulting seedlings were preliminary screened by NIR and tested by RT-qPCR to confirm ToBRFV absence. Afterwards, three seedlings were mechanically inoculated with ToB SIC01/19 ToBRFV isolate, while two non-inoculated seedlings were left as negative controls. NIR measurements were performed once every week post-inoculation, and virus replication was evaluated by RT-qPCR. The collected NIR reflectance spectra allowed to discriminate between infected and healthy plants 2 weeks before di appearance of symptoms, at the same time as molecular analysis detected the virus accumulation in the inoculated plants. Overall, these results suggest that NIR spectroscopy can reveal the virus presence in asymptomatic plants with a sensibility comparable to RT-qPCR and can be a valid tool for rapid, on-site screening of a high number of plants for ToBRFV infection in a sustainable and cost-effective manner.

P4 Screening of seven citrus viroids incidence in commercial orchards of the main Sicilian citrus areas

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The genus *Citrus* includes several tree crops both for fruit production and ornamental market, making it one of the most valuable cultivations in the Mediterranean basin. However, many pathogens, such as viroids, constantly threaten citrus industry. Viroids cause symptoms in some scion/rootstock combinations, but remain latent in others; it is therefore important to ensure the absence of these pathogens from propagation material, to limit their spread. During spring 2025, a survey was conducted by collecting random samples in commercial citrus orchards in Catania, Siracusa and Messina provinces (Sicily, Italy), to evaluate the dispersion of citrus viroids: citrus exocortis viroid (CEVd), citrus bent leaf viroid (CBLVd), hop stunt viroid (HSVd), citrus dwarfing viroid (CDVd), citrus bark cracking viroid (CBCVd), citrus viroid V (CVd-V) and citrus viroid VI (CVd-VI). A total of 138 symptomatic/asymptomatic citrus samples were collected, and total RNA was extracted using a commercial kit, quantified, and adjusted to ≈50 ng/µL. Several TaqMan RT-qPCR (one for each viroid) were developed for the detection of these viroids and subsequently used for their incidence evaluation. The highest incidence was observed for CEVd (47.83%) with 66 positive samples out of 138, followed by HSVd (46.38%), CDVd (45.64%), CBCVd (39,86%), CBLVd (32,61%) and CVd-V (7,25%), while no samples resulted positive to CVd-VI. Moreover, several samples showed mixed infections. In conclusion, since these pathogens were found in almost all collected samples, this study provides a preliminary assessment of their dispersion in Sicily, suggesting the need for more rigorous surveillance.

P5 Survey on *Xanthomonas campestris* pv. *campestris* strains from *Brassica* spp. in Latium Region

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Black rot of cabbage, caused by *Xanthomonas campestris* pv. *campestris* (Xcc), is one of the most pervasive diseases of *Brassica* spp. worldwide. Symptoms can be observed on leaf presenting V-shaped necrosis on major veins that can progress through the inflorescence and the corymb. Control techniques nowadays rely mostly on the use of copper which could have been caused the emergence of resistance within the bacterial populations. The aim of the work was to collect and characterize wild strains of Xcc from different farms with relevant cabbage crops in Northern Latium Region and screen them for copper sensitivity. Samples were firstly isolated from diseased leaves of different *Brassica* species. Several Xcc strains were obtained and 79 tested positive for the colony PCR assay with specific primers. Subsequently, a *in vivo* test was run to assess the pathogenicity of the isolated strains by inoculating them on seedlings of Brassica oleracea L. convar. botrytis L. var. Italica *cv.* Naxos; at the same time, the strains were screened to verify the amylolytic activity in a starch-composed media and the copper tolerance on nutrient agar amended with two different $CuSO_4$ concentrations (100 ppm and 200 ppm).
Confirmed Xcc strains provoked the expected symptoms at 7-10 days post-inoculation. All the selected strains tested positive for the amylolytic activity; all the strains were able to grow on copper media at 100 ppm and only 7 strains did not grow at 200 ppm, indicating a potential threat to the effectiveness and the sustainability of the current protection strategies based on copper.

P6 Pathotype diversity of *Plasmopara halstedii* in Central Italy: preliminary data and establishment of a monitoring system

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In sunflower, downy mildew disease control by seed coating is difficult to achieve, as the oomycete *Plasmopara halstedii* (Farl.) Berl. et de Toni has developed the resistance to the chemical Metalaxyl-M. Consequently, an Integrated Pest Management (IPM) approach that relies on mechanisms of genetic resistance must be adopted. Each *P. halstedii* resistance gene (*Pl*) is effective only against specific pathotypes. Therefore, downy mildew pathotype composition in Italy must be investigated, to select the most suitable commercial sunflowers hybrids carrying the appropriate resistance genes. To gather preliminary data on the genetic variability of *P. halstedii*, we focused on the Marche region (Central Italy), which accounts for nearly 40% of national sunflower production. Over a three-year period (2020 – 2022) we collected 18 *P. halstedii* isolates from various sunflower-growing locations across all five districts of the Marche region (Ancona, Ascoli Piceno, Fermo, Macerata, Pesaro-Urbino). The identification of the downy mildew races was conducted using the Universal System for race determination and designation of *P. halstedii* based on the “triplet” system and involving nine sunflower differential lines. As result, several pathotypes were detected, confirming findings from numerous reports that indicate similar pathogen evolution across Europe. To further investigate disease evolution, we are establishing four experimental fields. Two fields were set up between years 2023 and 2025 — one in Osimo (Ancona district) and the other in Monteleone (Fermo district). Two additional locations will be selected in 2026.

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P7 Preliminary results on the control of *Fusarium* wilt on lettuce by insect frass and exuviae from *Hermetia illucens*

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Fusarium wilt is a fungal disease caused by *Fusarium oxysporum*, threatening several crops including lettuce. Control methods include resistant cultivars, fungicides, fumigants, physical methods, soil amendments, and biocontrol agents. Among soil amendments, insect frass – a material composed of feces, exoskeletons, and residual rearing substrate from insect farming – has recently gained attention as an alternative to conventional fertilizers and pesticides. This study evaluated *Fusarium* wilt suppression in lettuce using insect frass and exuviae in greenhouse conditions. Frass and exuviae were obtained from *Hermetia illucens* larvae reared on the Gainesville diet (50% wheat bran, 30% alfalfa meal, 20% corn; 70% humidity) at the DiSAFA experimental facility – University of Turin. Two trials were carried out on potted lettuce plants. Heat-treated frass (70°C for 60 minutes) was mixed with peat at 10% (v/v). Exuviae were mixed at 1, 5, 10, and 20% (v/v) in nursery trays, and lettuce seeds were sown immediately. After 3 weeks, seedlings were transplanted into 2 L pots filled with peat previously inoculated with *F. oxysporum f. sp. lactucae* race 4 at 1 g/L (in wheat kernels). An untreated inoculated control and a chemical control (Enovit metil® FL, thiophanate-methyl, 1 ml/L) were included. One lettuce plant was transplanted per pot, with five replicates per treatment. Exuviae at 1, 5, and 10% significantly reduced disease severity in both trials, while the 20% dose was not effective. Frass was effective only in one of the two trials. The higher efficacy of exuviae is likely due to their high chitin content.

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P8 Rhizosphere microbiome dynamics associated with Esca disease in Barbera vineyards

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The soil microbiome plays a crucial role in grapevine health, yet its dynamics in Esca-affected vineyards remains poorly characterized. This study examined taxonomic and functional shifts in fungal and bacterial communities from rhizosphere soils of *Vitis vinifera* cv. Barbera vineyards in Piedmont (Italy) showing high (HE) and low (LE) Esca incidence. ITS2 and 16S rRNA gene metabarcoding revealed disease-associated microbial signatures: HE soils showed significant enrichment of grapevine trunk disease (GTD) associated fungi, including *Phaeomoniella* (15.3% vs 10.4%), a key Esca-related pathogen, and *Neofusicoccum* (4.9% vs 0.1%), one of the genera associated with Botryosphaeria dieback., while LE soils contained higher abundances of the core grapevine endophyte *Malassezia* (12.5% vs 2.1%) and plant growth-promoting *Mortierella* (7.2% vs 1.0%). Bacterial communities differed markedly, with *Vicinamibacterales* dominating HE soils (22.1% vs 10.5%), while LE soils showed increased relative abundance of *Candidatus Xiphinematobacter* (1.95% vs 1.06%) and *Staphylococcus* (1.6% vs 0.6%). Metabolic analysis (BIOLOG®) further indicated a higher utilization of carbon sources linked to stress tolerance (e.g., D-mannitol, erythritol) and antimicrobial compound synthesis (e.g., itaconic Acid, 2-hydroxy-benzoic acid) in LE compared to HE soils. Culture-dependent analysis isolated potential biocontrol fungi (*Trichoderma*, *Clonostachys*) from LE soils, while HE soils yielded predominantly *Penicillium* spp. and the root pathogen *Ilyonectria*. These results reveal distinct microbiome and metabolic profiles associated with Esca incidence in vineyard soils. The observed differences in microbial community structure and function provide a foundation for understanding vine-soil microbe interactions in this pathosystem. This study establishes baseline data for the development of biological indicators of vineyard health status.

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P9 Climate change, poplar adversities and innovative sustainable defense in Italy

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Climate change, with frequent temperature peaks and recurrent and persistent droughts, is causing significant shifts in Italy regarding impact of poplar pathogens and pests, and of abiotic adversities on plantations as well. In this regard, it must often be considered the effects of change in clonal composition together with climate change. For example, *Venturia* – specific pathogen – has currently almost disappeared during monitoring, after the gradual demise of susceptible clones in association with the occurrence of dry springs and summers. Instead, water stress connected with frequent droughts has increased the risks of attacks by more aspecific bark parasites such as *Citospora*, *Phomopsis* or *Fusarium*. Intense drought itself, however, simultaneous with high heat picks in summer, can induce severe dieback in plantations by early filloptosis and embolism occurrence, with death of whole branches. The high insecurity of such context is worsened by the narrow spectrum of molecules still allowed in intensive poplar cultivation, that has taken away usual tools of farmers to cope with pathogens and pests. Fortunately, improved methods of recurrent genetic crossing have led to the selection of a wide range of new clones (called MSA) with good and stable resistance to the main biotic adversities, and needing almost no chemical treatment, thus highly sustainable with respect to concurring annual crops. Promising results in resistance to the most aggressive pathogens and pests are being achieved by New Genomic Techniques (NGT), searching for resistance loci, as already obtained e.g. for poplar woolly aphid. In the future, inducing a suitable bark microbiome could also help us to reduce attacks of weak pathogenic fungi.

P10 Fluorescently tagged *Plenodomus tracheiphilus* to investigate the infection process on lemon

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Plenodomus tracheiphilus is a tracheomycotic fungus that causes mal secco disease in Citrus, causing the dieback of twigs and branches. In the severe cases, infections have affected up to 100% of the plants of susceptible lemon cultivars, with consequent reduction of yield and fruit quality. Consequentially, it is imperative to better understand the infection process of *P. tracheiphilus* in order to develop novel control strategies for the disease. In this work, we fluorescently labeled *P. tracheiphilus* to explore its pathogenicity mechanism using laser scanning confocal microscopy (LSCM). For this purpose, we used two different strategies: i) a plasmid carrying the GFP coding gene optimized for fungal expression was inserted into *P. tracheiphilus* conidia via *Agrobacterium tumefaciens* transformation. Some transformants, showing strong fluorescence, phenotype, growth rate, and pathogenicity not significantly differing from the wild-type isolate, were selected; ii) wheat germ agglutinin (WGA) conjugated with a fluorophore was used as an efficient alternative to GFP transformation enabling high resolution visualization of fungal morphology. After 7 days post inoculation (dpi) of lemon leaves, *P. tracheiphilus* successfully colonized the epidermal cells at the inoculation point. From 14 to 21 dpi, hyphae grew along the veins of leaves from the inoculation site toward the petiole. At 35 dpi *P. tracheiphilus* was found in petioles and the first part of the stem. Microscopical visualization has been molecularly confirmed by Real-Time PCR analysis. Ongoing investigations are focused on comparing the colonization dynamics and infection progression in susceptible and tolerant lemon cultivars.

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P11 Endotherapy applications for sustainable management of Flavescence dorée and esca diseases in Northern Italian vineyards

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Flavescence dorée (FD) and esca are among the most damaging diseases affecting grapevines in Northern Italy, threatening vineyard sustainability and productivity. In recent years, the need for effective, low-environmental-impact disease control measures has driven research toward alternative strategies. Within the Spoke 2 of the Agritech National Research Center (WP2.3, Task 2.3.3), we evaluated an innovative endotherapy approach for the targeted application of natural active compounds in commercial vineyards. Field trials were established in six vineyards located across Emilia-Romagna and Tuscany, involving more than 2,800 symptomatic vines. The trials targeted phytoplasmas associated with grapevine yellows and fungi involved in esca disease. Treatments were performed through endotherapeutic injection of formulations based on natural extracts previously shown to inhibit FD-associated phytoplasmas. In the vineyards affected by esca, a natural compound with *in vitro* antifungal activity was applied. Results from the 2023 season - marked by particularly favourable conditions for symptom expression - indicated a consistent and statistically significant reduction in symptom incidence in treated vines compared to untreated controls. In particular, two products showed significant effectiveness, reducing symptomatic vines by approximately 20–30%. These findings confirm the potential of endotherapy as a viable, sustainable strategy for managing grapevine trunk and yellows diseases. However, climatic variability in 2024 influenced symptom expression, highlighting the importance of multi-year trials to ensure robust conclusions, accounting for environmental variability and disease dynamics. Ongoing work aims to refine protocols and support future integration into vineyard management practices.

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). This manuscript reflects only the authors' views and opinions, neither the European Union nor the European Commission can be considered responsible for them.

P12 Net blotch of barley caused by *Pyrenophora teres*: the Italian scenario.

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Net blotch (NB) is a foliar disease of barley caused by the fungus *Pyrenophora teres* (*Pt*), which occurs in the net or spot forms caused by *P. teres* f. *teres* (*Ptt*) and *P. teres* f. *maculata* (*Ptm*), respectively. Given the economic impact of this disease and the limited information available in Italy, an overview on recent findings about the occurrence and management of *Pt* within the Italian context is presented. The possible presence of fungicide resistance was also evaluated in a population of Italian *Pt* isolates. As *Pt* is also a seed-borne pathogen, its presence was molecularly detected in barley grain samples in different seasons. A widespread and uniform distribution of the pathogen across the country was detected, with a strong predominance of *Ptt* with respect to *Ptm*, which was observed only occasionally. Field plot trials showed the relevant impact of agronomic practices, cultivated genotype and fungicide applications on NB management. High sowing density and nitrogen fertilization promoted NB symptoms, even under unfavorable environmental conditions. Conversely, delaying nitrogen application reduced disease pressure. Two-row Spring malting genotypes were the most impacted by NB, both regarding symptoms on leaves and DNA accumulation in grain, compared to six-row genotypes. Fungicide treatments, commonly used in cereal crop protection, showed an efficient control of NB by limiting symptoms development and fungal accumulation in grain, thus improving barley yield. Strains carrying genetic mutations associated with fungicide resistance were identified, and some multi-resistant strains were also observed. Overall, these results provide updated insights into NB in Italy, highlighting the importance of integrated disease management strategies for barley.

P13 Development of rapid in-field detection of *Erysiphe corylacearum* in hazelnuts using Loop-Mediated Isothermal Amplification

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Erysiphe corylacearum, the causal agent of powdery mildew in hazelnut (*Corylus avellana L.*), has become an emerging pathogen of increasing concern in Piedmont's hazelnut production, causing a new and aggressive form of powdery mildew compared to that provoked by *Phyllactinia guttata*. Accurate and early detection of this pathogen is crucial for effective disease management and for preventing its spread. It was developed and validated a Loop-mediated Isothermal Amplification (LAMP) assay for the rapid and specific detection of *E. corylacearum*. A set of novel LAMP primers were designed targeting a specific genomic region of *E. corylacearum* and selected to ensure specificity against closely related powdery mildew species. Symptomatic leaves that showed the characteristic symptoms of powdery mildew associated with *E. corylacearum* (round, white, powdery spots visible mainly on the upper surface of the leaves) were collected from Piedmont's hazelnut orchards for total DNA extraction and crude plant extract. The LAMP method was applied to fungal DNA and to crude plant extract. Successful results were obtained by LAMP assays performed on total DNA extracted from symptomatic hazelnut leaves or directly from crude plant extract in field. The assay proved as specific, sensitive, and replicable producing results in less than half an hour. The rapidity and robustness of the developed LAMP assay make it a valuable diagnostic tool for early detection and epidemiological studies of *E. corylacearum* directly in the field, supporting timely phytosanitary actions in hazelnut orchards.

P14 Decentralized solutions for tomato virus control: a sustainable approach to crop protection

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Prevention through early detection remains the most effective control strategies against viral diseases; to improve plant virus surveillance in tomato cultivation, a decentralized monitoring network was established for the major viral diseases affecting Sicilian tomato crops. Four diagnostic Point-of-Care (PoCs) were installed in Agrigento, Ragusa, Siracusa and Trapani provinces, each equipped with a portable thermocycler for real time LAMP and PCR assays. Results were analyzed through a cloud platform by the Plant Virology CMA-Lab (University of Palermo). Five-hundred tomato samples were collected from each province and sent to each PoC. Samples were analyzed for Tomato brown rugose fruit virus (ToBRFV), Tomato spotted wilt virus (TSWV), Southern tomato virus (STV), and Tomato leaf curl New Delhi virus (ToLCNDV). Moreover, two-hundred *Bemisia tabaci* MED adults were collected and analyzed in Ragusa province to understand the *B. tabaci* ToLCNDV-infected rate. Ready-to-use kits with a rapid sample extraction method were used for real time LAMP and PCR assays. The highest incidence in all provinces was showed by STV (>70%), followed by ToBRFV with higher incidence in Ragusa (65%) and Siracusa (55.6%) provinces, and ToLCNDV mainly detected in Siracusa (61.4%) and Trapani (60.2%) provinces. The lowest incidence was recorded for TSWV, ranging from 5.4% in Agrigento to 31.2% in Trapani provinces. ToLCNDV presence in *B. tabaci* confirmed the vector's role in field transmission, with an incidence reaching up to 100%. This system provides highly accurate results, facilitating real-time monitoring with an integrated approach to plant diseases prevention, reducing costs compared to a traditional laboratory.

P15 Integrated Strategies for the Containment of *Gnomoniopsis castaneae* in Chestnut Orchards of the Campania Region

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Gnomoniopsis castaneae is an emerging fungal pathogen causing significant damage to chestnut (*Castanea sativa*) production in southern Italy, particularly in the Campania region. This study focused on strategies for monitoring, controlling, and mitigating the spread of the pathogen within chestnut orchards. Integrated management approaches, including phytosanitary practices, pruning, removal of infected plant material, and application of biological and chemical treatments, were evaluated under laboratory and field conditions. Sensitivity baselines were constructed for 80 isolates on 4 commercial formulations, relating to 4 categories of fungicides: "biological" (copper oxychloride; Eugenol + Geraniol + Thymol); triazoles (Tetraconazole); sterol biosynthesis inhibitor in fungi (Fenhexamid); inhibitor mitochondrial respiration (Boscalid). In 2024, the incidence of *G. castaneae* was monitored in chestnut orchards in the Campania region following the application of the most effective active substances identified through *in vitro* assays. Treatments were integrated with rational and sustainable agronomic practices. In 2024, although disease pressure was relatively low, a 6% reduction in the incidence of *G. castaneae* was recorded in chestnut trees treated with four of the tested active substances (copper oxychloride, Eugenol + Geraniol + Thymol, Tetraconazole, Fenhexamid). These preliminary results support the potential of selected compounds to contribute to disease mitigation, even under less favorable conditions for pathogen development. The aim was to evaluate the field performance of selected compounds within an integrated disease management framework under real cultivation conditions. The results of this study indicate that, beyond sound agronomic practices, rational orchard management—such as the removal of infected plant material and the application of effective phytosanitary treatments—can play a key role in reducing the impact of *G. castaneae* and enhancing disease control in chestnut orchards.

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P16 Agroecological Strategies for the Management of Soilborne Pathogens in Strawberry Cultivation in Campania Region

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Strawberry crops in the Campania region are increasingly affected by soilborne pathogens such as *Macrophomina phaseolina*, *Neopestalotiopsis* spp., and *Phytophthora* spp., which cause significant yield losses and threaten the sustainability of production systems. The progressive restriction of synthetic fumigants and other Plant Protection Products highlights the urgency of identifying alternative disease management solutions that are both effective and environmentally sustainable. This 2024 study presents preliminary findings from an agroecological pathogen suppression strategy grounded in the "*healthy plants in healthy soils*" principle, in comparison with the conventional cultivation system widely adopted in the region. Key strategies include innovative soil solarization method (Solin®), organic amendments, crop rotation with non-host, and the application of antagonistic microorganisms such as *Trichoderma* spp. and *Bacillus* spp. The agroecological approach - based on the incorporation of organic amendments and effective soil solarization - resulted in a 97.4% efficacy in the control of *M. phaseolina* when integrated with the use of biocontrol agents. In addition, the pathogenic organisms, reported above, were not detected after the implementation of the agroecological strategy. Preliminary greenhouse trials conducted in strawberry-growing areas of Parete (Caserta) in Campania indicate a consistent reduction in disease incidence and an improvement in plant vigor when these practices were integrated. The role of microbial diversity and organic matter quality emerges as central in disease suppression. This agroecological framework offers a promising direction for agroecological disease control of soilborne pathogens in strawberry, aligning with current goals in plant pathology for sustainable and ecologically based disease control.

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P17 Plant colonization and survival of *Pseudomonas synxantha* DLS65, the active ingredient of the biopesticide *Microfighter*: essential keys for optimized and effective field applications.

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Copper-based pesticides are widely used to control bacterial and fungal diseases of key crops in Europe, such as downy mildew on grape, bacterial speck on tomato and olive knot disease. Widespread use of copper, however, is negatively affecting the soil microbiota in terms of abundance and biodiversity; therefore, it's not environmentally sustainable. As an alternative to control such diseases, the EU-funded project "LIFE Microfighter" has led to develop an innovative biopesticide named *'Microfighter'*, in which *Pseudomonas synxantha* strain DLS65 is the microbial active ingredient. In the current study, we assessed the colonization pattern and survival of DLS65, on tomato, olive, and grapevine. Under controlled conditions, DLS65 successfully colonized both the epiphytic and endophytic compartments of tomato leaves (cv. Roma), after one week post inoculation, with an abundance of 2.2×10^3 and 4.3×10^4 CFU g^{-1} leaf fresh weight, respectively. However, in the root compartment, DLS65 was only observed in the rhizosphere, with an abundance of 5.9×10^6 CFU g^{-1} root fresh weight. Microscopic visualization of eGFP-tagged DLS65 with a confocal laser scanning microscopy confirmed both rhizospheric and phyllospheric competence of *Pseudomonas synxantha* in tomato. In field condition, after a foliar application of *'Microfighter',* strain DLS65 exhibited crop-dependent survival within the phyllosphere of olive and grapevine plants. Competent colonization and bacterial survival on target crop plants are essential prerequisites towards an efficient application of the biopesticide in field: for instance, the establishment of the most suitable/effective concentration per gram of strain DLS65 viable cells in the product and the most appropriate product spray intervals.

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P18 Root colonization pattern of *Pseudomonas* spp. strains: a key step in the biocontrol of soilborne pathogens in hops

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The control of soil-borne diseases in hops, such as Verticillium wilt remains challenging due to the limited effectiveness of fungicides, the perennial nature of hop cultivation, and the long-term persistence of the pathogens in the soil. Microbial biocontrol agents (*m*BCAs) with plant growth-promoting (PGP) and antagonistic effects offer a sustainable ecofriendly alternative for hops protection. Two *Pseudomonas* spp. strains from the UniMORE microbial collection were selected for this study based on their strong antagonistic activity against *Verticillium* spp. and multiple plant growth-promoting (PGP) traits. Rhizospheric and endophytic colonization capacities of the strains DLS1929 and DLS2318 were evaluated in hop plants (cv. *Cascade*) under controlled conditions at seven- and fourteen-days post-inoculation (DPI). Both bacterial strains were rhizosphere and endorhiza competent, with slight differences in their abundances. The highest cell density was observed at 7 DPI for the strain DLS2318, reaching $\log_{10}$ 6.39 CFU g^{-1} root fresh weight in the rhizosphere and $\log_{10}$ 4.75 CFU g^{-1} root fresh weight in the endorhiza; at 14 DPI, colonization results were in line with the previous assessment. Confocal laser scanning microscopy visualization of both eGFP-tagged *Pseudomonas* spp. strains confirmed their rhizosphere competence in hop. Additionally, root colonization by these bacteria enhanced the photosynthetic capacity in hop leaves, supporting their potential as a PGP agents observed *in vitro*. Successful root colonization and PGP effects are key prerequisites for an effective biocontrol of soilborne pathogens. Further studies are required to assess the consistent efficacy in the field of these beneficial *m*BCA candidates.

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P19 Identification and Evaluation of *Alternaria* Strains Involved in Black Point Disease of Durum Wheat

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The Black Point Disease (BPD) affects wheat worldwide, causing yield losses, mycotoxin contamination, and deterioration of grain, semolina, and flour quality. Three *Alternaria* sections associated with BPD have been identified in wheat grains: *Alternaria*, *Infectoriae*, and *Japonicae*. Among these, *A. alternata* is the most widespread in wheat-growing regions. These species produce mycotoxins both *in vitro* and *in planta*, including alternariol, alternariol monomethyl ether, tentoxin, and tenuazonic acid, all frequently detected in wheat grains. Some of these mycotoxins have harmful effects on human health. Consequently, the EU Commission Recommendation 2022/553 includes draft guidelines for monitoring *Alternaria* mycotoxins in foods, especially cereal-based products for infants and young children. For this reason, samples of durum wheat (cv. San Carlo) grown in the province of Ravenna and exhibiting black point and shrivelling symptoms were analyzed for the presence of *Alternaria*. An initial morphological screening led to the isolation of seven *Alternaria* strains from symptomatic durum wheat seeds. These isolates were selected for molecular characterization using multi-locus analysis, including *ITS* region, *Alt a1*, *TEF-1α* and *RPB2*, to assess species identity and genetic diversity. Among the seven *Alternaria* strains isolated, four were selected for pathogenicity tests on wheat ears due to their higher sporulation capacity on solid culture media. These strains were subsequently evaluated for their ability to induce black point symptoms in greenhouse trials. Preliminary analyses are currently ongoing to elucidate the role of *Alternaria* species in BPD of durum wheat, with the aim of informing more effective management and control measures.

P20 Hands up, I will disarm you! Anti-bacterial and anti-virulence effect of bio-based extracts against plant pathogens

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The strategic management of plant biomass offers a promising approach to mitigating climate change challenges. Each year, forestry, agriculture, and industry produce globally an estimated 200 billion tons of lignocellulosic biomass. The objective is to valorise this biomass in high-values products while minimizing waste and by-products, advancing circular economy strategies. Wood residues are rich in bioactive molecules, especially phenolic compounds. Chestnut contains high levels of tannins, which have demonstrated effective in plant disease management and protection, besides their direct antimicrobial properties. In this study, we evaluated some biological bioactivities of commercial wood vinegars and of a laboratory-scale extract, all derived from chestnut. Antimicrobial assays were carried out against both Gram negative and Gram positive phytopathogenic bacteria, as well as beneficial microorganisms such as *Sinorhizobium meliloti* and *Bacillus amyloliquefaciens.* Furthermore, we investigated the inhibitory activity of these extracts on the type three secretion system (T3SS) and quorum sensing (QS) of *Pseudomonas savastanoi* pv. *nerii*, and on the T3SS of *Pseudomonas amygdali* pv. *tabaci* and *Sinorhizobium meliloti.* These effects were assessed using a *gfp*-promoter fusion system targeting genes involved in these pathways, that are *hrpA* and *psnI*. In *Pseudomonas syringae*-related species *hrpA* encodes the major structural component of the T3SS pilus, while *psnI* encodes a LuxI-homolog lactone synthase essential for QS. Bacterial growth assays showed a species-specific effect, affecting different strains differently, as well as showing greater inhibition at higher concentrations. Lastly, extracts here studied have inhibitory activity on both the T3SS and QS of pathogens bacteria, but also of *S. meliloti.*

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P21 The strange case of sweet orange essential oil (SOEO)

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Mal secco is an infective disease caused by the fungus *Plenodomus tracheiphilus* mainly affecting citrus survival in the Mediterranean basin, since 100 years. Lemon is one of the crops most burdened by the pathogen. In this study, we evaluated *in vitro* the activity of a commercial pesticide ("multi-crop polyvalent insecticide-fungicide-acaricide": MCPIFA) based on sweet orange essential oil (6%) (SOEO), compared to SOEO itself and its main component limonene. SOEO was tested at concentrations of 20, 200 and 2000 mg/L; moreover, its chemical composition was determined by gas chromatography-mass spectrometry (GC-MS) technique. Limonene was tested at 20, 200 and 2000 mg/L. MCPIFA was tested at 350, 4000 and 8000 mg/L (according to the label instructions). A copper-based fungicide [$CuSO_4 \cdot 5H_2O \cdot 3Cu(OH)_2$] and an untreated control were included for comparison. Limonene was determined as the major component in SOEO accounting for 91% of the total oil. *In vitro* studies demonstrated that MCPIFA, at concentrations of 8000 mg/L and 4000 mg/L, provided the best protection against the target pathogen, achieving effectiveness rates of 87% and 85.3%, respectively. These results surpassed the effectiveness of the copper-based fungicide, which exhibited a 75.5% protection rate. Additionally, MCPIFA significantly inhibited fungal growth (48.4%) at a concentration of 350 mg/L. Regarding SOEO, it exhibited antifungal activity with an effectiveness of 40.3% at concentration of 2000 mg/L. Conversely, limonene did not demonstrate any antifungal activity, which is a notable anomaly. Further studies are in progress to understand these contradictory results.

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P22 Preliminary evaluation of two formulations for the control of *Plenodomus tracheiphilus* in lemon trees

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Lemon is commercially valuable due to its content of compounds such as flavonoids, vitamins, minerals, carotenoids with recognized antioxidant properties. Between 2014 and 2023 years, lemon production in Italy tripled, increasing from 232.858 tons (ISTAT, 2014) to 780.245 tons (ISTAT, 2023), with Sicily contributing over 80% of the total. Sicily holds three of the seven global Protected Geographical Indication (PGI) designations for lemon: "Limone dell'Etna," "Limone di Siracusa," and "Limone Interdonato Messina". Mal secco, caused by the fungus *Plenodomus tracheiphilus*, is a major threat to lemon cultivation, leading to branch dieback and plant death. In Italy, the disease is regulated by Ministerial Decree 17 April 1998. In 2021, the Sicilian Region, and the University of Catania, issued guidelines promoting good agricultural practices and, where necessary, copper-based fungicide treatments. Given the environmental concerns associated with synthetic fungicides, research is increasingly focusing on sustainable alternatives. This study evaluated, in *semi-vivo* trials on lemon plants, the effectiveness of two treatments against *P. tracheiphilus*: a commercial multi-crop insecticide-fungicide-acaricide (MCPIFA) containing 6% sweet orange essential oil, and a formulation based on Natural Phenolic Compounds with ionic and non-ionic surfactants (NPhC), applied at 8000 mg/L and 1200 mg/L, respectively. Treated lemon plants continued to grow despite confirmed pathogen presence (via confocal microscopy and Real Time-PCR analysis), whereas untreated inoculated control did not survive. These results hint at the possibility of new, low-impact means of treating pathogen-affected plants and suggest the importance of further studies on the efficacy of using MCPFIFA and NPhC in the field for pathogen containment.

This research was funded by the Agrivita research project, titled "Protecting Italian citrus groves from the tracheomycotic fungus Plenodomus tracheiphilus" (MASAF D.M. 689142, dated 15/12/23).

P23 From the lab to the field: testing the antagonistic activity of three *Pseudomonas* strains against two genera of KVDS-associated oomycetes

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Kiwifruit vine decline syndrome (KVDS) is a soil-borne disease widespread across all Italian regions, impacting roughly 80% of the cultivated area. KVDS has been constantly associated with the presence of oomycetes belonging to the genera *Phytopythium* and *Phytophthora*. While some oomycetes, such as *Phytopythium vexans*, were proven to be pathogenic, the pathogenicity of others, such as *Phytophthora sojae*-like, remains unconfirmed. Currently, the research aims to identify possible non-chemical strategies targeting these genera. To create an efficient consortium of biocontrol agents to manage KVDS, we evaluated the antagonistic activity of three *Pseudomonas* strains against some oomycetes, and their compatibility in the same environment. In this study, the efficacy of *Pseudomonas asplenii*, an endophyte of the kiwifruit plant, and two *Pseudomonas protegens*-related strains, Pf4 and Pf11, isolated from lamb's lettuce, was assessed. Using a dual culture assay, we have proven the antagonistic activity of all selected bacteria against *Phytopythium vexans*, and three *Phytophthora* spp. (*P. plurivora*, *P. cinnamomi* and *P. acerina*) associated with KVDS. All *Pseudomonas* strains showed good *in vitro* inhibition (~70%) against all the oomycetes tested. We then evaluated their mutual compatibility through a streak test or a VOCs assay. An imaging process on the Petri dishes evaluated the possible mutual inhibition of the selected biocontrol agents. Generally, the three *Pseudomonas* strains have shown good compatibility, allowing us to proceed with *in planta* studies. Thus, a greenhouse test has been performed to demonstrate the *in vivo* efficacy of all the strains either singularly or in consortium.

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P24 Investigating the role of wild plants in flavescence dorée epidemiology in north-eastern Italy: a complexity beyond expectations?

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Flavescence dorée (FD) is a destructive disease of grapevine associated with phytoplasmas of 16SrV-C and -D subgroups and mainly transmitted by the leafhopper *Scaphoideus titanus*. Recent findings have revealed that the FD epidemiology is more complex than previously thought, involving several wild plants, acting as alternative hosts within the agroecosystem. The *map* gene sequence is the most widely used to finely differentiate phytoplasma strains characterized by a specific epidemiological trait or geographic distribution. In addition, the *vmpA* gene sequence provides information about their transmissibility by *S. titanus*. This study aimed to investigate the role of wild plants as possible reservoirs in five vineyards in north-eastern Italy, in the provinces of Udine, Pordenone, and Treviso. Thus, in 2023-2024 molecular detection based on 16Sr DNA was performed on samples of *A. glutinosa*, *A. altissima*, *C. vitalba*, *Corylus avellana* and *Salix* spp. besides grapevine. FD-related phytoplasmas were subjected to genotyping based on *map* and *vmpA* genes. In grapevine the typical map genotypes of the area, M54/VmpA-II (about 90%) and M3/VmpA-III (about 10%) were present; whereas samples of *C. avellana* and *Salix* spp. were negative. Concerning the other wild plants the same genotype M51/VmpA-III was present in *C. vitalba* and *A. altissima*; whereas in *A. glutinosa*, phytoplasmas (including those belonging to M6 and M50/VmpA-III) were often present in mixed infections. Although the genotypes found in grapevine and wild plants were different, the latter contain genotypes (M51, M6 and M50) found in other European regions with FD outbreaks, suggesting their potential role as a reservoir.

P25 Temporal dynamics and molecular characterization of a still uncultured oomycete associated with KVDS

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In the last decade, kiwifruit vine decline syndrome (KVDS) has significantly impacted Italian fruit production. Several studies have shown a constant association of oomycetes with the disease; among them, *Phytopythium vexans* is regarded as one of the most important and widespread pathogens. However, in northeastern Italy, a metabarcoding approach underlined the association of the disease with another oomycete, belonging to *Phytophthora* spp. We have previously proved its genetic similarity with *Phytophthora sojae* and other members of subclade 7b based on ITS region sequence analysis; thus, we referred to it as *Phytophthora sojae*-like. Despite several attempts, *P. sojae*-like has never been isolated from KVDS symptomatic samples. Nevertheless, we were able to confirm its identification by Sanger sequencing of the elongation factor gene and by exploiting metagenomics using long-reads MinION sequencing on symptomatic roots. To monitor the presence of *Ph. vexans* and *P. sojae*-like over the vegetative season, samples collected from KVDS-affected plants in three farms were subjected to molecular detection using specific primers in nested-PCR and PCR, respectively. These analyses revealed an increased presence of the two oomycetes throughout the season and suggested that they are actively involved in the syndrome process, especially *P. sojae*-like, which was the most abundant since it was readily detected by one-round PCR, even at the beginning of the vegetative season. A deeper insight into its molecular and biological characterization may help define cultivation methods that would allow its *in vitro* growth and provide hints to clarify host-pathogen interactions in this puzzling disease.

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P26 Exploring wood distillate as an eco-friendly strategy to control basil downy mildew

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Wood distillate (WD), a by-product of woody biomass pyrolysis rich in organic acids and phenolic compounds conferring biostimulant and antimicrobial properties, was evaluated in this study on *Ocimum basilicum* cv. Riviera Ligure infected by *Peronospora belbahrii*, a foliar pathogen. Here, the role of a commercial WD BioDea® was evaluated as both (i) a protective agent and (ii) an inducer of plant defence. One month-old plants were foliar-sprayed with WD (0.2% v/v in water) once per week for three consecutive weeks and were artificially inoculated with *P. belbarhii* (10^5 CFU mL^{-1}) at leaf level, one week after the first treatment. Stomatal conductance (g_s) and CO_2 assimilation (C_i) were measured after each treatment. Levels of signalling molecules [ethylene (ET), jasmonate and salicylate (JA and SA)] were quantified at 0, 1, 3, 24 and 48 hours post inoculation (hpi). Disease severity was assessed at the end of the experiment. WD-treated plants showed reduced g_s and C_i values in both uninoculated (–51 and –13%) and inoculated plants (–41 and –18%) from the first and second week of treatment, respectively (compared to WD-untreated control). In addition SA levels and the JA/ET ratio rose by +12 and +40% (at 24 and 48 hpi, respectively) in inoculated plants treated with WD. Finally, WD treatment reduced disease incidence by 22%. These results indicate that WD foliar treatment can activate both pre-inoculation structural defences and the post-infection signalling pathways, particularly those mediated by JA and SA, offering a promising strategy for managing *P. belbahrii* in basil cultivation.

P27 AI-Driven Epidemiological Modeling of *Gnomoniopsis castaneae* in Chestnut Orchards

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The European chestnut (*Castanea sativa* Mill.) plays a key role in European agricultural and forestry systems due to its economic, ecological, and cultural importance. However, its cultivation is increasingly threatened by pathogens and pests, including *Gnomoniopsis castaneae* Tamietti, an emerging fungus responsible for severe damage to fruits and vegetative tissues. To support epidemiology modeling of *G. castaneae*, a multi-scale collection of climatic and environmental data is being carried out in collaboration with local authorities, universities, and farmers in Campania region. A monitoring station, equipped with various types of sensors, records parameters such as air temperature and humidity, atmospheric pressure, leaf wetness, solar radiation (PYR, PAR, UV), wind direction and speed, precipitation (pluviometry), and soil variables at different depths, such as volumetric water content (VWC), temperature, and electrical conductivity (EC). In parallel, systematic sampling of plant tissues and fruits is conducted to isolate pathogens, mainly *G. castaneae,* whose presence will be monitored throughout the plant annual cycle. The integration of heterogeneous data, originating from different sources and conveying diverse types of information, thanks to the support of artificial intelligence (AI) technologies (including machine learning and deep learning algorithms) will allow the design of an epidemiological and forecasting model for *G. castaneae* development. This model will be integrated into a decision support system (DSS), designed to guide chestnut growers in adopting sustainable and timely crop protection practices. The project aims to improve resilience and productivity of chestnut orchards, reduce management costs and environmental impact, and promote an innovative and efficient agricultural approach.

P28 Influence of Soil Microelement Availability on Esca Disease Incidence in Grapevines

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Esca complex is one of the most economically damaging grapevine trunk diseases. Abiotic factors such as cumulated rainfall in May and June appear to be strongly linked to the yearly fluctuation of symptom expression. One factor that has received limited attention is the influence on symptom development of the amount of spring and early summer rain in relation with soil composition, presence and bioavailability of microelements. To assess this relationship three vineyards with long-term disease monitoring (≥5 years) were selected: two in Tuscany (Bolgheri and San Casciano) and one in Emilia-Romagna (Bozara). Within each vineyard, 10 high-incidence micro-areas (clusters of vines showing foliar symptoms for at least two years) and 10 low-incidence areas (clusters without symptom history) were identified. From each cluster, four soil samples were collected around the most symptomatic vines (north, south, east, and west) at a depth of 40 cm, and then pooled. The pooled samples underwent both Electron Paramagnetic Resonance (EPR) spectroscopy and Inductively Coupled Plasma-Mass Spectrometry (ICP-MS) analysis to determine the presence and concentration of 20 microelements. Preliminary ANOVA results indicate statistically significant differences in several elements between high- and low-incidence areas. Notably, boron was found in lower concentrations in high-incidence areas, and an interesting trend towards a higher concentration of manganese was also observed, though not significant. Previous studies have suggested that boron may suppress wood-infecting fungi such as *Eutypa lata*. These findings support the need for further investigation into soil chemistry as a contributing factor in Esca development.

P29 Smoke signals for plant health: wood vinegar effects on stress tolerance and performances in tomato, basil, and lettuce

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Wood vinegar (WV), a pyrolytic condensate derived from lignocellulosic biomass, is increasingly studied as a sustainable biostimulant and plant health promoter. This study investigated the effects of an experimental WV formulation (total phenolic content: 2.3 g/L) on agronomically relevant species, *Ocimum basilicum*, *Lactuca sativa*, and *Solanum lycopersicum*, under abiotic stress conditions, with emphasis on plant vigor, chlorophyll accumulation, and the incidence of physiological disorders.
Experiments were carried out in both hydroponic and soil-based systems. Hydroponic trials on lettuce and basil were performed under nutrient-limited conditions to assess whether WV could support growth while reducing synthetic fertilizer inputs. Tomato plants were grown in pots under salt (2 g/L NaCl) and water-limiting conditions. WV was applied weekly at dilutions of 1:300 and 1:1,000 in hydroponics, and 1:500 and 1:1,000 in soil-based systems. At 1:1,000, WV improved growth and chlorophyll content in basil and lettuce under nutrient stress. However, higher concentrations showed signs of phytotoxicity. In tomatoes subjected to salt stress, WV treatment promoted earlier and more abundant fruit set compared to untreated controls. Nonetheless, the incidence of blossom-end rot (BER) was variable, with both healthy and BER-affected fruits often occurring on the same plant, suggesting complex interactions between WV, salinity, calcium homeostasis, and fruit development. These findings suggest that WV can modulate crop responses to abiotic stress in a dose- and context-dependent manner. Further research is needed to elucidate the molecular, hormonal and physiological mechanisms involved.

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P30 Exploring native soil microbiota for biocontrol potential in Moroccan almond orchards

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Understanding soil microbial communities of native plants is essential to uncover functional interactions and identify potential biocontrol agents. This study combined culture-dependent and amplicon-based metagenomic approaches to assess bacterial diversity in soils associated with *Prunus dulcis* var. *Beldi*, a traditional Moroccan almond, and four native plant species from central Morocco. Our aim was to bioprospect native microbiota and identify beneficial microbes to support almond growth and health. Alpha-diversity indicated that almond soil exhibited significant lower richness compared to the other soils, while *Rhus pentaphylla* soil showed the lowest overall diversity. Beta-diversity analysis showed distinct bacterial community compositions across the different soils. Nevertheless, Actinomycetota, Pseudomonadota and Acidobacteriota remained the most represented phyla in all samples, accounting for over 50% of the total abundance. Culturable bacteria were isolated using multiple culture media, yielding a total of 177 bacterial isolates. To assess the overall taxonomic diversity, all colonies from each soil were pooled for total DNA extraction. Amplicon-based metagenomic 16S rRNA gene sequencing was performed on five pooled samples, revealing 26 bacterial genera. Most isolates belonged to genera well known for their biocontrol potential, such as *Bacillus*, *Pseudomonas*, and *Streptomyces*. Comparative analysis between soil metagenomic data and the cultivable fraction revealed that the cultivated isolates represent genera within the 10% of the bacterial families detected by metagenomics. Individual bacterial strains showing the highest biocontrol activity against both bacterial and fungal pathogens of almond were identified through Sanger sequencing of the 16S rRNA gene and now form a foundational collection for *in vivo* screening.

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P31 Emerging diseases caused by *Neofusicoccum* and *Phytophthora* species on fig tree (*Ficus carica* L.) in Italy

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Monitoring surveys, conducted during 2024 in four Italian regions (Apulia, Marche, Sardinia and Veneto), revealed the widespread occurrence of young and mature fig trees (*Ficus carica* L.) showing sudden death, crown thinning, shoot and branch dieback, sunken cankers and root rot symptoms. Given the unusual diffusion and severity of these symptoms, a study was conducted to identify the main causal agents associated. To achieve this goal, 86 samples including rhizosphere with fine roots (11) and branch with bleeding and sunken cankers (75) were collected from 11 symptomatic fig trees. In vitro isolations performed on universal and selective medium yielded colonies belonging to three families: *Botryosphaeriaceae, Diaporthacee* (Ascomycetes) and *Peronosporaceae* (Oomycetes). Based on morphological features and DNA sequences, seven species namely *Botryosphaeria dothidea* (14 isolates), *Diaporthe cinerascens* (10), *Neofusicoccum australe* (9), *N. mediterraneaum* (10), *N. parvum* (28), *Phytophthora citricola* (3) and *P. plurivora* (6) were identified. In addition, two *Phytophthora* isolates could not be assigned to any formally described species. For the three *Phytophthora* species, *N. australe* and *N. mediterraneaum* are reported here for the first time on fig trees worldwide, Koch's postulates were satisfied inoculating 5-year-old seedlings in laboratory conditions. Sixty days after inoculation, all inoculated plants showed the same symptoms observed in the field. Overall, the data obtained highlights the involvement of multiple *Botryosphaeriaceae* and *Phytophthora* in the aetiology of the emerging diseases affecting fig trees in Italy.

P32 Characterisation of *Hanseniaspora uvarum* PGL5, a grapevine berry inhabiting yeast with a promising potential in controlling *Botrytis cinerea*

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Botrytis cinerea, the causal agent of grey mould, is one of the most relevant plant pathogenic fungi affecting grapevine production worldwide. Concerns about fungicide-resistant *B. cinerea* populations underscore the critical need for alternative control strategies. To address these issues, there is growing interest in testing new plant-beneficial (micro)organisms. Recently, we directed our focus on *Hanseniaspora uvarum* PGL5 (PGL5), a yeast strain isolated from grapevine berries with promising biocontrol properties. To evaluate biocontrol efficacy, experiments were conducted on grape berries treated with a PGL5 conidia solution (10^7 conidia/mL) 24 and 48 h before the inoculum of B. cinerea (10^6 conidia/mL). The highest efficacy was achieved by inoculating PGL5 48 h before *B. cinerea*. In this case, PGL5 showed a significant higher efficacy than that of iprodione (1.5 g/L). To characterise the PGL5 mode of action, inhibition of *B. cinerea* mycelial growth through diffusible secondary metabolites and volatile organic compounds (VOCs) was assessed. In the dual culture assay, PGL5 reduced *B. cinerea* mycelial growth by 41.36% compared to the control. In the VOC assay, *B. cinerea* mycelium growth was drastically inhibited compared to the untreated control, indicating that PGL5 emitted a VOC blend highly toxic to *B. cinerea*. To investigate its biocontrol potential, the PGL5 genome was sequenced and annotated to identify genes involved in VOC production. Overall, the results achieved in this study support the possible development of PGL5 as a biopesticide against *B. cinerea* on grapevine. However, further studies are needed to understand the impact on grapevine production and vinification.

P33 Application of IRRIGOPTIMAL® for smart farming of citrus orchards and phytosanitary aspects of the use of reclaimed water for irrigation

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The reuse of wastewater treated in constructed wetland (CWs) for crop irrigation is a sustainable strategy to face water scarcity. IRRIGOPTIMAL® is an integrated decision-support platform for optimizing the irrigation in citrus orchards with reclaimed water (RW). Specific objectives of this study were: i. To investigate if RW from a CW may be a source of citrus oomycete pathogens. ii. To test the anti-oomycete effectiveness of biocontrol agents (BCAs), such as *Trichoderma asperellum*, *T. atroviride*, *T. harzianum*. and *Epicoccum nigrum*, or two commercial bioproducts containing chitosan and nosodes (Ascoma® and Verde®). The detoxification potential of *Trichoderma* spp. makes them interesting also as bioremediation agents of wastewaters. Only oomycetes with an aquatic lifestyle and weakly pathogenic to citrus, including *Phytophthora gonapodyides*, *P. inundata*, and *Phytopythium litorale*, were recovered from CW, while only soilborne aggressive oomycetes, including *P. nicotianae*, *P. citrophthora* and *Phtopythium. vexans*, were recovered from the rhizosphere soil of citrus trees irrigated with RW. These findings indicate that oomycetes residing in CW and those associated to citrus rhizosphere occupy distinct ecological niches, excluding the hypothesis that irrigation with RW constitutes a phytosanitary risk for citrus orchards. Despite the inhibitory activity shown *in vitro* against all aforementioned oomycetes, all candidate BCAs applied singularly *in planta* were ineffective in preventing infections of *P. nicotianae*, the most virulent among these oomycetes. Conversely, the application of either a mixture of *Trichoderma* species or the two commercial bioproducts, singularly, reduced significantly the disease severity caused by this pathogen.

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P34 Resveratrol bioconversion into dimeric stilbenoids using fungal biofactories

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Resveratrol bioconversion by fungi is a fascinating area of research, as they possess a wide range of enzymes that can metabolize various organic compounds such as stilbenoids and convert them into valuable products. *In vitro* antifungal assays have demonstrated different activity levels of grape stilbenoids - such as viniferins - against *Pyricularia oryzae, Plasmopara viticola* and *Botrytis cinerea.* These compounds can be synthesized or extracted from different natural sources or raw materials, however, the potential of fungal whole cells as a tool to provide biologically active dimers of resveratrol has been poorly investigated. In this study, the ability of *Botrytis cinerea* and *Cryphonectria parasitica* to convert resveratrol into dimers was investigated in liquid cultures. Both fungal species grew in broths amended with resveratrol, but their morphology was affected in the presence of resveratrol dissolved in DMSO. Reverse-phase HPLC analysis confirmed that *B. cinerea* produces delta-viniferin, epsilon-viniferin and pallidol, and with this study, we report for the first time the same ability also for *C. parasitica* hypovirulent strain. The stilbenoid production dynamics revealed that *B. cinerea* quickly converted resveratrol into dimers that are not detectable 24 hours later in nutrient-rich medium. On the contrary, *C. parasitica* required more time than *B. cinerea* to convert resveratrol, but the dimers could be detected even after 48 hours. These data open the perspective to use *C. parasitica* hypovirulent strains for the sustainable and zero-waste production of bioactive molecules to be used for plant protection.

P35 Preliminary *in vitro* and *in vivo* Screening of Biological Products Against *Colletotrichum* spp. Causing Apple Bitter Rot and Glomerella Leaf Spot on apple orchards

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Apple Bitter Rot (ABR) and Glomerella Leaf Spot (GLS), caused by *Colletotrichum* spp., are emerging diseases of *Malus domestica* in Europe, particularly damaging in Italian organic orchards where chemical control options are restricted. This study investigates the *in vitro* and *in vivo* efficacy of several commercial biological products (based on *Bacillus subtilis*, *Bacillus amyloliquefaciens*, potassium hydrogen carbonate, orange oil, calcium polysulfide, copper, sulphur, rock and diatomaceous powders, and a mix of essential oils containing eugenol, geraniol, and thymol) against four *Colletotrichum* species (*C. chrysophilum*, *C. fioriniae*, *C. siamense*, and *C. grossum*). These were compared to conventional chemical fungicides (Ditianon, Captan, and Fluazinam). *In vitro* assays showed high inhibition rates (>80% GI) for formulations containing *B. amyloliquefaciens* D747, *B. subtilis* (IAB/BS03 and QST 713), orange oil (60 g/L), copper (124 g/L and 20%), sulphur (80%), and the essential oils mix. Selected effective products were further tested in semi-field conditions on 2-year-old 'Gala' apple trees inoculated with *C. chrysophilum* (2×10^5 conidia/mL) and maintained for 12 days at 25 °C. Biological treatments resulted in a reduction of disease with values ranging from 18% (orange oil) to 41.5% (*B. amyloliquefaciens* D747) in terms of severity and values between 9.8% (Rock powder) and 37.3% (sulphur) in terms of incidence. In comparison, the best chemical treatment (Fluazinam) showed a reduction in severity and incidence of 78% and 62.4% respectively. Considering the moderate disease pressure, these preliminary results highlight potential biological alternatives for ABR and GLS management, supporting future development of sustainable control strategies in apple orchards.

P36 Intercropping of medicinal and aromatic plants in vineyards can make a contribution to the control of *Plasmopara viticola*

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Salvia officinalis (sage) and *Origanum vulgare* (oregano) have a potential in disease control; their secondary metabolites have been recognized as active compounds against several plant pathogens and some of their volatile organic compounds (VOCs) may stimulate the upregulation of defense-related genes in grapevine. A 3-year experiment was conducted in a vineyard by planting oregano and sage plants between vines along the vine rows, in plots of 52 m^2 (4 rows, 22 m long); control plots were also considered, in which there were no intercrop plants. The 3rd or 4th grapevine leaves from the apex of active growing shoots were randomly sampled from the plots with sage, oregano, or control, at three different grapevine growth stages (BBCH 65, 71, 75). Discs were excised from these leaves and artificially inoculated with a sporangial suspension of *Plasmopara viticola* in Petri dishes. Results showed a significant reduction in disease severity in the leaves from intercropped rows, with an overall efficacy of 27% for oregano and 34 % for sage compared to the control. In some Petri dishes, leaves of oregano or sage were added, which further increased the efficacy to 45 and 51% for sage and oregano, respectively. These results confirm the interest of the oregano and sage VOCs for disease control, even when these plants are grown in consociation with grapevines. Further studies are ongoing to understand metabolomic processes of grapevine leaves following the exposition to sage VOCs by plants grown in consociation, and artificial inoculation with *P. viticola*.

This study was supported by the PhD in Agro-Food System (Agrisystem) of the Università Cattolica del Sacro Cuore (Italy).

P37 Sustainable Management of *Fusarium* Diseases in Durum Wheat: Field Testing of Seed and Spike Biological Treatments

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Fusarium Crown and Root Rot (FCR/FRR) and Fusarium Head Blight (FHB) pose significant threats to global durum wheat production, particularly in organic farming systems where chemical control is not available. This study explores biological control agents (BCAs) as sustainable and effective alternatives, validating laboratory findings under field conditions through differet application methods. To address seed-related infections, seed priming with beneficial bacterial strains was applied during open-field trials over two consecutive growing seasons (2023–2025) in the Ravenna area. Durum wheat seeds (cv San Carlo) were co-sown with autoclaved barley inoculated with *Fusarium culmorum* Fc1126. Early seedling emergence was manually recorded, with additional assessments at BBCH 30–31 stages using drone technology. In the first year, *Bacillus amyloliquefaciens* CAAd increased germination by 50% compared to untreated seeds, while LAB strains improved emergence by up to 37.3%. Drone surveys confirmed a consistent 15% emergence improvement for CAAd in both years, despite reduced disease pressure in the second season. For FHB trials at the University of Bologna Experimental Station, spray treatments with a LAB strain following artificial inoculation with *F. culmorum* (Fc383 and Fc820) and *F. graminearum* (Fg566 and Fg913) achieved the lowest disease index (13.8) in the first year. Its cell-free supernatant further reduced the FHB index to 4.2 in the second year compared to 7.6 in the inoculated control, suggesting potential antifungal metabolite activity. These results highlight BCAs' potential as effective tools for organic durum wheat cultivation, with future research needed to optimize formulation and stability for enhanced practical use.

This research 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) – M4 C2, Investimento 1.4 – D.D. 1032 17/06/2022, CN00000022) and the project PRIN 2022 PNRR (M4 C2. Investment 1.1.) - D.D. n. 1409 of 14/09/2022-BICONTRARIUM.

P38 A rapid tool for resilient orchards: a qPCR assay supporting sustainable peach disease management

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Diaporthe amygdali, the causal agent of twig canker in peach (*Prunus persica*), poses a considerable threat to peach production, leading to substantial yield losses and significant economic impact in Italian orchards. Early and accurate detection of this pathogen is therefore essential to support sustainable disease management strategies, improve orchard health, and reduce unnecessary fungicide applications. In the present study, a species-specific quantitative PCR (qPCR) assay targeting the β-tubulin gene was developed and validated for the sensitive and rapid detection of *D. amygdali* in various peach tissues. The assay displayed exceptional specificity, as evidenced by its performance in testing against a wide array of *Diaporthe* isolates and a selection of non-target fungal species commonly associated with peach trees. Notably, the method was successfully implemented on field-collected samples from multiple peach-producing regions across Italy, thereby demonstrating its robustness, reproducibility, and applicability under field conditions. The complete diagnostic workflow, from sample preparation to result acquisition, can be accomplished within a short time, providing a substantial temporal advantage over conventional diagnostic approaches such as culturing or microscopy. This molecular diagnostic tool could provide timely and accurate monitoring of pathogen presence in the field, thereby supporting the development of dynamic predictive models within the integrated pest management (IPM) programs, contributing to the development of more sustainable peach production systems.

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P39 Peach bud microbiome profiling reveals cultivar-dependent microbial signatures related to susceptibility to *Diaporthe amygdali*

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Diaporthe amygdali, a fungal pathogen, is a primary causal agent of twig canker in peach trees (*Prunus persica*), posing a significant threat to Italian peach production. The different susceptibility of various cultivars suggests that plant genotype could play a role in disease outcomes. To explore whether plant-associated microbial communities contribute to disease tolerance, a metagenomic analysis was conducted on three peach cultivars characterized by contrasting susceptibility to *D. amygdali*. Total DNA was extracted from surface-sterilized buds collected during dormancy, and community profiling was performed using high-throughput Illumina sequencing of the ITS1 and V3-V4 of 16S rRNA gene regions to characterize fungal and bacterial communities, respectively. Bioinformatic analyses revealed distinct microbial profiles associated with each cultivar. *Pseudomonas, Sphingomonas*, and *Methylobacterium* predominantly represented bacterial communities across all cultivars. Notably, the most susceptible cultivar also harbored the bacterial genus *1174-901-12*, which was reported as pathogenic in several tree species. Fungal communities displayed a more homogeneous pattern, with *Aureobasidium* consistently abundant. However, *Diaporthe* was detected exclusively in the most susceptible cultivar, together with *Alternaria* and *Cladosporium*. Interestingly, *Vishniacozyma*, a genus including species with potential plant-beneficial properties, was enriched in the medium-susceptible cultivar. These findings underscore the potential influence of the endogenous microbiome in shaping cultivar-specific responses to *D. amygdali*, thereby providing a foundation for future studies aimed at developing new strategies based on natural antagonists for sustainable disease management in peach orchards.

This research was funded by National Recovery and Resilience Plan (NRRP), Mission 4, Component 2, Investment 1.1, Call for tender No. 104 published on 2.2.2022 by the Italian Ministry of University and Research (MUR), funded by the European Union – NextGenerationEU– Project Title IMPEACHMENT "IMproving PEACH manageMENT of emerging and re-emerging pests and diseases" – CUP J53D23006820006 - Grant Assignment Decree No.0001015 adopted on 07.07.2023 by the Italian Ministry of Ministry of University and Research (MUR).

P40 *Fusarium* spp. as decline agents in young vineyards in Northern Italy

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Young vine decline is often associated with pathogens involved in Grapevine Trunk Diseases (GTDs). Recently we have been recording several cases of poor growth up to death in young vineyards (2-9 yrs.-old) with negligible presence of GTDs pathogens. Symptomatic vines showed stunted growth, and at the base of the rootstock and in some of the main roots, a dark brown to black woody tissue and vascular discolouration extending upwards or even reaching the graft union or the scion. They were sampled in six commercial vineyards in the province of Verona (Northern Italy). Adventitious root formation above the primary root system was often noticed, a symptom that is usually related to hypoxia in the root zone and poor drainage conditions. Wood tissues were sampled in 4 sites from roots to scion, disinfected, and cultured on MEA medium. While one vine showed a heavy colonization by *Armillaria mellea*, all the others showed a high presence of *Fusarium* isolates, mostly *Fusarium oxysporum*, expecially from dark brown to black tissue, with variable incidence and severity. In the root system, in the collar and in the middle position of the rootstock, 100% of the wood sections sampled were colonized by *Fusarium*, around 40% even in the scion. The colonization severity varied from 60 to 78.9% over the total chips sampled in each plant. These results suggest a potential important role, to be verified by the artificial infections under way, of *Fusarium* spp. in grapevine decline under stress conditions, where poor drainage can here be found as the main stress inciting factor.

P41 Early detection of *Flavescence dorée* in grapevine via hyperspectral leaf reflectance: A case study from Tuscany (Central Italy)

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Flavescence dorée (FD), caused by *flavescence dorée phytoplasma* (FDp), is one of the most severe grapevine (*Vitis vinifera*) diseases in Europe. There are no resistant grapevine varieties or effective treatments, so infected plants must be removed to stop the spread. Despite the quarantine status of FDp and the mandatory monitoring and vector control, FD continues to spread. Traditional visual field inspections are slow and often inaccurate, especially in early infection stages. In this study, we explored the potential of full-range hyperspectral data (400–2,400 nm), collected at the leaf level, as a high-throughput and non-destructive tool for in-field detection of FD infection. The research was conducted in a Sangiovese vineyard (red grape) located in the Chianti Classico region (Tuscany, Central Italy), an area severely affected by FD. Our results demonstrate that hyperspectral analysis enables: (i) early detection of FDp infection, even before visible symptoms appear (accuracy >70%); (ii) discrimination between different symptom severity levels, including asymptomatic and mildly symptomatic leaves (accuracy ~80%); (iii) physiological characterization of plant responses to FDp, with spectral estimations indicating impaired photosynthetic activity in early stages and accelerated leaf senescence later in the season, potentially impacting vine performance and grape quality. While not intended to replace molecular diagnostics, the proposed hyperspectral approach can complement conventional methods and significantly enhance field monitoring and early warning systems. Further investigations across less severely affected vineyards and different grapevine varieties, including white cultivars with yellowing symptoms, are recommended to validate and broaden the applicability of this technique.

This study was conducted during and with the support of the Italian national inter-university PhD course in Sustainable Development and Climate change (https://www.phd-sdc.it/). This study was also funded by 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).

P42 Systemic Stress and Resilience: a meta-Analysis of grapevine response to *Flavescence dorée*

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Flavescence dorée (FD) is a major phytoplasma-associated disease severely affecting *Vitis vinifera* in European vineyards, causing substantial yield losses and a decline in grape quality. The causal agent, *flavescence dorée* phytoplasma (FDp), is transmitted primarily by the leafhopper *Scaphoideus titanus* through phloem feeding. FD symptoms generally appear one-year post-infection and progressively intensify during the summer. During this latent period, asymptomatic infected vines act as inoculum sources, contributing to further disease spread. Despite its status as a quarantine pest, FD continues to expand across Europe, underscoring the need for improved understanding of grapevine responses to FDp. This meta-analysis synthesizes data from 22 European studies published over the past two decades, encompassing 67 genetic and biochemical parameters related to FD infection. The findings reveal a consistent upregulation of genes involved in flavonoid biosynthesis, stress signaling, and pathogen defense pathways in FDp-infected grapevines. Biochemical profiles show increased concentrations of sucrose and salicylic acid, indicative of enhanced stress response. Conversely, a significant decline in photosynthetic pigments, especially chlorophylls, suggests compromised photosynthetic capacity and metabolic stress. These results demonstrate that FDp infection triggers a complex physiological response in grapevines involving carbohydrate redistribution, defense activation, and photosynthetic disruption. The consistency of these responses across cultivars and studies highlights their potential as biomarkers for disease detection and targets for breeding programs. This work provides a foundation for future research aimed at developing resistant grapevine varieties and more effective disease management strategies.

P43 *Plenodomus tracheiphilus* and 'Mal Secco' disease: selection of tolerant genotypes based on phenotyping and molecular analysis

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Plenodomus tracheiphilus, the causal agent of 'Mal secco' disease, is one of the most serious threats to lemon cultivation in the Mediterranean. It causes extensive damage to lemon and citron trees, leading to substantial economic losses. The fungus's pathogenicity, which primarily affects the plant's vascular system, makes the disease management complex. The control of the disease is particularly challenging due to the limited understanding of the genetic resistance mechanisms in host plants, making field phenotyping the most reliable method to identify sources of resistance or field tolerance.

To investigate the pathogen-host interaction and identify new tolerant/resistant genotypes, CREA has started a genetic improvement program based on hybridization and clonal selection. Since 2020, lemon hybrids resulting from three distinct crosses have been planted in two experimental farms in Sicily and Calabria, areas characterized by high natural pathogen pressure. The plants were monitored monthly through visual assessments of symptoms. Moreover, 170 nucellar selections derived from tolerant lines were subjected to field evaluation, with susceptible cultivars included as controls. To support visual diagnosis, molecular analysis using qPCR has been performed on woody tissues from both symptomatic and asymptomatic clonal selections to detect the pathogen.

After five years of observations in natural conditions of strong infection, clones and hybrids with significant tolerance to the pathogen were selected. These resistant hybrids represent a strategic resource for pre-breeding and for future research on genetic resistance. Moreover, the tolerant clonal selections will be tested in multiple environments to confirm field tolerance

The results highlight the key role of field phenotyping in the identification of *P. tracheiphilus*-resitant/tolerant accessions.

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P44 The quest is on for natural resistance to Flavescence dorée

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Flavescence dorée (FD) is an economically important disease of grapevine caused by a phytoplasma (FDp). FDp is transmitted in a persistent propagative manner by the leafhopper *Scaphoideus titanus*. Control of the disease relies on planting of healthy material, roguing of infected plants and compulsory insecticide treatments against the vector, these latter having raised concerns about non-target effects and human health. Grapevine genotypes show different susceptibility to FD in the field, but complete resistance has not been confirmed under controlled conditions. In a quest for natural resistance to FD, we evaluated several typical cultivars from the Veneto and from Piedmont regions, which were selected based on: i) a close parental relationship with a resistant cultivar and ii) a high-frequency introgression of genomic elements belonging to a resistant genotype; iii) apparent low FD incidence and severity in the field. The most resistant of these accessions, together with others previously ranked as FD-tolerant, were analysed using electropenetrography (EPG) to distinguish between resistance due to the plant's response to phytoplasmas and repellency/antibiosis towards the vector. Our results showed that a relationship with a resistant parental genotype confers lower FD susceptibility in a context of vector repellence and that vector feeding on some varieties results in increased insect mortality, suggesting a possible resistance mechanism based on a reduced transmission efficiency.

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P45 Biotechnological approaches to determine the mechanisms involved in UV resistance in biocontrol *Lysobacter* spp. strains

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Bacterial biocontrol agents generally show promising results when tested under controlled conditions, such as laboratories and greenhouses. However, they are characterised by inconsistent performance in open-field environments, primarily due to the germicidal effects of UV light. While this limitation applies to many bacterial strains, there are certain exceptions. For instance, species within the *Lysobacter* genus produce xanthomonadins, yellow pigments that not only give colonies their characteristic colour but also provide protection against UV light. Based on this premise, the present study aimed to investigate the survival of the biocontrol agent *L. capsici* AZ78 (AZ78) cells exposed to UV light conditions through the production of xanthomonadins. To identify the genes involved in xanthomonadin biosynthesis, we employed a biophysical transformation technique using electroporation (12,5 kV/cm) and the transposon vector pUT/mini-Tn5 Cm. To make the AZ78 cells electrocompetent, the initial exponential phase culture was pelleted and washed twice on ice with 10% glycerol, then resuspended in 10% glycerol. The ratio between cells and plasmid varied: 40 or 80 µL of electrocompetent cells were electroporated with 500 or 1000 ng of pUT/mini-Tn5 Cm. At the end of the process, a total of four white AZ78 colonies were selected and will be tested for their resistance to UV light. These preliminary findings will be the basis for understanding the importance of molecular pathways involved in xanthomonadin biosynthesis in *Lysobacter* spp. biocontrol strains.

P46 Phytosanitary profiling of local tomato variety Pomodorino di Manduria

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An impressive work of valorization of local Apulian tomato varieties recently led to recovery six Pomodoro di Manduria ecotypes. To valorize this source of biodiversity, a phytosanitary profiling of the ecotypes was conducted evaluating the presence of seed-borne fungal, bacterial pathogens, phyto-viruses and culturable microbiota. No relevant ectophytes were identified, while 8 bacterial and 1 fungal species, further identified by 16s and ITS region sequencing, represented the endophytic population. *Clonostachys* sp. was isolated with a frequency of 72% from ecotype 5/21, while bacteria were mostly plant growth promoters or biocontrol agents belonging to *Bacillus* sp. or *Stenotrophomonas* sp.. *Agrobacterium tumefaciens* was frequently isolated (40%) from ecotype 5/17. The susceptibility to *Fusarium oxysporum f.sp. lycopersici* and *Pseudomonas syringae pv tomato* was compared to the commercial hybrid Roma. All the populations were susceptible to *F. oxysporum* infections and were found less susceptible to *P. syringae* infection than 'Roma'. None of the ecotypes proved to be positive to tomato infection chlorosis virus (TICV) tobacco mosaic virus (TMV), potato virus Y (PVY), tomato yellow leaf curl virus (TYLCV), tomato spotted wilt virus (TSWV) and tomato mosaic virus (ToMV), while all were positive to tomato brown rugose fruit virus (ToBRFV). Furthermore, in post-harvest conditions, Pomodoro di Manduria showed longer shelf life compared to other varieties. Important information on the phytosanitary status of self-propagated seeds and on the susceptibility of Pomodorino di Manduria to important tomato pathogens was assumed. Nevertheless, to assure a phytosanitary safe guaranteed use of local tomato ecotypes, additional studies are necessary.

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P47 Bioactive extracts from *Agaricus bisporus* spent mushroom substrate and *Aureobasidum pullulans* bioformulations effect on *Rhizoctonia solani* of *Lactuca sativa* L.

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New challenges are expected in the future, such as ensuring food security, managing waste, and tackling emerging pathogens. Bioformulations and bioactive compounds obtained from agricultural waste could provide solutions to these challenges, particularly with regard to the management of soil-borne pathogens. This study tested the use of *Aureobasidium pullulans* strain AP1, as active substance in an oil dispersion (OD) formulation, and bio-extracts derived from spent mushroom substrate (SMS) of *Agaricus bisporus* as sustainable strategies to manage *Rhizoctonia solani* of lettuce. *In vitro* assays showed that AP1OD at 600 mg/L inhibited pathogen mycelial growth by 57%, while SMS extracts stimulated lettuce seedling growth. In *in vivo* assays, the AP1OD formulation reduced the incidence of the soil-borne pathogen *R. solani* on lettuce plants by 66.6%, and the SMS bio-extracts significantly stimulated lettuce leaf and root growth (>200%). The AP1OD formulation and the SMS extracts increased the expression levels of the lettuce genes (*ggps* and *hppd pdx1*), which are involved in plant antioxidant potential, vitamin E and vitamin B6 biosynthesis. This study demonstrates the potential of a new yeast formulation and bio-extracts derived from agricultural waste to use against *R. solani* of lettuce, with respective antifungal and biostimulant properties.

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P48 Assessment of effectiveness by natural and biological means to control soilborne fungi on tomato crop

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Starting from the "Green Revolution" the overuse of chemical and synthetic products leaded to negative effects for human and environmental health. The application of chemical compounds represented the only way to satisfy the food request for a long time. Due to these reasons, aware that according to FAO the global population will increase to 10 billion by 2050, the research started to focus on the application of harmless means to control the parasites and guarantee food for the population. Thus, we focused on the identification of the most promising agricultural wastes and biological agents to control the fungal pathogens of tomato. The preliminary part of the experiment was performed *in vitro* and consisted of the application of six agricultural wastes as putative inhibiting products (bergamot, eucalypt, laurel, pomegranate, sage, false pepper) and three biological strains against nine fungal pathogens strains (*Athelia rolfsii*, *Fusarium graminearum*, *F. oxysporum*, *F. solani*, *Fusarium* spp., *Sclerotina sclerotiorum*, *Verticillium dahliae*). Based on results obtained in *in vitro* condition, bergamot and pomegranate, an inorganic product (EP5), and a microorganism (*Streptomyces* sp. Strain Strep_22) were selected to perform the *in vivo* experiment. This was carried out in greenhouse to control three fungal pathogens (*A. rolfsii*, *F. oxysporum* and *S. sclerotiorum*) on tomato by the setting of 80 theses. The putative inhibiting products protected the roots and collars in some cases, while the microorganism Strep_22 protected them significantly. Moreover, it has been observed that the *Streptomyces* strain was able to promote the growth of the tomato plants.

P49 Evaluation of the efficacy of a commercial chitosan-based formulation applied as a seed treatment in different host-pathogen systems

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Chitosan, a natural biopolymer derived from chitin, has gained considerable attention as an eco-friendly biocontrol agent in agriculture. Its application in plant disease management is based on its ability to elicit plant defense responses, directly inhibit pathogen growth, and enhance overall plant vigour. In this study, we evaluated the efficacy of a commercial chitosan-based formulation applied as a seed treatment on tomato, snap beans, and broccoli in the presence of various plant pathogens including *Alternaria brassicicola* (Altb), *Leptoshaeria maculans* (Lm), *Fusarium* spp. (Forl and Fsp), *Pseudomonas syringae* pv. *tomato* (Psto), *Xanthomonas euvesicatoria* pv. *perforans* (Xep), and *Clavibacter michiganensis* subsp. *michiganensis* (Cmm). Independent trials assessed both the direct effect on seed inoculum (Forl/tomato, Fsp/snap beans, Altb/broccoli) and plant-mediated responses via a seed biopriming approach (Xep, Psto, and Cmm on tomato, Lm on broccoli). The efficacy varied depending on the host-pathogen combinations. On tomato, seeds artificially inoculated with Forl and treated with chitosan, developed seedlings with a significantly lower disease severity. Similarly, the product significantly reduced the number of spots on tomato cotyledons induced by Xep as well as the bacterial canker severity caused by Cmm. However, no reduction in the severity of bacterial speck caused by Psto was observed. In the Fsp/snap beans combination, seed treatment with chitosan-based product resulted in a significantly low disease incidence and severity compared with non-treated seeds. Conversely, chitosan-based product was not effective in reducing the symptoms of Altb e Lm on broccoli. Overall, chitosan is a promising tool in integrated disease management strategies aimed at reducing chemical inputs and promoting sustainable agriculture.

P50 Effect of cropping system on structure and function of citrus tree rhizosphere microbiome in organically and conventionally managed orchards

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Soil microbiome plays a crucial role in plant health, influencing nutrient cycling, plant growth promotion, plant resilience to abiotic stresses and interactions between plant and soil-borne pathogens. This study investigated the impact of organic versus conventional management on the rhizosphere microbiota, including prokaryotes, fungi and oomycetes in citrus orchards, focusing on the interactions between microbial diversity, soil physisochemical properties and agronomic practices. Metagenomic sequencing using BeCrop® technology was used to analyze microbial communities in 150 rhizosphere soil samples collected from 15 orchards (both conventionally and organically managed) in eastern Sicily during summer and winter. Geographical location was the primary driver of prokaryotic and fungal community structure. Other factors, including seasonality, soil physicochemical properties, soil tillage, irrigation system, and rootstock type, also had a significant but lower impact. Organic management was associated with higher microbial diversity and greater microbial network modularity and co-exclusion interactions, indicating it promotes a more structured and resilient microbiome. Moreover, this study revealed that organic practices enhance beneficial microbial functions, such as nitrogen fixation and phosphorus solubilization, more effectively than conventional practices. Organically managed orchards harbored a richer fungal microbiota (54 taxa vs. 25 in conventionally managed soils), including *Chaetomium convolutum*, a well-known biocontrol agent. Additionally, the bacterial genus *Nitrospira*, crucial for nitrification and nitrogen cycling, was exclusively detected in organically managed soils during winter, indicating a potentially higher nitrogen use efficiency. These findings suggest that organic management enhances microbial functional diversity, improving citrus resilience to stresses and reinforcing microbiome-based indicators for sustainable agriculture and soil fertility.

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P51 Development of a portable qPCR assay for early detection of *Plasmopara viticola* specie complex

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Downy mildew is a devastating grapevine disease worldwide caused by the oomycete *Plasmopara viticola*. In its native area, five cryptic species have been identified and the *aestivalis* clade is apparently the unique present in Europe, including southern Italy. A on-field quantitative SybrGreen®-based PCR (qPCR) assay for detection and quantification of *P. viticola* complex was developed employing an *on-site* molecular lab station (Generon S.p.A., San Prospero (MO), Italy). A primer set (PLAV19) was designed to target the ITS1 region of the pathogen. Three primer concentrations (200, 300 and 400 nM) and three annealing temperatures (56, 58 and 60°C) were evaluated and 200 nM primer and an annealing temperature of 58°C yielded the most efficient and specific amplification. Under these conditions, the assay showed a limit of detection (LoD) of 1.5 fg μL^{-1} of *P. viticola* DNA, corresponding to a quantification cycle (Cq) value of 34. Specificity tests conducted using a panel of more than twenty grapevine pathogens and beneficial microorganisms, and seven table grape cultivars, showed no evidence of unspecific amplification. The assay was further validated using sporangia suspensions of *P. viticola* at 6 different concentrations (from 10^5 to 10^0) confirming its high sensitivity (even 1 sporangia). *On-field P. viticola* quantitative detection was carried out on grape leaves and inflorescences with unspecific symptoms, bunches with larvata-like symptoms, as well as on capture-spores tape, confirming the validity of the protocol for early, rapid and accurate pathogen detection, which can be useful for improving sustainable and effective management of downy mildew.

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P52 First report of *Fusarium redolens* infecting wild rocket in Italy and identification of candidate virulence genes

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Fusarium redolens is a plant pathogen known to infect several crops, including chickpea, asparagus, lentil, and durum wheat. For the first time in Italy, we isolated *F. redolens* (called Ruc1) from symptomatic wild rocket (*Diplotaxis tenuifolia*) grown in greenhouses in Pontecagnano Faiano (SA). To evaluate its virulence, we conducted infection assays on the susceptible line Diplo1 accession from the IPK Gene Bank. Upon infection, Diplo1 developed yellowing of leaf veins, wilting, root rot and eventually died. To test if *F. redolens* has the intrinsic ability to infect Diplo1, four additional strains of *F. redolens* (*ITEM 2787, ITEM 5168, ITEM 5174 and ITEM 5176*), not isolated from wild rocket and kindly provided by the CNR-ISPA of Bari, were tested. We also carried out infection tests using two *Fusarium oxysporum f. sp. raphani* (*For* and *CREA*). Interestingly, only *For* showed the ability to infect Diplo1 plants as Ruc1 does. To investigate the genetic basis of this difference in virulence between these *Fusarium* strains, we sequenced the genomes of all *F. redolens* isolate, *For* and *CREA* strains using Oxford Nanopore technology. Subsequently, we performed comparative genetics and, by using RNA-seq data of infected Diplo1 plants by *F. redolens* strain Ruc1, we identified 11 candidate genes. Of these genes, five are in common between Ruc1 and *For*. Interestingly, two of them are also common to other *F. oxysporum* strains that can infect Brassicaceae. These two candidate genes will be knocked-out and mutants used in disease assays on *D. tenuifolia*.

P53 Influence of GTDs on grapevine microbial communities: a case study on Apulia and Sicily

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In recent years, the symptomatic expressions related to grapevine trunk diseases (GTDs) exacerbated, particularly in southern environments such as Apulia and Sicily. Given the scarcity of effective chemical control methods, the use of biocontrol agents remains the most appropriate perspective for the containment of etiological agents of GTDs. Furthermore, knowledge on the balances of microbiomes of table grape vines affected by GTDs is still insufficient. In this work, the microbial community of table grape vines of different commercial cultivars and symptomatic GTDs was investigated in comparation with asymptomatic vines, in Apulia and Sicily areas. The microbial community was studied through different approaches. The portion of culturable microorganisms was assessed by isolating fungi and bacteria on Potato Dextrose Agar (PDA) and Nutrient Agar (NA), respectively. In the sampled Apulian vineyards *Diplodia seriata*, *Neofusicoccum parvum, Botryosphaeria* spp. and *Phaeomoniella chlamydospora* were the mostly re-isolated pathogens. The re-isolation proportion of the fungi belonging to *Botryosphaeriaceae* was slightly higher in symptomatic plants. In the Sicilian area, *Phaeoacremonium minimum, P. chlamydospora,* and *Diaporthe* spp. were the most common re-isolated fungi from both symptomatic and asymptomatics vines, without significant differences between the two conditions. Additionally, the endophytic bacterial community is under study. From the same samples, total DNA was extracted and metagenomic analysis is in progress. These results will allow to better understand the relationships established between resident microorganisms and GTDs pathogens at pruning, a crucial time for their spread, and further improve knowledge on the interactions in the microbiome of plants affected by GTDs.

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P54 Characterization of *Neopestalotiopsis* species associated with crown rot of strawberry in Italy

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Pestalotiopsis-like fungi have been widely reported in strawberry worldwide as casual agents of leaf spot, root and crown rot. Accurate species identification requires both morphological and molecular analyses to resolve cryptic phylogenetic relationships. Recent multi-locus studies reclassified several *Pestalotiopsis*-like isolates from strawberry as members of the *Neopestalotiopsis* genus, emphasizing their role in root and crown rot diseases. In recent years, numerous disease outbreaks caused by *Neopestalotiopsis* have been observed in Italian strawberry fields, suggesting that it is an emerging pathogen of significant concern. During 2022-2023, a comprehensive survey was conducted in the Piedmont region to assess the diversity and distribution of *Neopestalotiopsis* species. Isolates were identified through morphological characterization and phylogenetic analysis based on ITS, *tef1*, and *tub2* locus sequences. Four species were identified: *N. rosae*, *N. iranensis*, *N. hispanica* (syn. *vaccinii*), and *N. scalabiensis*. Pathogenicity tests on strawberry cv. Portola confirmed the four species as wound pathogens, associated with crown rot symptoms. Among them, *Neopestalotiopsis rosae* was confirmed to be the most prevalent and virulent species. This study represents the first report of *N. scalabiensis* associated with strawberry crown rot in Italy, and the first global report of *N. iranensis* in association with strawberry diseases. These findings underscore the emerging threat posed by *Neopestalotiopsis* species to strawberry cultivation worldwide, highlighting the need for continuous monitoring to support effective management strategies.

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P55 *Moringa oleifera* seed cake yielded pure glucomoringin with potential for biocontainment of tomato Fusarium wilting

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The vascular fungus *Fusarium oxysporum* f. sp. *lycopersici* is an important soil-borne pathogen of tomato in cultivated areas worldwide. Coating seeds with phytochemicals has been reported to prevent seed transmission and control seedlings' infection, as well. In this work, the defatted seed cake of *Moringa oleifera*, that is rich in bioactive compounds including 4-(α-L-rhamnosyloxy)benzyl glucosinolate (glucomoringin), was explored as a valuable source of antifungal molecules. Glucomoringin, indeed, is the precursor of 4-(α-L-rhamnosyloxy)benzyl isothiocyanate (moringin), which is obtained through myrosinase (EC 3.2.1.147) catalyzed hydrolysis. Therefore, an extraction pipeline of pure glucomoringin on the multigram scale was set up. The commercial defatted residue of *M. oleifera* PKM-2 (Indena India Pvt. Ltd) (100 g) showed a glucomoringin content of 13.9% (w/w), determined according to the ISO 9167:2019 method. After extraction in boiling water, glucomoringin (4.2 g) was obtained in 99% pure form by two chromatographic steps. The pure compound and the moringin-rich solution obtained after hydrolysis with a commercial myrosinase were evaluated against the pathogen both *in vitro* and *in planta*. *F. oxysporum* f. sp. *lycopersici* conidia germination and mycelial growth were significantly inhibited by the moringin-rich suspension in the range 1-0.001 mM, in a dose-dependent manner, compared to glucomoringin and control treatments, which didn't differ significantly. Interestingly, the preventive treatment (coating) of tomato var. crovarese seeds with glucomoringin and the respective hydrolysis product (0.1 mM) resulted equally effective in reducing (-70%) the disease severity in post-emergence, suggesting a putative plant-mediated mechanism underlying the phytochemical efficacy.

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). This manuscript reflects only the authors' views and opinions, neither the European Union nor the European Commission can be considered responsible for them.

P56 Evaluation of the antifungal activity of olive mill wastewater enriched with citrus juices against *Verticillium dahliae*

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The olive oil industry by-products, such as olive mill wastewater (OMW), are rich in phenolic compounds, so they have a potential application in phytopathogen control. In this study, we evaluated the antifungal activity of three OMW-based extracts against *Verticillium dahliae* defoliating strain (D), the causal agent of Verticillium wilt of olive (VWO). We tested a pure OMW extract and two extracts enriched with bergamot (OMWB) and tarocco orange juice (OMWO), respectively, to enhance their phenolic content. Results obtained from in vitro tests showed that OMWB powder completely inhibited fungal growth, in a dose-dependent manner, whereas OMW and OMWO only reduced colony diameter, indicating a partial fungal activity. Based on these outcomes, in vivo trials were initiated on ten olive cultivars, including Frantoio and Picual (tolerance and susceptibility references, respectively), along with: Borgese, Laurina, Mignola, Minuta, Morellona di Grecia, Rastellina and Verde Verdelho. Plants were artificially inoculated by root-dipping in a conidial suspension of *V. dahliae* (D) and divided into four experimental groups: (i) inoculated only; (ii) inoculated + OMW; (iii) inoculated + OMWB; and (iv) uninoculated control treated with water. Extracts were administered at regular intervals to ensure gradually exposure. Disease progression will be monitored weekly over a 10-weeks period, assessing symptom severity, wilting, and other infection-related parameters. Preliminary observations indicate variability among plants in the different experimental groups. Final results will allow to establish the possible efficacy of the phenolic extracts tested, potentially contributing to the development of eco-sustainable strategies for the management of VWO.

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P57 Exploring the genome variability of *Fusarium musae.*

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Fusarium musae is a recently described species which causes crown rot disease on banana fruits and infections in humans. Genomic tools can help decipher the mechanisms of adaptability and success of a pathogenic species in multiple environments. Previous data suggest that both strains isolated from humans and bananas share the ability to cause a similar level of disease on banana fruits and Galleria mellonella (used as a model for human infection). Genome size of 18 strains obtained from the two hosts shows variability of more than 2 Mbs with unique genes compared to the sister species *F. verticillioides.* Telomere-to-telomere complete genomes obtained by combining nanopore and Illumina sequencing of two strains collected from a banana and a human patient, reveal the existence of supplementary chromosomes, which partially explain genome diversity. Transposons are active in some strains, likely contributing to genome rearrangements. This variability might explain the cross-kingdom adaptation of the species.

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P58 Development of a Novel Real-Time PCR Protocol for the Detection of *Plenodomus tracheiphilus* in Lemon Trees

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Plenodomus tracheiphilus is the etiological agent of Malsecco, a tracheomycotic disease of citrus that causes severe dieback of twigs and branches. Given its status as a quarantine pest, though in Italy mandatory controls have been recently abandoned, the development of rapid and reliable detection protocols is essential for timely diagnosis and effective management. We present a novel real-time PCR method based on EvaGreen intercalating dye and TaqMan probe chemistries. Primers and a hybridization probe were designed based on the internal transcribed spacer (ITS) region of DNA ribosomal genes. Standard curve analyses demonstrated nearly best fitting amplification efficiency in both assays, even in the presence of DNA extracted from healthy or necrotic lemon wood. The detection limit (LOD) was respectively 20 fg and 10 fg per PCR reaction of *P. tracheiphilus* gDNA in EvaGreen and TaqMan assays. Even in the LOD evaluation no significant interference by the host tissue was recorded. Tests of analytical specificity confirmed the assay's reliability: all 36 non-target fungal species tested to date were negatively detected (exclusivity), while all 23 *P. tracheiphilus* isolates tested to date were positively detected (inclusivity). A comparative evaluation with two previously published qPCR protocols showed that while TaqMan-based results were comparable, our method was the only one to provide specific/reliable detection using EvaGreen assay. These results indicate that our dual-chemistry Real-Time PCR assay is a promising tool for early detection of Malsecco and for quantitative monitoring of fungal colonization in susceptible and resistant citrus species.

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P59 Virome analysis of *Euonymus japonicus* unveil the presence of a new Fabavirus and a new Rhabdovirus

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Native to Japan, euonymus (*Euonymus japonicus* Thunb.) is a perennial shrub used in landscape and private gardens appreciated for its glossy and green foliage. Euonymus plants with viral-like symptoms consisting in mottling and vein clearing were collected from a private garden in Campania region (South Italy). Total RNA was extracted from leaves of a single plant and submitted to high-throughput sequencing (HTS). A total of 24.909.354 trimmed reads were analysed and contigs for a possible new species in the *Rhabdovirus* genus and a new species in the *Fabavirus* genus have been identified, having less than 80% similarity with reference genomes available in NCBI. Rhabdoviruses are ssRNA(-) viruses, bullet shaped, enveloped while fabaviruses are segmented bipartite ssRNA(+) not enveloped. Near complete genomes were obtained and RT-PCR with specific primers, designed on the assembled genomes, confirmed the presence of both viruses in the original sample and in ten additional different foliar samples collected from plants with similar symptoms. Phylogenetic analysis indicate that the new *Rhabdovirus* is closely related to maize fine streak virus (MFSV) a *Gammanuclearhabdovirus*, while the new *Fabavirus* is closely related to physostegia virginiana crinkle-associated virus 1 (PVCaV1), a recently described member of the *Fabavirus* genus. These findings illustrate the phytovirome features from a new pathosystem, emphasizing the importance lesser-monitored plants as potential viral reservoir of new emerging viruses.

P60 Metagenomic profiling of soil microbiota associated with *Xylella fastidiosa*-infected olive plants

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Xylella fastidiosa (Xf) subsp. *pauca* is a devastating bacterial pathogen that colonizes xylem vessels of many plants, including olive trees on which causes the olive quick decline syndrome. While several studies have recently addressed the characterization of changes in the microbial communities associated to xylem vessels following Xf infections, the impact on the rhizosphere microbiome remains unexplored. In this work, we performed a metagenomic analysis of rhizosphere soils from potted plants of two olive cultivars grown under controlled conditions, comparing artificially infected plants with uninfected controls. Total genomic DNA from soil samples was submitted to Illumina shotgun sequencing and analyzed through the SqueezeMeta pipeline for co-assembly, gene prediction, binning, and comprehensive taxonomic and functional annotation for KEGG, COG, GO, Pfam, CAZy, MEROPS terms. Differential abundance analysis was conducted using SQMtools in R. Similarly to what was observed in the xylem niche of infected olives, infection induced significant shifts in soil microbial community, notably an enrichment of taxa involved in nitrogen-cycling, including ammonia-oxidizing archaea (*Nitrosarchaeum*) and nitrite-oxidizing bacteria (*Nitrobacter*). Functional changes were observed in carbon fixation, glycolysis/gluconeogenesis, glutathione metabolism, and microbial competition mechanisms such as quorum sensing, biofilm formation, and secondary metabolite biosynthesis. Nevertheless, different levels of enzymes linked to volatile organic compound production were also found. The identified microbial and functional signatures hold promise as ecological indicators contributing to understand the alterations occurring in severely affected plants *versus* resistant plants, and to gather novel information on soil microbial community with potential outcomes in the framework of integrated pest management strategies.

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SESSION 2

Sustainable Strategies for Plant Disease Management

FLASH TALKS FROM “YOUNG RESEARCHERS IN TRAINING”

FT1 Improved tolerance to grey mold of tomato plants fertigated with micronutrient amounts of zinc

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Zinc (Zn) is a key micronutrient involved in numerous physiological processes in plants, including defense responses against biotic stress. However, its role in mediating tolerance to fungal pathogens such as *Botrytis cinerea* remains poorly explored. In this study, we investigated the impact of Zn fertilization on grey mold tolerance in tomato (*Solanum lycopersicum* L.) under controlled conditions. To select a responsive genotype, several tomato lines were screened for their Zn accumulation capacity. Based on leaf tissue analysis, line LA-4068 was chosen due to its superior ability to accumulate Zn following fertigation with 2 or 10 μM $ZnSO_4$. Plants were subsequently challenged with *B. cinerea*, and lesion development was assessed using an excised leaf assay. Plants treated with 10 μM Zn showed a significant reduction in lesion area, with an average decrease of nearly 40% compared to plants treated with 2 μM Zn, confirming a protective effect. These results highlight zinc's capacity to modulate the tomato defense system at the physiological level. At the molecular level, comparative proteomic analysis is currently being performed to identify which defense-related proteins are involved in the lesion containment. In addition, RT-qPCR analysis is being used to investigate the modulation of specific stress-related genes in Zn-treated tissues. The findings reinforce the functional involvement of zinc in plant nutrition and present evidence for its potential use, at micronutrient levels, to enhance crop resistance against grey mold.

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FT2 Sustainable Control of *Plasmopara viticola* in Grapevines via SafeWax: A Bioinspired Passive Coating Strategy

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SafeWax is a bioinspired antifungal coating designed as a sustainable alternative to conventional fungicides. Its fatty acid–based formulation mimics the superhydrophobic and self-cleaning properties of natural cuticles of superhydrophobic plants, forming a stable, water-repellent barrier that hinders pathogen adhesion and colonization while ensuring sustainable, environmentally friendly protection. *In-vitro* assays on grapevine leaf discs demonstrated complete inhibition of *Plasmopara viticola* at a SafeWax dosage of 35 µL/cm². Treatments applied both prior to and following pathogen inoculation indicated that SafeWax primarily exerts preventive and protective effects rather than curative action. Long-term efficacy was confirmed through *in-vivo* trials on whole grapevine plants. Leaves inoculated up to 9 days post coating application consistently showed significant pathogen suppression, with inhibition rates ranging from 47% to 80% when compared to uncoated leaves, showing a substantial protective activity over time. Coating persistence was evaluated by scanning electron microscopy (SEM) on leaves 3, 6, 20, and 40 days after application, revealing strong adhesion and stable structural integrity, essential for prolonged field effectiveness. Ongoing field trials are running to assess SafeWax applicability under standard vineyard conditions, comparing its performance with conventional and organic treatments including copper and essential oil-based fungicides. Overall, SafeWax offers a promising passive strategy to reduce synthetic inputs while maintaining effective grapevine protection.

This project has received funding from the European Union's Horizon Europe research and innovation program under grant agreement No 101099462.

FT3 Unveiling the antibacterial potential of nanoparticles: a game-changer in crop bacterial disease management

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Plant diseases are a major challenge to agriculture, threatening biodiversity and food production. With climate change accelerating their spread, bacterial infections are becoming increasingly severe, causing devastating economic losses. However, in the European Union, disease control options are limited. Thus, developing sustainable strategies is crucial. Eucalyptus essential oil (EEO) is well-known for its antibacterial activities, but its high volatility and hydrophobicity can hinder its large-scale application. So, this study aimed at developing nanoparticles incorporating the EEO and assessing their antibacterial effects against tomato plants' pathogens. Briefly, EEO was incorporated into lipid (LN-EEO) and keratin (KN-EEO) nanoparticles. Then, their bactericidal properties were evaluated against *Xanthomonas euvesicatoria (Xeu), Pseudomonas syringae* pv. *tomato (Pst),* and *Clavibacter michiganensis michiganensis (Cmm)* after 48 h of exposure to different concentrations of LN-EEO, KN-EEO, and EEO. Here, *Xeu* presented the highest susceptibility, followed by *Cmm* and *Pst.* While all treatments had similar bactericidal activities against *Xeu,* KN-EEO was 47% more effective than EEO against *Cmm*, showing that KN-EEO enhanced EEO bactericidal effects. To complement these data, ongoing research is being conducted to assess the effectiveness of these nanoparticles in treating *Xeu*-infected tomato plants. Furthermore, to assess if bacterial exposure to nanoparticles triggered the release of volatile organic compounds (VOCs) that could inhibit neighboring cells' growth, a subsequent experiment was performed. Results revealed a stronger inhibitory effect when bacteria were closer to the VOC source, particularly to KN-EEO. Overall, these findings highlight that KN-EEO could be a promising strategy for sustainable bacterial disease management in agriculture.

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FT4 Varietal Susceptibility and Biological Approaches for the Management of Albugo occidentalis in Spinach Cultivated in the Capitanata Area

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White rust of spinach, caused by the oomycete *Albugo occidentalis*, is one of the main threats to spinach cultivation, especially in the Capitanata area, where climatic conditions strongly favor the spread of the pathogen. In this context, limiting the use of chemical control methods is essential, and this can be achieved through the selection of resistant or tolerant cultivars and the adoption of biological control strategies, promoting an integrated and sustainable disease management approach. This study evaluated the susceptibility of fifteen *Spinacia oleracea* L. cultivars — eight traditionally grown in Capitanata and seven non-local varieties considered for introduction — through artificial inoculation with *A. occidentalis*. In parallel, the effectiveness of three biological control strategies was assessed: antagonistic microorganisms (*Bacillus subtilis*, *Aureobasidium pullulans*, and *Streptomyces lydicus*), natural substances (basalt powder, silicates, and ozonated oil), and a plant extract (nettle macerate). Varietal trials revealed considerable differences in infection response. Among local cultivars, "Warthog" exhibited the highest resistance, while "Lignite" and "Kangaroo" were the most susceptible. The other local cultivars showed intermediate tolerance levels. Among the non-local cultivars, "Andromeda" stood out for its superior performance, showing delayed and milder symptoms. Field trials confirmed the superior efficacy of antagonistic microorganisms, especially *Bacillus subtilis*, in reducing disease development compared to natural substances and the plant extract. These results highlight the potential of integrating varietal selection and biological control strategies for the sustainable management of spinach white rust, offering valuable insights for integrated crop protection in Mediterranean farming systems.

This research was funded through a co-financed PhD fellowship under the program "Biotechnology and smart practices for a sustainable management of natural resources, food and agriculture," Cycle XL, pursuant to Ministerial Decree 630 of April 24, 2024.

FT5 Plant products as putative botanical fungicides assayed in *in vitro* and *in vivo* conditions against fungal soilborne pathogens on fennel seedlings

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The increasing restrictions on the use of chemical products in agriculture due to environmental and health concerns have highlighted the need to investigate on sustainable alternatives for controlling fungal soilborne pathogens. This study aimed to evaluate the antifungal efficacy of five natural plant-based powders as botanical fungicides (*Citrus bergamia*, *Eucalyptus globulus*, *Punica granatum*, *Solanum lycopersicum*, and EP), applied individually and in combination, against six severe soilborne fungal pathogens, such as *Diaporthe foeniculina*, *Fusarium oxysporum*, *Rhizoctonia solani*, *Sclerotinia sclerotiorum*, *Sclerotium rolfsii*, and *Verticillium dahliae*. Two commercial products, a resistance inducer, EP, and a fungicide (Rizolex®, active ingredient: Tolclofos-methyl) were included as reference controls. In vitro assays were conducted by inclusion of the natural powders (2% g/ml) into growth PDA medium, alone or in binary combinations. The colony growth has been recorded for 21 days. The *in vivo* trials were performed under greenhouse conditions in 1 L pots to protect *Foeniculum vulgare* seedlings against the above-mentioned fungi artificially inoculated. The putative botanical fungicides were used individually (8%; v/w) and combined in consortium (2% for each; v/w). After 45 days, the plant health status was assessed through disease severity ratings, shoot and root measurements, swollen base morphology, and biomass analyses. Results from both *in vitro* and *in vivo* experiments indicated that the natural powders, alone and each other combined exhibited different antifungal activity. Mycological re-isolation performed to ascertain the presence of inoculated fungi detected their incomplete suppression, highlighting that natural products deserve further investigations to optimize the application methods.

FT6 *Salvia* spp. extracts contain bioactive terpenoids against grapevine downy mildew

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Alternative products to synthetic fungicides are required to develop sustainable plant protection strategies. The interest in plant-derived products as biofungicides has increased over time, since they could play a crucial role in pest management. In particular, *Salvia* spp. extracts previously showed inhibitory activity against different phytopathogens. *Plasmopara viticola* is the causal agent of grapevine downy mildew, and leads to significant economic losses to viticulture, especially in areas with warm and humid climate conditions. This study aims to characterize the activity of *Salvia* spp. alcoholic extracts against grapevine downy mildew and to identify bioactive compounds. Alcoholic extracts of sage shoots, leaves, and flowers showed strong disease reduction in grapevine leaf disk assays, while stem extract was only partially active against *P. viticola*. Moreover, shoot extracts decreased downy mildew symptoms in potted grapevine plants under greenhouse conditions. Fractions of shoot extracts were obtained using preparative liquid chromatography and subjected to inhibitory activity tests. Active fractions were analyzed with untargeted metabolomics using liquid chromatography-high resolution mass spectrometry (LC-HRMS), and 25 putative bioactive compounds were annotated as terpenoids. The annotation of five compounds was validated by reference standards, and the activity against downy mildew was confirmed on leaf disk assays. The concentration of each bioactive compound in sage alcoholic extracts will be quantified using LC-HRMS. The identification of novel bioactive compounds from *Salvia* spp. and the characterization of their mode of action will pave the way for the development of new alternative products for sustainable plant protection.

ORAL PRESENTATIONS

OP10 Italian peanuts: an integrated approach to ensure safety and sustainability

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Peanut is cultivated and consumed globally, but its high susceptibility to *Aspergillus flavus* infection raises significant concerns regarding aflatoxin (AFs) contamination. In Italy, peanut cultivation has been recently reintroduced, and in this study, an integrated approach was assessed to ensure both safety and sustainability along the supply chain. Preliminary field investigations, conducted in 2022 and 2023, delivered promising pre-harvest results with concentrations of aflatoxin B_1 (AFB_1), the most toxic among AFs, consistently below European legislation limits. Optimal crop management is crucial to maintain this high-quality standard, especially in account of increased AFs risk driven by warmer and drier conditions linked to climate change (CC). Predictive modelling and biocontrol using non-aflatoxigenic *A. flavus* strains offer effective tools for risk management. Models that identify AFs risk at harvest can also support improvements in post-harvest handling. A mechanistic weather-driven prototype model, AFLA-peanut, was developed and showed strong potential in accounting for weather variability, highlighting its usefulness in risk prediction. Furthermore, the biocontrol agent "AF-X1", already in use in Italy on maize, inhibited AFB_1 production by over 70% under simulated CC conditions *in vitro,* comparable to normal conditions. Implementing these tools in the peanut value chain could significantly improve AFs risk management, and integrating the behaviour of biocontrol agents into the AFLA-peanut model may further enhance farmer support. Finally, in line with sustainability and circular economy goals, the rearing of *Hermetia illucens* larvae on peanut by-products, with or without fungal contamination, has shown promising results, offering a valuable opportunity for the valorisation of by-products.

This study was supported by the Doctoral School on the Agro-Food System (Agrisystem) of the Università Cattolica del Sacro Cuore (Italy).

OP11 Metabolomics-guided optimization of *Trichoderma*-based bioformulates for sustainable crop improvement in grapevine and sorghum

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Modern agriculture is shifting towards sustainable practices, promoting microbial-based products to reduce the use of synthetic chemicals. The use of a metabolomic approach enables comprehensive analysis of metabolic shifts resulting from interactions between beneficial microbes and plants, with the aim of selecting of novel and improved bioformulates. Two strains of *Trichoderma* (*T. harzianum* M10 and *T. afroharzianum* T22) and one *Trichoderma*-derived secondary metabolite (6-pentyl-α-pyrone, 6PP) were used in the present study. Single strain inoculants and 6PP were applied to grapevine plants, while formulations of single strains or synthetic consortium with a natural carob-derived adhesive (polysaccharide hydrogels from *Ceratonia siliqua*) were used for seed coating and application to sorghum plants. Samples including vineyard leaves and grapes, and sorghum leaves and grain, were collected and analyzed through an untargeted metabolomics approach. Results showed that *Trichoderma* and 6PP treatments increased ascorbic and m-hydroxybenzoic acids content, improving grapevine leaf oxidation resistance, and enhanced grape polyphenol levels, essential for aroma, shelf life, and health benefits. Metabolomic analysis of sorghum demonstrated that *Trichoderma* applications significantly influenced plant and grain metabolome, specifically increasing grain sugar content. Targeted analysis for mycotoxins revealed that the combination of T22 and M10 significantly reduced the levels of all analyzed mycotoxins compared to control group, except fumonisin B1 (45.04 ppb) and α-zearalenol (44.92 ppb). Overall, these findings highlight the potential of metabolomics to guide the optimization of microbial and metabolite-based formulations by evaluating their effects on plant, including the identification of specific biochemical markers that may support the selection of effective strains and biomolecules.

OP12 *Diaporthe amygdali* inside out: leveraging genetic insights for sustainable and precision control strategies

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In recent years, symptoms related to Twig Cankers and Shoot Blight disease (TCSB) have re-emerged in several Italian peach orchards, particularly in key production districts of the Emilia-Romagna region. The fungal pathogen *Diaporthe amygdali* is recognized as the primary causal agent of TCSB, inducing the rapid drying of shoots, flowers, leaves, and branches, often accompanied by resin exudation from cankers observed in late winter or early spring. Given Italy's status as the second-largest peach producer in Europe, ensuring sustainable production and maintaining high fruit quality requires a deeper understanding of *D. amygdali* biology and the development of effective detection and management strategies. As part of the Italian IMPEACHMENT project (PRIN 2022), this study utilised a hybrid whole-genome sequencing approach, combining Illumina short-read and PacBio long-read technologies, to generate the first high-quality genome assembly of D. amygdali isolated from peach. This genomic resource facilitated the identification of candidate virulence-associated effectors and other pathogenicity-related genes, thereby providing novel insights into the infection mechanisms of this emerging pathogen. It is reasonable to hypothesise that molecular-precision treatment, such as that based on dsRNA molecules, could be developed for a spray-induced gene silencing method, given these results. The integration of pathogen genomics and molecular diagnostics constitutes the cornerstone of this research, thereby establishing a foundation for the development of more effective TCSB management strategies. The outcomes of this research are expected to contribute to the enhancement of sustainability and resilience in peach production, both in Italy and in other regions.

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OP13 Antifungal factors or resistance elicitors? Role of polycyclic tetramate macrolactams in the biological control of *Peronospora belbahrii* and *Plasmopara viticola* by *Lysobacter capsici* AZ78

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Biocontrol *Lysobacter* spp. strains are emerging as potential candidates for the development of microbial biopesticides to control plant pathogenic oomycetes. Their efficacy is associated with polycyclic tetramate macrolactams (PTMs), thermostable antifungal compounds stored in cell membranes. In this study, we explored how PTMs participate in the plant protection efficacy of *L. capsici* AZ78 (AZ78) against *Peronospora belbahrii* and *Plasmopara viticola* in basil and grapevine, respectively. Firstly, we tested the plant protection efficacy of heat-treated (HT) AZ78 cells. Viable (V) and HT AZ78 cells, when applied to both pathosystems, significantly reduced disease severity by over 90–95% across all trials, providing efficacy similar to that of commercial products. Interestingly, V and HT AZ78 cells had a toxic effect against pathogen sporangia and were able to stimulate the production of callose and Reactive Oxygen Species (ROS) in basil and grapevine leaves. Dihydromaltophilin (DMP) and maltophilin (MP), two PTMs, were isolated from AZ78 cells and, subsequently, tested for the control of *P. viticola* on grapevine leaf disks. DMP and MP were able to reduce the *P. viticola* infection drastically. Moreover, the application of DMP and MP mixture at 2.5 mg/L resulted in a 100% reduction in *P. viticola* sporulation. Importantly, this mixture was toxic against *P. viticola* sporangia and stimulated the production of callose in grapevine leaf disks. These findings underscore the potential of AZ78 and PTMs as a broad-spectrum, sustainable tool for downy mildew management in sustainable agriculture, inspiring future research and applications in the field of plant pathology and biocontrol methods.

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OP14 Circular Plant Protection Measures against *Xanthomonadaceae* Plant Pathogens: Antibacterial Potential of Pomegranate Peel Extract and Cellulose Nanocrystals

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Pomegranate peel extract (PGPE) and cellulose nanocrystals (CNC), derived from agro-waste, are promising bioactive compounds, potentially useful in crop protection. PGPE, rich in polyphenolic compounds like ellagic acid, gallic acid, and punicalagins, has demonstrated significant antibacterial effects. Our studies show that PGPE inhibits the growth, motility, and biofilm formation of *Xanthomonas campestris* pv. *campestris* (Xcc), the pathogen responsible for black rot in cruciferous crops, along with a significant decrease in disease severity when applied as protective treatment. PGPE fully inhibited *Xylella fastidiosa* subsp. *pauca* (Xf), under *in vitro* conditions, when applied at 0.5%; furthermore, PGPE reduced Xf biofilm formation, a critical factor in managing pathogen virulence and persistence. Phenotypic and molecular studies on olive cuttings and 2 years old olive plants, showed that PGPE exhibits biostimulant effects enhancing chlorophyll metabolism and plant defense-related genes, when applied at the root level in combination with CNC. Indeed, CNC, a biodegradable nanomaterial, has also shown promising potential for controlling Xf by modulating biofilm production and reducing the bacterial growth *in vitro*. Ongoing research is focusing on developing combined formulations of the compounds to optimize the delivery by endotherapy and soil application, though the synthesis of novel thermo-reversible polymer and soil amendments, improving their efficacy in field conditions, both for disease control and biostimulant activity. This research underscores the potential of PGPE and CNC as sustainable, circular solutions for bacterial plant disease management, which are under evaluation on model pathosystems (eg. tobacco) and on naturally infected plants in the Apulia region.

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OP15 Combined *Trichoderma-Clonostachys* reduce Fusarium head blight infection and mycotoxin content of wheat under greenhouse conditions.

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Wheat is the third most-produced staple crop globally and a basic component of the human diet. The production is affected by several factors, with plant pathogens being one of the major threats. Fusarium head blight (FHB), caused primarily by *Fusarium graminearum (Fg),* is the most widespread in Europe over the past 30 years. Biological control agents (BCAs) offer sustainable alternatives to manage such threats. *Trichoderma gamsii* T6085 (*Tg*) and *Clonostachys rosea* IK726 (*Cr*) have shown efficacy in reducing *Fg* impact on wheat and oat. In previous growth chamber experiments, combined *Tg-Cr* treatment reduced number of infected spikes by 93%. In this study, we evaluated the efficacy of their co-inoculation under greenhouse conditions. To enhance performance, *Tg* spores were primed in water for 15 hours before inoculation while *Cr* spores were inoculated immediately after harvest. Spikes were sprayed with *Fg* spores 3 days later. The co-inoculation reduced both, disease incidence and disease severity by 45%, in comparison with *Fg* control whereas the content of *Fg* DNA was reduced by 94%, outperforming both individual treatments. The quality of harvested kernels was significantly improved by *Tg-Cr* as compared to the *Fg* control. Hence, thousand kernel weight was increased by 28% while kernel damage was reduced by 59%. Furthermore, the deoxynivalenol (DON) level was decreased by 59%. These results support the potential of *Tg-Cr* co-inoculation for FHB control and justify a further progress to field-scale trials.

OP16 Integrated control strategies for managing crown and fruit rot of pomegranate caused by *Coniella granati* in southern Italy

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Pomegranate cultivation has gained interest in southern Italy, driven by the tree's drought tolerance and temperature requirements, which make it a suitable alternative to traditional crops such as olives, cereals, and vineyards. However, production is increasingly threatened by wood canker diseases, particularly crown and fruit rot caused by *Coniella granati*, which severely impacts yields, fruit quality, and tree health. In addition, abiotic stresses and physical injuries can compromise fruit integrity. In Italy, the limited availability of registered fungicides and alternative compounds highlighted the need for an integrated and/or multidisciplinary approaches to diseases management. In alignment with the European Union's Farm to Fork (F2F) strategy, this study evaluated the *in-vitro* efficacy of several biological agents and organic products against *C. granati*. Tested biocontrol agents included *Bacillus* spp., *Clonostachys roseum*, *Coniothyrium minitans*, *Trichoderma* spp., *Streptomyces* sp., a yeast extract, and chitosan chlorhydrate and EP-Protect as organic means. Based on *in-vitro* performance, the most promising control means were selected for *in-vivo* trials on 12-year-old 'Wonderful' pomegranate trees under field conditions. The organic control means were applied individually or in combination either with each other or with conventional fungicides used for managing wood diseases in fruit trees. To ascertain the absence of chemical residues, multi-residue analyses were performed on fruit samples. The canopy's phytosanitary status was evaluated, while fruit quality was assessed at harvest. Results showed that integrated treatments combing organic, biological and chemical means preserved both fruit yield and quality, improving the potential of biocontrol strategies in integrated pomegranate disease management.

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SESSION 3

Diagnosis and Characterization of Plant-Associated Pathogens

FLASH TALKS FROM "YOUNG RESEARCHERS IN TRAINING"

FT7 A new molecular seed detection method to quantify *Ustilago nuda* and reduce prophylactic seed treatments

C. Panzetti[1,2], E. Jenny[3], I. Bänziger[3], A. Kägi[3], S. Vogelgsang[3], T. Hebeisen[4], P. Büttner[5], D. Croll[2], F. Widmer[1], K. E. Sullam[1]

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Seed health tests are performed to avoid sowing untreated seeds with problematic plant pathogen levels, thus limiting their spread. The detection of internal seedborne pathogens like *Ustilago nuda* – the causal agent of loose smut in barley (*Hordeum vulgare*) – is challenging because symptoms only appear when teliospores replace barley inflorescences and smutted ears develop. Current *U. nuda* detection methods rely on the visual analysis of extracted embryos or field inspections of crops used for seed production, both of which are laborious and can be unreliable. We developed a novel multiplex qPCR method that targets *U. nuda* and *H. vulgare* DNA to test seed. Naturally infected seed lots with varying levels of *U. nuda* were analyzed with our qPCR method and the visual analysis of extracted embryos. To evaluate the performance of these laboratory detection methods, seeds from the same lots were grown during two field seasons, and the observed field infections were used as the reference infection level. The qPCR results, normalized by the ratio of *U. nuda* to *H. vulgare* DNA copies, showed a stronger correlation with field infection levels than the number of infected embryos detected. Compared to the visual embryo analysis, our qPCR method discriminated more accurately between seed lots with infection levels above and below the field tolerance threshold. Overall, our qPCR approach offers a reliable alternative to visual embryo inspection. Its integration with field observations can prevent *U. nuda* infections and reduce the reliance on synthetic prophylactic seed treatments, contributing to an integrative pest management strategy.

This research was founded by Foundation Sur-la-Croix, IP Suisse, the Swiss Association of Cereal Producers, Swiss granum, and swisssem.

FT8 Exploiting actinomycete biodiversity in Arctic soils to find new biocontrol agents of fungal pathogens

L. Pisoni[1], S. Viganò[1], C. Pizzatti[1], A. Kunova[1], P. Cortesi[1], M. Pasquali[1], M. Saracchi[1], L. Bertini[2], C. Caruso[2], D. Bulgari[1]

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Fungal plant pathogens pose a significant threat to global crop production. Although synthetic fungicides are commonly used in the field to control these pathogens, their application can have detrimental effects on the environment, the broader biosphere, and human health. The sustainability of the agricultural sector is closely linked to the development of alternative approaches to chemical control. In this context, actinomycetes are particularly important due to their ability to produce a wide range of secondary metabolites with antimicrobial activity. The exploitation of this group of bacteria could lead to the discovery of new possible biocontrol agents (BCAs) or bioactive molecules. In this study, soil and rhizosphere samples were collected in different regions of Greenland. A total of 167 bacteria isolates were obtained and characterized using cultivation-dependent methods. Based on morphological traits, sixty-four strains of actinomycetes were selected for screening of their biological control activity. Their direct antagonistic activity was evaluated using a dual culture assay against six phytopathogenic fungal species (*Sclerotinia sclerotiorum*, *Botrytis cinerea*, *Fusarium culmorum*, *Fusarium oxysporum* f.sp. *basilici*, *Alternaria alternata*, and *Alternaria tenuissima*), belonging to three families (*Sclerotiniaceae*, *Nectriaceae*, and *Pleosporaceae*). Some actinomycetes caused strong fungal growth inhibition exceeding 75%, with the strongest antimicrobial activity against *S. sclerotiorum*, reaching up to 86%. Phylogenetic analysis based on 16S rRNA gene sequencing allowed to identify these isolates and assess the microbial diversity of Greenlandic soils and rhizosphere, revealing a predominance of the *Streptomyces* genus.
These results support the discovery of novel BCAs or active compounds for sustainable plant pathogen management.

This research was funded by INTERACT-Horizon 2020.

FT9 Image-based time series analysis for the early evaluation of the biocontrol efficacy of *Trichoderma gamsii* T6085 on Fusarium head blight disease progression in wheat.

D. Mencarini[1], A. Petrucci[1,2], G. Del Cioppo[3,4], S. Poque[3,4], K. Himanen[4,5], K. Mäkinen[3], S. Sarrocco[1]

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Wheat, considered as a staple food, is constantly threatened by several diseases as Fusarium head blight (FHB), and the related risk of mycotoxins contamination. In view of the use of sustainable strategies for the management of FHB, one of the most promising alternatives to fungicides is the exploitation of biocontrol agents (BCAs) such as *Trichoderma gamsii* T6085, whose beneficial effects have been profusely demonstrated. Detecting, quantifying and preventing the progression of a plant disease, and the effect of a BCA, is challenging and susceptible to bias inherent in visual assessment. Aim of this study is to evaluate the early effects of *T. gamsii* T6085 application on FHB progression using high-throughput, multi-sensor, image-based time series. The experiment was performed at the National Plant Phenotyping Infrastructure (NaPPI) at the University of Helsinki, Finland. Dissected spikelets of *Triticum aestivum*, inoculated successively with T6085 and *F. graminearum*, one of the causal agents of FHB, were imaged every 6 hours after treatments. Disease progression could be monitored through RGB imaging by tracking color changes associated with disease symptoms, chlorophyll fluorescence imaging to detect disruptions in photosynthetic activity, and thermal infrared (IR) imaging to evaluate stomatal response to infection and treatment. Altogether, these imaging are expected to provide quantifiable information about the effect of T6085 on host-pathogen interactions. Results obtained with these controlled phenotyping methods could contribute to an early assessment of the preventive use of BCAs together with an early detection of plant diseases through a time-based monitoring.

FT10 Strains of *Aureobasidium pullulans* from extreme environments: new potential biocontrol agents?

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Extreme environments are an unexplored reservoir of microbial diversity, with a remarkable potential to be exploited in agriculture. One hundred seventeen yeast isolates, derived from different ecosystems, were molecularly identified, and the most represented genus was *Aureobasidium* (57%). A phylogenetic analysis based on a multi-*locus* sequence typing (ITS, ELO, EF-1alpha) was conducted to characterize the 'black yeasts' population. To investigate *A. pullulans* extremophilic and extremotolerant behaviour, different temperatures, pH, and enzymatic production were evaluated. The strains were tested by *in vitro* and *in vivo* assays against the postharvest fungal pathogen *Monilinia fructicola* as potential biocontrol agents (BCAs). Results displayed a great ecological variability concerning strains' growth and cells production depending on different culture conditions. However, a remarkable thermotolerance aptitude was detected in almost all the strains. In particular, the strains belonging to Group 2 (Algerian Desert) and Group 3 (Alto Adige Region) showed, respectively, a higher thermotolerance and biocontrol ability. These findings showed how some extreme environments could represent a promising source for new potential BCAs. However, further studies are needed to investigate the mechanisms of action of these putative BCAs for application during the postharvest phase.

FT11 Genetic Insights of *Aspergillus flavus* Population in Azerbaijan and Perspectives on the Use of Aflatoxin Biocontrol Products.

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Hazelnuts (*Corylus avellana L.*) are widely used for direct consumption and as ingredients in confectionery and chocolate industry. However, hazelnuts are susceptible to *Aspergillus flavus* infection, which diminishes their commercial value and presents significant health hazards due to aflatoxin contamination, with the Caucasus region being notably affected. Employing native non-aflatoxigenic (non-AF) *A. flavus* strains as a form of biocontrol is highly effective in reducing aflatoxin contamination in several crops, and formulated products are currently employed in USA, Africa and Europe. This research examined genetic diversity of *A. flavus* in three major hazelnut-producing regions of Azerbaijan, with the purpose of getting insight on *A. flavus* population structure and to evaluate the prevalence of genotypes closely related to non-AF isolates currently used in biocontrol products, with a particular focus on MUCL54911, the active ingredient of AF-X1, labelled for use in Italy. From 2022-2024, 827 isolates were recovered from hazelnut kernel and inflorescence in Zaqatala, Khachmaz and Gebele regions of Azerbaijan. All isolates were subjected to simple sequence repeat (SSR) genotyping and results revealed high genotypic diversity across regions, years and stages of hazelnut value chain. SSR results from clone corrected isolates highlighted how non-AF genotypes are native to Azerbaijan, and haplotypes closely related to MUCL54911 are already present in hazelnut orchards. These findings suggest the potential use of AF-X1 for reducing aflatoxins in this geographical region.

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ORAL PRESENTATIONS

OP17 *Botryosphaeriaceae* and *Phytophthora* species involved in the decline and mortality of ornamental trees on Albarella Island (Italy)

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Since autumn 2023 severe decline phenomena and sudden death symptoms on ornamental tree and shrub species were observed throughout the Albarella Island (Veneto, Italy). Given the landscape and economic importance of the green areas of the island, an in-depth study was conducted to establish the causal agents. To this end, a phytosanitary monitoring has been conducted in 26 micro-areas of the island chosen based on the spread of disease outbreaks. A total of 91 samples of rhizosphere including roots and necrotic aerial plants tissues were collected from 16 plant species for diagnostic analyses. Isolation performed on universal (PDA) and selective (PDA+) substrates yielded in pure culture 99 colonies belonging to 10 species of oomycetes and 14 species of ascomycetes, two of which not yet formally described. In particular, 9 fungal species belonging to the *Botryosphaeriaceae* family were obtained from branch samples showing typical sunken cankers. Among these, *Diplodia sapinea* and *D. corticola* were isolated with a high frequency. Ten species of *Phytophthora* were obtained from both root (rhizosphere) and shoot samples. *Phytophthora limosa* (first report in Europe) and *P. plurivora* were found to be the most widespread species. The results obtained highlight a very complex symptomatology and etiology characterized by the presence of multiple pathogens even on the same plant. The discovery of 9 species of *Botryosphaeriaceae* and 10 species of *Phytophthora* in a small geographical area such as the one under investigation suggests that this plethora of pathogens have potentially been introduced through human-related activities.

OP18 Advancing plant health monitoring: Nanopore sequencing for quarantine pathogen diagnostics

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Effective phytosanitary surveillance requires diagnostic tools capable of accurately detecting and identifying regulated pathogens directly from plant material, even in asymptomatic conditions. To address this challenge, a reliable diagnostic system was developed based on Oxford Nanopore Technologies (ONT) sequencing, using the portable MinION device, and data analysis through MONICA®, a custom bioinformatics pipeline specifically designed for ONT data. Two approaches were tested: (i) amplicon-Nanopore sequencing, involving the development of multiplex-PCR assays targeting selected housekeeping genes; (ii) a preliminary shotgun metagenomic approach that bypasses gene amplification, further reducing sample processing time. Amplicon-Nanopore sequencing was applied to target key EU-regulated quarantine pathogens, including *Xylella fastidiosa* subspecies (comprising different sequence types), *Xanthomonas citri* pv. *citri* and *X. citri* pv. *aurantifolii*, and *Pantoea stewartii* subsp. *stewartii*. These subspecies, pathovars and sequence types are characterized by distinct host ranges and geographic distributions. Therefore, high-resolution taxonomic identification is essential to guide appropriate phytosanitary measures. The amplicon-based approach was successfully applied to plant samples spiked with known pathogen concentrations as well as to naturally infected samples, achieving high sensitivity and specificity. Preliminary results of the shotgun metagenomic approach performed on host samples spiked with *Xylella fastidiosa* subsp. *pauca*, using cost-effective ONT Flongle flow cells, were promising, enabling reliable detection at high bacterial concentrations. However, further testing is needed to improve sensitivity and ensure detection at low bacterial loads. The overall findings of the study highlight the value of this system as a portable, reliable, and accessible solution for quarantine pathogen diagnostics and plant health monitoring.

This research was funded by the Project "La diagnosi come strumento di prevenzione per il contenimento di Xylella fastidiosa: sviluppo ed ottimizzazione (DIACOX)" funded by Ministry of Agriculture, Food Sovereignty and Forests (MASAF) –DM n. 664531 28/12/2022.

OP19 Invisible foes: cutting-edge non-destructive diagnostics for quarantine pathogens in legume seeds in a globalized market

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Legumes are essential to global food security and sustainable agriculture, owing to their high protein content, nitrogen-fixing ability, and adaptability to marginal soils. Since the 1960s, global demand has increased significantly. However, this growth also raises the risk of spreading seed-borne pathogens such as *Curtobacterium flaccumfaciens* pv. *flaccumfaciens* (*Cff*), a Gram-positive bacterium causing bacterial wilt in common beans. *Cff* is a quarantine-regulated organism in the EU and poses a serious threat to legume-producing and -importing countries, including Italy, where legumes are largely imported. Detection in plant materials and control of *Cff* are particularly challenging due to its xylem-limited colonization of bean plants and long latency period in seeds, which often remain asymptomatic. Conventional diagnostic methods such as PCR and LAMP are highly specific and sensitive, but often costly, labor-intensive, and destructive, making them less suitable for large-scale or port-of-entry screening. This study presents two innovative, cutting-edge, non-destructive diagnostic approaches: volatile organic compound (VOC) fingerprinting and photoacoustic detection. VOC profiling identified unique volatile molecules, particularly phenylmethanol and 2-methoxy-4-vinylphenol, that distinguish *Cff* from other bean pathogens. Simultaneously, photoacoustic analysis leveraged the pigment-based optical signatures of *Cff*, enabling its rapid and sensitive detection in simulated infected seeds, demonstrating for the first time in agriculture the feasibility of this technique for pathogen diagnosis. Together, these approaches offer a promising shift toward early, non-invasive, and scalable pathogen diagnostic systems. In the context of international trade and phytosanitary regulation, implementing such tools is pivotal for protecting legume value chains, reducing biosecurity risks, and strengthening crop resilience.

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OP20 Assessing the spread and impact of candidate priority pests to support risk management in the EU: EFSA's method and results

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In 2022, the European Food Safety Authority (EFSA) was mandated by the European Commission's Directorate-General for Health and Food Safety to provide technical assistance on identifying EU quarantine pests that qualify as priority pests, in line with Regulation (EU) 2016/2031 on protective measures against plant pests. EFSA assessed the lag period, rate of expansion and impact on crops and the environment for 46 shortlisted pests through expert knowledge elicitations carried out in 2023 and 2024 with 130 experts. Probability distributions were fitted to the elicited values using a statistical software. The resulting reports and datasets, including 200 probability distributions and 150 environmental impact values, were delivered to the European Commission's Joint Research Centre to support the Impact Indicator for Priority Pests model and complete the pest prioritisation ranking. The 11 plant pathogens assessed include the fungi *Bretziella fagacearum*, *Phyllosticta citricarpa*, *Phymatotrichopsis omnivora* and *Pseudocercospora pini-densiflorae*; the bacteria '*Candidatus* Liberibacter' spp. (causal agent of Huanglongbing), *Ralstonia pseudosolanacearum*, *Xanthomonas citri*, *Xylella fastidiosa*; Grapevine flavescence dorée phytoplasma; the nematode *Bursaphelenchus xylophilus;* and the virus *Nepovirus myrtilli*. The estimated parameters vary widely across pathogens i.e., median lag periods range from 21 days [95% probability interval: 8-34] (*R. pseudosolanacearum*) to 30 years [8-56] (*N. myrtilli*), expansion rates from 2 meters [0-10] (*P. omnivora*) to 15 kilometers per year [1-29] ('*Ca.* Liberibacter' spp.), and yield losses from 0.5% [0.0-1.8] (*P. pini-densiflorae* in *Pinus* spp.) to 67% [15-94] ('*Ca.* Liberibacter' spp. in *Citrus* spp.). This study provides evidence-based support for managing key plant pests across the EU.

OP21 Innovative e-probe detection of 11 viruses infecting tomato using e-probes Diagnostic Nucleic-acid Analysis and Microbe Finder (EDNA-MiFi)

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Electronic-probes (e-probes) were developed with the bioinformatic pipeline EDNA-MiFi® for screening of High-Throughput Sequencing (HTS) outputs to detect 11 tomato-infecting viruses, *Orthotospovirus arachinecrosis* (GBNV), *Carlavirus pisi* (PeSV), *Potexvirus pepini* (PepMV), *Potyvirus nicotianainsculpentis* (TEV), *Nepovirus nigranuli* (TBRV), *Tobamovirus fructirugosum* (ToBRFV), *Blunervirus solani* (ToFBV), *Ipomovirus lycopersici* (TMMoV), *Ilarvirus TomNSV*, *Nepovirus lycopersici* (TomRSV), and *Torradovirus marchitezum* (ToMarV), of economic significance worldwide. EDNA constitutes the basis of the MiFi® platform. It includes MiProbe, for generating e-probes, and MiDetect, to detect and identify viruses in metagenomic datasets. A large-scale multiple parallel genome alignment of all targeted virus sequences and close neighbors was made using MiProbe, and four sets of raw e-probes of different lengths (30, 40, 60, and 80 nucleotides) were generated for each virus. The e-probe sets were curated, removing non-specific hits at species level, and the theoretical limit of detection (LoD) was estimated *in silico* simulating serially diluted virus-infected datasets of high-throughput sequencing (HTS) samples. The LoD varied among virus species from 8 to 1030 pathogen reads. A tandem of e-probes was used to generate a synthetic artificial positive control that was serially diluted (1 ng to 1 fg). E-probe detection with different e-value parameters and numbers of hits is consistent for all e-probe sets except for TomRSV. Viruses ToBRFV, PepMV, and ToFBV were detected by EDNA-MiFi® in two HTS metagenomes from tomato collected in Italy. RT-PCR confirmed these findings. E-probe screening of datasets enables sensitive and time-saving virus detection, an alternative to *de novo* assembly and reference genome mapping.

POSTER SESSION II

Poster list from 61 to 120

61. **Resistance mechanisms in wild potato relatives against *Botrytis cinerea* and *Phytophthora infestans***
F. Di Virgilio, G. Coppola, G. Ianiri, T. Docimo, D. Carputo, D. Palmieri, R. Castoria, G. Lima, V. D'Amelia, F. De Curtis

62. **Uncovering a novel *Pseudomonas* from the tomato endosphere with dual lifestyle traits**
G. Dimaria, M. E. Massimino, D. Nicotra, P. Bella, V. Catara

63. **Phytophthora pathogens, their presence and impact in public gardens**
F. Drizou, D. Frederickson Matika, S. Green

64. ***Trichoderma harzianum* for sustainable agriculture: metabolic versatility, biocontrol potential, and plant growth promotion**
A. Esposito, N. Vassilev, M. Aragona, R. Fiorani, A. Polito, L. Canfora, S. Mocali, V. Scala

65. **Development of an extraction protocol and untargeted UHPLC-HRMS Orbitrap method for uncovering the polar metabolome of olive xylem tissue**
F.L. Ferrante, L. Lascala, F. Colais, M. Reverberi, V. Scala

66. **Assessing cross-kingdom pathogenicity of *Fusarium verticillioides* isolates from human infections and maize plants.**
M. Ferrara, F. Antonelli, G. Simonetti, M. Reverberi, L. Faino

67. **Thermotolerant *Trichoderma* Strains as Potential Biocontrol Agents Against *Rhizoctonia solani***
A. Ferrentino, M. Ruggiero, D. Lotito, A. Staropoli, G. Iacomino, F. Vinale, M. Lorito

68. **The system analysis for Bull's Eye Rot in apple production**
A. Francavilla, A. di Francesco, P. Battilani, M. Camardo Leggieri

69. **Are Tiny Forests® a Potential Boost for Soil Suppressiveness or Threats for pathogens emergence?**
S. Frasca, G. Gramegna, M. Beccaccioli, L. Faino, V.C. Cuccaro, V.E. Cambria, M. De Sanctis, M. Reverberi

70. **Unveiling the Role of *Stemphylium vesicarium* Extracellular Vesicles in Pear Brown Spot Disease**
TQ. Gao, XQ. Chen, M. Karas, EG. Kabeto, F. Pacini, F. Pizzuti, C. Ratti, E. Baraldi

71. **Efficacy of soil storage protocols for long term preservation of bacterial and fungal communities associated with crop plants**
M. Garello, F. Sbarra, F. Aloi, F. Sevi, E. Colantoni, B. Aracri, S. Tabacchioni, A. Visca, G.C. Varese, A. Bevivino, D. Spadaro

72. **Disruption of RPP13-like Impairs β-Ionone-Induced Priming in Tomato**
S. Gargiulo, D. D'Esposito, F. Palomba, M. Cangemi, G. Schiavone, V. D'Amelia, A. Facchiano, D. Giordano, F. Loreto, M. Ruocco, M. M. Monti

73. ***Fusarium incarnatum-equiseti* species complex occurring on durum wheat in Southern Italy**
A. Gatto, P. Anelli, V. Balmas, D. Carella, G. Cozzi, M. Haidukowski, M. Masiello, S. Oufensou, G. Porqueddu, S. Somma, Q. Migheli, A. Susca, A. Moretti

74. **Feruloyl-amides as natural antimicrobials for crop and food protection**
S. Ghosh, D. Dozio, D. A. Consolini, J. L. Ermini Starna, L. Pinto, F. Baruzzi, M. L. Contente, A. Pinto, P. Cortesi, S. Princiotto, A. Kunova, S. Dallavalle

75. **P75 Fast-tracking *Citrus* health: a portable molecular platform for *Plenodomus tracheiphilus* monitoring**
A. Giovino, I. Granata, M. Airò, C. Mandalà

76. **Probabilistic modelling provides clues to draft management guidelines for the conservation of *Fraxinus excelsior* threatened by *Hymenoscyphus fraxineus***
M. Giraudo, G. Lione, D. Giunta, S. Prencipe, A. Ebone, P.G. Terzuolo, L. Zarantonello, P. Gonthier

77. **Plant performance and metabolomic profile of wheat in response to seed application of *Trichoderma atroviride***
G. Golzi, V. Cirino, S. Sarrocco

78. **Preliminary study on the presence of *Biscogniauxia nummularia* in beech seeds of selected Italian populations**
G. P. S. Graham, H. Berto, F. Pecori, A. L. Pepori, B. Mariotti, A. Santini, A.M. Vettraino, L. Ghelardini, N. Luchi

79. **Exploring the mode of action of Tramesan from *Trametes versicolor* as a plant defense inducer in *Arabidopsis thaliana***
G. Gramegna, E. Romanelli, M. Beccaccioli, V. Cecchetti, M. Reverberi

80. **The role of soil physicochemical properties and related in-field sensors in mycotoxin model development: a review**
E. Granata, M. Camardo Leggieri, D. Trinchero, P. Battilani

81. **Raising public awareness on plant protection: the role of the Plant Pathology Diagnostics Laboratory**
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P61 Resistance mechanisms in wild potato relatives against *Botrytis cinerea* and *Phytophthora infestans*

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The search for the increase of potato resistance to diseases to reduce the massive use of agrochemicals is a very active field of research. The objective of our research is to carry out a multidisciplinary approach to investigate the different levels of tolerance/resistance of wild potato germplasm to fungal pathogen attacks. To this aim, we artificially infected potato leaves with *Botrytis cinerea* or *Phytophthora infestans*. Then, we assessed the level of sensitivity in different wild *Solanum* tuber-bearing species in comparison with *Solanum tuberosum* cv "Desirée" and "Blue Star" by investigating the influence of pathogens inoculation on metabolome and transcriptome in these plants. Wild potato accessions showed a more pronounced biochemical response to *B. cinerea* as compared to cultivated potato, and qPCR analysis revealed a reduced fungal growth on wild potato species. As to *P. infestans*, some of the tested accessions, such as *Solanum bulbocastanum* and *S. hougasii*, showed hypersensitivity responses, while in other ones, such as *S. commersonii* and *S. fendeleri*, we observed delayed and less severe symptoms as compared to cultivated potato. In conclusion, we identified phenotypic differences among wild potato accessions inoculated with pathogens with two different lifestyles, necrotrophic and hemibiotrophic. Ongoing metabolomic and pan-transcriptomic analyses will provide further insights into the molecular mechanisms underlying these differential responses.

P62 Uncovering a novel *Pseudomonas* from the tomato endosphere with dual lifestyle traits

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Bacteria of the genus *Pseudomonas* colonize a wide range of habitats, assuming roles spanning from pathogenicity to plant growth promotion. During a greenhouse survey, tomato plants (*Solanum lycopersicum*) exhibiting symptoms of wilting, leaf chlorosis, and xylem and parenchymatic discoloration of the stem were observed. On nutrient-dextrose agar, bacteria were isolated whose colonies exhibited undulate margins, a wrinkled surface and the production of a peculiar diffusible black pigment. Similar bacterial colonies were obtained from the farm soil. All isolates were fluorescent on King's medium B, indicating their affiliation to the genus *Pseudomonas sensu stricto*. Pathogenicity tests by prick-inoculation in tomato plantlets revealed the isolates' ability to induce stem pith and xylem discoloration, the symptoms observed in the field. When inoculated into the rhizosphere, the same isolates colonized the entire plantlet endophytically but without inducing symptoms, suggesting functional versatility within the plant microbiome. The 16S rRNA and *rpoD* genes sequence analysis placed the isolates within the *P. fluorescens* species complex, in the *P. corrugata* subgroup. Comparative genomics of one strain indicated taxonomic proximity to *P. zanjanensis*, although digital DNA–DNA hybridization and average nucleotide identity values suggested its belonging to a novel species. AntiSMASH analysis revealed the presence of a so-called pathogenicity island designed LPQ, harboring homoserine lactone quorum-sensing (QS) system genes; in addition, the biosynthetic gene clusters for two families (Mycin and Peptin) of cyclic lipopeptides, known phytotoxic and antimicrobial compounds, were predicted. The potential biological activities of these strains and QS-mediated interactions with other *P. corrugata* subgroup members were investigated.

P63 Phytophthora pathogens, their presence and impact in public gardens

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Phytophthora pathogens are known to cause significant diseases in agriculture and natural ecosystems, however little is known about their prevalence in public gardens. Considering that public gardens attract millions of visitors for their unique and rare plant collections and outstanding plant displays and, that to fulfil these demands, the gardens procure huge numbers of variable plant genera, receive plant donations from collectors and exchange plant specimens with other gardens, the risk of introducing and spreading Phytophthora diseases is potentially high. The aim of the present study, which was part of the Euphresco Phyto-gard Project, was to identify the prevalent *Phytophthora* spp. in UK public gardens, the possible associations between *Phytophthora* spp. and hosts as well as the impact of biosecurity practices on managing the pathogens. Soil, plant and water samples were collected from gardens and their nurseries. Their analysis consisted of DNA extraction and nested PCR (Scibetta et al, 2011) to verify the presence (or absence) of *Phytophthora* DNA. All *Phytophthora*-positive samples were processed using an established metabarcoding approach involving Illumina sequencing (Green et al. 2021). More than 60% of the samples were positive, with the majority being *Phytophthora* sequences, suggesting that *Phytophthora* species are widespread in garden enviroments. Additionally, significant differences were detected between oomycete abundance and the type of sample, as well as the host genera. Finally, having biosecurity facilities *per se* is not sufficient to eliminate *Phytophthora* spread and needs to be combined with improvements in overall garden management practices and stakeholder and public awareness.

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P64 *Trichoderma harzianum* for sustainable agriculture: metabolic versatility, biocontrol potential, and plant growth promotion

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Trichoderma harzianum are well known for their biocontrol capabilities. In addition to protecting crops, it stimulates plant development and increases their resistance to abiotic stress, underscoring an effective plant growth promoting fungi (PGPF). Among abiotic stress, salt stress is a limiting crop development and yield. This study aimed to assess the multifunctional potential of *T. harzianum* and explore strategies to optimize its growth by: i) evaluating its in vitro antagonistic activity against three common tomato phytopathogens; ii) assessing the effect of different concentrations of gazpacho soup in the culture medium on fungal growth, phosphate solubilization, and salt tolerance; and iii) analyzing its impact on morphological parameters and rhizosphere microbiome composition in tomato plants subjected to 100 mM NaCl in a pot experiment. *In vitro* assays showed that *T. harzianum* effectively inhibited over 70% of pathogen mycelial growth, confirming strong antagonistic activity. Gazpacho supplementation significantly enhanced fungal biomass production and improved the solubilization of rock phosphate (RP), identifying it as a promising, low-cost substrate for inoculum production. Furthermore, the combination of NaCl and gazpacho stimulated fungal sporulation, highlighting *T. harzianum*'s adaptability to stress. In pot experiment, *T. harzianum* inoculation improved tomato plant height and leaf number under both normal and salt stress conditions. Additionally, it influenced the rhizosphere microbiome by increasing microbial diversity. These findings demonstrate *T. harzianum* metabolic versatility and underline its potential as a sustainable biocontrol and plant growth-promoting agent, especially under saline conditions.

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P65 Development of an extraction protocol and untargeted UHPLC-HRMS Orbitrap method for uncovering the polar metabolome of olive xylem tissue

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Xylella fastidiosa subsp. pauca (Xfp) is a xylem-limited phytopathogenic bacterium implicated in Olive Quick Decline Syndrome, which has severely affected olive orchards in Apulia (southern Italy) over the past decade. The significant economic and ecological consequences of this disease, along with the absence of effective treatments, highlight the need for in-depth investigation of the molecular and biochemical bases of host-pathogen interaction mechanisms, to develop containment strategies. While most metabolomic studies on the Xfp-olive pathosystem have focused on leaves, metabolic changes within the xylem vessels, the primary site of bacterial colonization, remain largely unexplored during disease progression. In this study, we tried different extraction protocols suitable for olive woody tissue, coupled with an untargeted UHPLC-HRMS Orbitrap metabolomics approach to directly characterize the metabolome within xylem vessels. For method development, different experimental parameters were assessed, including sample matrix selection, pretreatment and storage conditions, and extraction solvent choice. The resulting data were initially assessed qualitatively for extraction efficiency, repeatability, and chromatographic quality. Subsequently, univariate and multivariate statistical analyses were performed using Compound Discoverer™ (Thermo Scientific™) and MetaboAnalyst software to compare experimental conditions, enabling the identification of optimal parameters for the extraction protocol. Overall, this study provides a method for metabolomic analysis suitable for investigating molecular interactions occurring directly within the xylem vessels, offering new insights into the pathogenesis of Xfp in olive trees and supporting future efforts to control this devastating disease.

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P66 Assessing cross-kingdom pathogenicity of *Fusarium verticillioides* isolates from human infections and maize plants.

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Fusarium verticillioides is a major fungal pathogen of maize and an opportunistic agent of human infections. In this study, we investigated its cross-kingdom pathogenic potential by analyzing 38 isolates derived from both clinical cases and infected maize plants. Field infections were performed on maize, and disease symptoms were quantified. In parallel, survival assays were conducted in the invertebrate model *Galleria mellonella* through larval injection, and mortality was monitored over time. To further explore potential virulence-associated traits, we measured in vitro biofilm production for all isolates. Our results show significant differences in virulence among isolates in both plant and animal models, with some strains causing more severe disease outcomes. Moreover, biofilm assays revealed variability in biofilm-forming ability among isolates, independent of their origin (clinical or plant). This trait is particularly relevant in clinical settings, as it may facilitate persistence on hospital surfaces, increase the risk of transmission, and contribute to antifungal resistance. These findings provide preliminary evidence that clinical *F. verticillioides* isolates are capable of infecting both animal and plant hosts. This suggests the presence of common virulence factors that are not specific to a single host. Nonetheless, the virulence variability observed among strains suggests that fungal effectors and genome plasticity play a role in adapting to different environments and enabling cross-kingdom infections. Moreover, this study demonstrates the usefulness of *G. mellonella* as a model for virulence assessment in fungal pathogens and supports its integration into comparative pathogenicity studies involving plant and human fungal isolates.

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P67 Thermotolerant *Trichoderma* Strains as Potential Biocontrol Agents Against *Rhizoctonia solani*

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The widespread use of synthetic plant protection products in agriculture presents significant risks to human health, biodiversity, and environment. The application of beneficial microbe-based formulations offers a promising, sustainable alternative to chemicals, promoting both crop production and soil quality. *Trichoderma* species are highly effective biological control agents, known for their ability to enhance plant growth, improve nutrient uptake, and induce disease resistance. This study evaluated the growth and spore production of several *Trichoderma* isolates, under high-temperature stress conditions (28 - 34 °C). Observations recorded during *in vitro* thermal stress assays, measuring radial growth and spore production, led to the selection of five strains: *Trichoderma harzianum* TT1 and TT2, *T. asperellum* TT3 and TT4, and *T. asperelloides* TT5. These strains were also tested for their antagonism against *Rhizoctonia solani*, isolated from naturally infected tomato seedlings, at 34 °C. Results of dual culture assays showed 100% inhibition of the plant pathogen after 24 hours of incubation with TT2; however, after 72 hours, the inhibition percentage decreased to 27%. Conversely, TT1 showed lower inhibition at 24 hours (67%) but higher activity at 72 hours (53%). These two selected strains also demonstrated significant overgrowth after 96 hours of interaction. These findings indicate that, despite adverse conditions, *Trichoderma* strains TT1 and TT2 retain substantial inhibitory activity against *R. solani*, highlighting their potential application as biocontrol agents in agricultural environments affected by climatic stress. Overall, the results support the use of *Trichoderma* spp. as a sustainable biocontrol strategy, even under suboptimal agroecological conditions.

P68 The system analysis for Bull's Eye Rot in apple production

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Apple (*Malus domestica*) is a fruit crop with a significant economic importance, highly regarded by consumers and prevalently cultivated in the Northern Italy. Long-term storage of the fruits is a common practice, but it can lead to significant economic losses due to biotic and abiotic diseases. Exposure to these diseases frequently occurs in the pre-harvest phase, even if major symptoms can occur in postharvest. This is also confirmed for Bull's Eye Rot (BER), an important postharvest disease, caused by *Neofabrea vagabunda*. Among several actions to lower the disease impact, predict fungal infection could be an important goal for disease management. To reach this objective, comprehensive understanding of the pathosystem is necessary. Extensive literature research was carried out to gather all the qualitative and quantitative data available for each step of fungal infection cycle. Through system analysis, the prototype relational diagram of *N. vagabunda* was drawn and the link with crop growth stages, from the petal fall to the harvest, considered. Meteorological data regarding precipitation, relative humidity, and temperature were included as input variables, both for fungal infection cycle and apple growth stages. All data collected will contribute to develop proper functions and build a mechanistic predictive model whose output will be the *N. vagabunda* infection risk along the apple value chain.

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P69 Are Tiny Forests® a Potential Boost for Soil Suppressiveness or Threats for pathogens emergence?

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Urban afforestation is increasingly promoted as a nature-based solution to restore degraded ecosystems and enhance urban environmental quality. Soil microorganisms provide essential ecosystem services by regulating nutrient cycling, organic matter decomposition, and soil organic carbon dynamics. Nonetheless, the effects of afforestation on soil microbial communities remain underexplored, although their integration with well-established ecological indicators is critical for assessing restoration effectiveness. Shifts in soil microbial composition may trigger soil suppressiveness or facilitate the emergence and spread of pathogens, potentially enhancing or compromising the long-term conservation status of newly established forests. Moreover, these afforestation sites can act as *refugium* for alien pathogens also considering climate change dynamics in urban and peri-urban contexts. This study assessed bacterial and fungal community dynamics within the SMART-TINY project at two Tiny Forest® sites in Rome: La Mistica and Divino Amore. Each plot (10 × 20 m) was planted with native trees and shrubs and subdivided into fertilized and unfertilized subplots (10 × 10 m), to test the effects of management practices on soil microbiota. Soil samples were collected from each subplot and adjacent non-reforested control areas. We employed 16S and ITS DNA metabarcoding using Nanopore sequencing, along with functional group annotation, to explore the taxonomic and functional diversity of bacterial and fungal communities, focusing on putative beneficial (biocontrol agents) and pathogenic taxa. Results provided a baseline of soil microbial communities during the first year after planting, highlighting potential differences among sample types. Our findings underscored the importance of integrating soil microbial descriptors into afforestation monitoring to implement sustainable and pathogen-aware restoration strategies in urban settings.

P70 Unveiling the Role of *Stemphylium vesicarium* Extracellular Vesicles in Pear Brown Spot Disease

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Pear cultivation holds substantial economic importance in Italy, especially in the Emilia-Romagna region, which has recently suffered a dramatic decline in production due to the devastating impact of brown spot disease caused by the fungal pathogen *Stemphylium vesicarium* (Sv). While significant efforts have been made to understand the pathogenicity of Sv, a new frontier in plant–pathogen interactions is emerging from the study of the extracellular vesicles (EVs) traffic between plants and pathogens. These secreted membrane-bound structures have been shown to play crucial roles in intercellular communication, defense modulation, and virulence factor delivery. Despite their relevance, little is known about the EVs secreted by Sv, particularly in the context of its infection on pear. In this study, we aim to explore the functional roles of Sv-derived EVs, with the aim of uncovering how they might contribute to host colonization and disease progression. We employed a multifaceted approach: identifying candidate EV marker proteins, assessing expression patterns of EV-related genes under different conditions (in vitro and in planta), and isolating Sv-specific EVs from infected pear tissues using immunocapture-based techniques. This investigation outlines our experimental strategy and shares early findings that shed light on the role of Sv-derived extracellular vesicles in pear infection.

P71 Efficacy of soil storage protocols for long term preservation of bacterial and fungal communities associated with crop plants

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In recent years, soils associated with different crops have been studied as a source of fungal and bacterial isolated with interesting growth promotion and biocontrol properties. As such, a great interest has emerged for developing and validating techniques for long term storage of these communities. In the present work, soils were collected from grapevine, kiwifruit and strawberry fields and they were stored at 4°C, at 4°C after freeze-drying, and at -80°C for up to 12 months. Integrity of microbial communities was assessed at harvest, after 6 months of storage and after 12 months of storage using vitality assays (CFU number), metagenomics (metabarcoding) and metabolomics (BIOLOG). The results of these analyses indicated significant differences among the considered soils in their response to the three storage protocols. Original vitality was retained in all matrixes for bacteria stored at -80°C, while for fungi this was observed only in one of the considered matrixes, both at 4°C and -80°C. Composition over time shifted in all matrixes, although storage at -80°C proved to be the most conservative for both fungi and bacteria in two out of three matrixes. For the metabolic component, storage at 4°C and -80°C showed less differences compared to initial sampling time in two out of three matrixes. For all approaches, freeze-drying resulted in severe community degradation. In conclusion, no storage protocol by itself could thoroughly preserve the composition of the whole microbial community, although storage at -80°C proved to be the most effective for the bacterial communities.

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P72 Disruption of RPP13-like Impairs β-Ionone-Induced Priming in Tomato

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RPP13-like is a protein, not yet functionally characterized, belonging to the R-protein class, which includes transmembrane pattern recognition receptors. *In silico* analysis identified it as a potential Volatile Organic Compound (VOC)-binding protein. To investigate the molecular mechanisms underlying plant VOC perception, gene-edited tomato plants (cv. Micro-Tom) were generated using CRISPR-Cas9 to knock out the *RPP13-like* gene. β-ionone is a natural plant volatile derived from β-carotene, known for its role in plant communication and defense as a signaling molecule, triggering defense responses (priming). *In silico* protein-docking modeling suggested β-ionone as a potential ligand for the RPP13-like protein. A priming experiment was conducted using T1 progeny of biallelic mutants. Both mutant and wilde -type (WT) plants were exposed to β-ionone under controlled conditions, followed by inoculation with *Botrytis cinerea*. Physiological parameters appeared unaffected in non-challenged plants. However, VOC emissions, measured using real-time PTR-TOF-MS, showed both qualitative and quantitative differences among treatments. Following *B. cinerea* infection, primed WT tomato plants showed the least floral damage, whereas primed mutant plants exhibited responses comparable to those of non-primed WT plants. Transcriptomic analyses supported these phenotypic observations, revealing a strong upregulation of defense-related genes in primed WT plants under stress conditions. In contrast, the same genes were not significantly upregulated in primed mutant plants, suggesting that priming enhances stress responses exclusively in the WT genotype. The RPP13-like gene mutation appeared to impair the plant ability to respond to β-ionone as priming agent.

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P73 *Fusarium incarnatum-equiseti* species complex occurring on durum wheat in Southern Italy

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A survey of fungal diversity associated with *Fusarium* crown rot of durum wheat in Southern Italy led to isolation of multiple *Fusarium* species. Strains belonging to the *Fusarium incarnatum-equiseti* species complex (FIESC) were the second most frequently isolated group. The FIESC comprises over 30 phylogenetic species, most of which are cryptic and lack formal Latin names, making identification challenging. If FIESC strains are indeed pathogenic, their high frequency should be considered in field disease management and when evaluating mycotoxin contamination risks. Pathogenicity tests performed with 29 isolates showed a variable level of virulence (disease severity index range 0÷38%, on a 0-100 scale), with 13.4% average. Using single-gene phylogeny based on translation elongation factor 1-alpha, we identified 74 *Fusarium* strains belonging to 7 FIESC species. Based on phylogenetic analyses, strains have been shown to belong to *F. clavum* (63), *F. flagelliforme* (1), *F. croceum* (1), *F. guilinense* (1), *F. coffeatum* (3), *F. tanahbumbuense* (3) and the recently described *Fusarium mariecurieae* (2), here reported in Italy for the first time. To investigate the potential of *F. mariecurieae* to produce trichothecenes, a primer pair, targeting conserved regions of the TRI1 gene, was designed. An amplification fragment was obtained, and homologous sequences were assessed for the 2 isolates. Since the trichothecene cluster is reported in various FIESC members, and variation in the TRI gene cluster content can influence trichothecene analogue production, additional studies are necessary to confirm whether *F. mariecurieae* produces trichothecenes or other mycotoxins, and to evaluate its impact on food safety.

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P74 Feruloyl-amides as natural antimicrobials for crop and food protection

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Pyricularia oryzae is a major biotic threat constraining rice production worldwide. The increasing concern over the environmental impact of fungicide resistance spread in pathogens, and growing demand for sustainable crop protection and food safety solutions is driving interest in plant-derived bioactive compounds. Such natural and naturally derived compounds represent promising tools for integrated fungal disease management in crops. Phenylamides (PAs), naturally occurring in many plants including rice, are known for their involvement in plant defense. A set of ferulic acid-derived PAs was synthesized via chemical and chemoenzymatic approaches to evaluate their antifungal potential against *Pyricularia oryzae*, other key phytopathogens: *Botrytis cinerea* , *Fusarium culmorum*. Antifungal activity was assessed through inhibition of mycelial growth, spore germination, and, in the case of *P. oryzae*, appressorium formation—a critical structure for host penetration and disease establishment. A striking inhibitory effect on *P. oryzae* appressorium formation was observed for specific PAs; some significantly reduced appressorium development by up to 94% without affecting spore germination, suggesting a targeted disruption of virulence mechanisms rather than general antifungal toxicity. Structure-activity relationships indicated that the presence of hydroxyl- and guanidine- groups enhanced efficacy. Overall, the synthesized compounds showed modest effects on mycelial growth, with inhibition rates up to 25% in *F. culmorum*. Spore germination in *B. cinerea* and mycelial growth in *P. oryzae* was largely unaffected, indicating that these compounds do not interfere with early fungal development. These findings suggest that phenylamides may act by impairing fungal infection processes than inhibiting vegetative growth, offering a novel mechanism for disease control.

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P75 Fast-tracking *Citrus* health: a portable molecular platform for *Plenodomus tracheiphilus* monitoring

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“Mal secco”, caused by the vascular fungus *Plenodomus tracheiphilus*, is a severe disease leading to progressive shoot dieback and threatening the production of many *Citrus* species worldwide, especially in the Mediterranean basin. Therefore, detecting the disease in its early stages is crucial to prevent widespread epidemics and enable effective control strategies. This study assessed the suitability of portable molecular diagnostic tools for rapid and reliable detection of the pathogen in lemon leaves and twigs samples (var. Femminello Santa Teresa, Zagara Bianca, and Femminello Comune). Two DNA extraction protocols were compared: i) a traditional CTAB method and ii) an automated extraction using the Auto-Pure Mini system (Allsheng), followed by duplex qPCR analysis performed with the portable bCUBE™ device (Hyris Ltd.). Results showed that the CTAB method performed better than the Auto-Pure Mini extraction system. The qPCR assays, carried out directly with the bCUBE™ device, confirmed the presence of *P. tracheiphilus* even in asymptomatic samples, showing higher pathogen concentrations (lower Cq values) in twigs than in leaves. These findings highlight the promising role of portable molecular tools as valuable solutions for large-scale early disease screening, particularly in contexts lacking fully equipped diagnostic laboratories. Moreover, their adoption could support regular monitoring and enable timely phytosanitary control measures against “mal secco”, ultimately helping to safeguard *Citrus* production and promote more sustainable disease management in Mediterranean orchards.

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P76 Probabilistic modelling provides clues to draft management guidelines for the conservation of *Fraxinus excelsior* threatened by *Hymenoscyphus fraxineus*

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Ash dieback caused by the fungal pathogen *Hymenoscyphus fraxineus* is the most detrimental disease affecting *Fraxinus excelsior*, a forest tree species providing key ecosystem services. Because of the high mortality rates associated with dieback, *F. excelsior* is an endangered species in Europe. The goal of this study was modelling the probability of infection by *H. fraxineus* based on biometric, silvicultural and environmental variables to unravel which factors could trigger the onset of ash dieback. In 2023-2024, 30 sites in Northwestern Italy were monitored to assess the impact of *H. fraxineus*. Up to 20 trees per site were inspected and sampled. The presence and incidence of *H. fraxineus* were assessed through a species-specific qPCR diagnostic assay. Probabilistic risk models were built based on unbiased recursive partitioning, random forests algorithms and logistic regressions. Results showed that *H. fraxineus* was present in 85% of the sites, with an average incidence of 61%. Approximately 11% of ashes were potentially tolerant to *H. fraxineus* since they were infected, yet almost completely asymptomatic, despite their vicinity to visibly symptomatic trees. Models showed that the probability of infection raised significantly ($P<0.05$) with increasing stem diameter, tree height and canopy density, especially in high forest stands hosting tree species requiring abundant precipitation levels in colder and wetter stand locations. Assessing the risk of infection based on the above probabilistic models allowed for the design of management strategies targeting the conservation of ash. Management options include decreasing the stand density trough felling and releasing potentially tolerant ash trees.

P77 Plant performance and metabolomic profile of wheat in response to seed application of *Trichoderma atroviride*

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The growing demand for sustainable alternatives to pesticides and fertilizers - whose intensive use has contributed to environmental pollution and biodiversity loss - is driving continuous research into new biofungicides and biostimulants. Among these, fungi of the genus *Trichoderma* are widely studied and used for their beneficial effects including plant growth promotion, stress tolerance, and activation of defence mechanisms. This study evaluated the effects of a new *Trichoderma*-based product under development by the Spanish company Atens as wheat seed coating, focusing on its impact on wheat growth, metabolism and modulation of defence-related genes. Spores of *T. atroviride* were applied to wheat seeds alone or with different adhesives aiming to identify the best co-formulant that facilitates spore application without impairing fungal performance. Plant parameters - such as germination rate, root elongation, fresh and dry biomass – along with the metabolic profile (by LC-MS) were analysed. In addition, *T. atroviride* was tested for its ability to endophytically colonize wheat roots, to modulate defence-related genes, and to exhibit antagonistic activity against *Fusarium graminearum*. When applied as seed coating, *T. atroviride* promoted wheat growth, modulated plant metabolisms, exhibited antifungal activity via volatile and soluble metabolites, and upregulated defence-related genes. However, two adhesives significantly reduced its effectiveness, suggesting that formulation components can critically influence its performance. These findings support the need for targeted optimization of adhesive–fungus combinations to improve bioformulation efficacy Further studies are required to better understand the impact of adhesives on *T. atroviride* performance and to optimize the formulation for improved efficacy.

P78 Preliminary study on the presence of *Biscogniauxia nummularia* in beech seeds of selected Italian populations

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Biscogniauxia nummularia (Bull.) Kuntze is a fungal endophyte in the Graphostromataceae family, known to be related to strip-canker disease in European beech (*Fagus sylvatica* L.). The pathogen's spread is linked to environmental stressors such as drought and rising temperatures, which alter host plant defense and predispose the tree to decline. The shift of the interaction with this fungus raises questions about beech resistance to climate change and the conservation and management of the species in the future. Since *B. nummularia* has long been considered a secondary pathogen with reduced impact, this fungus is poorly known, and has been neglected until the recent increase in economic, ecological and landscape damage in the Mediterranean region. This study aimed at investigating the possible vertical transmission of this endophyte in beech. For this purpose, approximately 100 seeds from three Italian provenances were analyzed by real time quantitative PCR for the presence of *B. nummularia* in the tegument, endosperm and embryo tissues. Initial analyses showed no pathogen presence in the seeds, despite successful amplification of control genes. Further assessments indicated that the detection of fungal DNA was not hindered by host DNA. Ultimately, larger-scale seed analyses also yielded negative results for pathogen detection, suggesting a limited potential for *B. nummularia* transmission through seeds in the studied populations. The study is being continued with tests on the presence of the fungus in seedlings.

P79 Exploring the mode of action of Tramesan from *Trametes versicolor* as a plant defense inducer in *Arabidopsis thaliana*

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Fungal pathogens significantly reduce crop yield and quality. The intensive use of pesticides to control them has led to resistant strains and poses risks to both the environment and human health. European Regulation 128/2009 has restricted many agrochemicals, encouraging the use of natural alternatives. In this context, Tramesan, an exopolysaccharide from the basidiomycete *Trametes versicolor*, is a promising biocontrol agent. In fact, it has been previously demonstrated that Tramesan, in addition to inhibits aflatoxin biosynthesis by mycotoxigenic fungi *Aspergillus flavus* and *A. parasiticus*, enhances the resistance of wheat against Septoria Leaf Blotch Complex by inducing plant defense responses. To better understand the mechanisms of this elicitation, we explored the mechanism of action of Tramesan in the model plant *Arabidopsis thaliana* challenged with the foliar pathogen *Botrytis cinerea*. Therefore, we evaluated both the direct antifungal effect of Tramesan as well as its ability to induce plant immune responses, such as induction of defense genes, H_2O_2 accumulation and hormones production. These analyses indicate that Tramesan has only a slight inhibitory effect on Botrytis growth while it can induce Arabidopsis defense responses to the fungus, probably acting as a priming agent. To attempt clarifying this peculiarity, we analyzed the hormonal pathways involved in the activation of immunity induced by Tramesan, studying its effect in Arabidopsis *jar1.1* and *nahG* seedlings, defective in JA and SA response respectively.

P80 The role of soil physicochemical properties and related in-field sensors in mycotoxin model development: a review

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In recent years, the development of models for mycotoxins and mycotoxigenic fungal populations has predominantly relied on meteorological data and crop physiology. However, the potential contribution of additional data sources, such as soil characteristics, remains largely unexplored. A literature search was carried out in major scientific databases (Scopus, Web of Science, and OVID), covering the period from 2000 to 2025, with a focus on soil properties – temperature, water content, pH, electrical conductivity –, fungal communities – *Aspergillus* and *Fusarium* genera in particular – and different crop species – peanut, wheat and maize. The state of the art regarding in-field soil sensors applied was also investigated. From 2421 papers found, 178 were ultimately retained, based on inclusion/exclusion criteria. The soil variables mentioned were all reported as relevant for fungal metabolism and interaction with the plant. Disease incidence and mycotoxin occurrence increased under stressful soil conditions, such as more alkaline or acidic pH, high soil moisture or drought depending on the considered fungus, and soil temperatures above 25°C. To measure those parameters, laboratory techniques and equipment were used, such as pH/EC meters or oven drying. A very limited use of wireless sensor emerged, with few exceptions for soil temperature and moisture. Overall, soil characteristics are important aspects to consider for host-crop interactions yet not exploited in modelling. Existing IoT technologies are still not considered to collect widespread and dense data. Therefore, the groundwork for guiding future research to address existing gaps and improve predictive models with soil data is fixed.

P81 Raising public awareness on plant protection: the role of the Plant Pathology Diagnostics Laboratory

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Plants are essential components of our ecosystem and, like all living organisms, they are susceptible to diseases caused by bacteria, fungi, viruses, phytoplasmas, insects, and nematodes. These diseases not only threaten plant health but also compromise food security, biodiversity, and environmental well-being. Plant protection deserves particular attention, especially in a context marked by climate change and globalization, which can favor the spread of pathogens.
A key aspect is raising awareness about regulated and emerging pests and the risks they pose. In this regard, the EPPO standards PM 3/94 and PM 3/86 provide fundamental guidelines for informing both the general public and professional stakeholders about the dangers associated with plant pests. These international standards emphasize the importance of educating people—from professional growers to consumers—on the threats posed by both emerging and regulated pests, whose spread can severely impact crop health and entire ecosystems. It is possible to educate farmers and citizens to recognize the symptoms of infection caused by harmful organisms, and to adopt appropriate containment and management strategies. Every small action in support of plant health contributes to the preservation of biodiversity and to the overall well-being of the environment and human populations. This contribution aims to present the activities and outreach strategies developed over the years by the Plant Pathology Diagnostics Laboratory of the Edmund Mach Foundation, with the goal of engaging and empowering various segments of the population on the topic of plant protection.

P82 *Colletotrichum* spp. on walnut fruits in Trentino: Preliminary Studies on a Pathogenic Complex

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Colletotrichum spp. is considered one of the ten most important phytopathogen worldwide, affecting a wide range of fruit crops ranking eighth in order of importance for its significant impact on agricultural and forestry production. To date, 17 species of *Colletotrichum* have been reported globally on walnut, with *C. godetiae* and *C. fioriniae* being the most frequently encountered. *Colletotrichum* spp., the agent of walnut anthracnose, can damage fruits, leaves and branches.
In recent years, walnut fruits (*Juglans regia* L.) cultivated in Trentino (Northern Italy) have shown increasing symptoms consistent with *Colletotrichum*-associated diseases. In Trentino, particularly in the Giudicarie Esteriori and especially in Bleggio, walnut cultivation has a long tradition. It represents a distinctive feature of the local landscape and an important element of the community's identity. It also represents a strategic sector for both Italian and global fruit growing. In 2024, as part of the CANOSSA project — funded by the UNESCO Man and the Biosphere Programme — different walnut tissues (leaves, wood, buds, litter and mummified fruits) and walnut fruits with anthracnose symptoms were collected from several production sites in Bleggio at different sampling periods. Several isolates of the genus *Colletotrichum* were obtained, revealing the pathogen's spread across different geographical areas and overwintering sites. This study aims to characterize the *Colletotrichum* species associated with walnut anthracnose in Trentino, tracing the evolution of the fungus over time and space. Its findings will be fundamental for understanding the infection mechanisms and the risk factors driving the development of the disease. The results obtained will help to clarify the species causing walnut anthracnose in these areas, providing a scientific basis for the diagnosis and development of effective management strategies to control walnut anthracnose.

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P83 Plant extracellular vesicles production using a plant-based biotechnological platform

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Plant Extracellular Vesicles (EVs) are a diverse group of cell-derived membranous structures secreted by plant into the extracellular environment. EVs carry a diverse array of bioactive compounds (biocargo), including proteins, lipids, nucleic acids (such as RNA and DNA), and metabolites, of fundamental importance in regulating plant-microbe interactions by facilitating cross-species communication. In this perspective, EVs are promising delivery systems for crop protection in sustainable agriculture and innovative therapeutic tools in various biomedical applications. Herein, we propose a combined strategy to set up a biotechnological platform to collect plant EVs from tomato plants subjected to biotic challenges orchestrated by beneficial/pathogenic fungi individually and in combination. For EVs collection during tomato-*Trichoderma* and tomato-*Trichoderma*-*Botrytis* interplay, we employed a split-root hydroponic floating system specifically designed to exclude the co-purification of fungal EVs. For plant-*Botrytis* interactions, samples were collected from distal leaves relative to the initial *B. cinerea* spore inoculation site. Vesicle round-shape morphology of both apoplastic and root EV was confirmed by transmission electron microscopy (TEM). Preliminary metabolomic analysis identified tomatine and tomatidineol as primary bioactive compounds, suggesting EVs' potential in plant defense, especially against fungal pathogens, by enabling targeted distribution of antimicrobial molecules. A detailed EV proteome and miRNA profiling is underway, and along with data integration analyses will decode the 'SecreEVome' molecular messaging in plant-biotic interactions, making them suitable for applications in plant defense.

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P84 Towards a unified framework for *Colletotrichum* identification and management: case studies from citrus in Southern and apple in Northern Italy

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Colletotrichum is one of the most important genera of phytopathogenic fungi worldwide, including species with different behaviour ranging from endophytes to pathogenic. In Italy, recent outbreaks of *Colletotrichum*-associated diseases have raised concerns, particularly in citrus orchards in Southern Italy and apple orchards in Northern regions. Several symptoms caused mainly by *C. gloeosporioides* sensu stricto and further species members of the Acutatum and Boninense complexes, have become an increasingly severe threat in Mediterranean citrus-growing areas, while bitter rot and Glomerella leaf spot are emerging diseases on apple, caused by *Colletotrichum* species of the Acutatum, Gloeosporioides, and Orchidearum complexes. Taxonomic advances based on multilocus phylogenetic analysis have revealed a high number of cryptic species within these complexes, highlighting the limitations of traditional identification methods. An updated overview of *Colletotrichum* species distribution in Italian citrus and apple orchards, based on surveys conducted over the last 15 years and compared with the internation scenario, is provided. In citrus, *C. gloeosporioides* and *C. karsti* are the dominant species, while in apple, *C. chrysophilum*, *C. fioriniae*, *C. siamense*, *C. sojae*, and *C. grossum* were identified, with *C. siamense* being particularly virulent. Current and future research aims to: (1) re-evaluate *Colletotrichum* isolates preserved in EU culture collections; (2) reallocate historical records to clarify host associations and species distributions; and (3) develop a robust, user-friendly diagnostic protocol for accurate species-level identification. This work will improve the understanding of the biogeography of *Colletotrichum* spp. and enhance disease management strategies.

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P85 Dual RNA-Seq Analysis Reveals Host–Pathogen Interplay in Lupin Anthracnose

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Colletotrichum lupini is a hemibiotrophic fungal pathogen responsible for anthracnose in *Lupinus* spp., an agriculturally important crop. However, the molecular interplay between fungal effectors and host immune receptors remains poorly understood. We re-analyzed previously published dual RNA-seq data of *Lupinus albus* infected with *C. lupini* across five timepoints (24, 48, 60, 72, and 84 hours post-inoculation [hpi]), as well as fungal samples grown in liquid culture as controls. Raw reads were processed using standard pipelines and aligned separately to host and pathogen genomes. Differential gene expression was assessed using DESeq2, comparing fungal samples to liquid culture controls and plant samples to the 24 hpi reference point. Upregulated genes were identified ($|\log_2 FC| > 1$, adjusted $p < 0.05$) for both the plant and fungus at each timepoint. Protein sequences of upregulated plant genes were annotated using InterProScan to predict domains associated with plant immunity. Candidate PTI and ETI receptors were classified based on domain architecture. Fungal DEGs were cross-referenced with a curated effector dataset filtered through secretion and effector prediction pipelines. Heatmaps of expression patterns revealed that most predicted fungal effectors were upregulated during both early and late infection stages, while expression of candidate host receptors intensified at later stages (72–84 hpi). Together, these results provide a foundational transcriptomic map of the *Lupinus*-*Colletotrichum* interaction. This resource lays the groundwork for future functional studies to elucidate effector–receptor interactions and support the development of anthracnose-resistant lupin cultivars.

P86 Evaluating Wood Vinegar's Chemical Properties and Biological Impact on Crops and Pests

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Industrial wood vinegar (WV), a liquid byproduct from woody pruning waste pyro-gasification, was thoroughly investigated for its chemical composition and diverse biological activities. Its composition was characterized using advanced analytical techniques, specifically liquid chromatography (LC) and gas chromatography-mass spectrometry (GC-MS). Analyses revealed an acidic pH of 3.2, along with high concentrations of acetic acid (27840.16 mg/L) and phenols (54.00 mg/L). WV's biological efficacy was evaluated across multiple agroecosystem components. Two-year field trials in an olive grove showed no significant repellent effect against the olive fruit fly, *Bactrocera oleae*, when undiluted WV was applied as an aerosol. In controlled greenhouse experiments, higher WV concentrations (5% and 10%) demonstrated pronounced phytotoxicity to strawberry plants, leading to a reduced total yield across plant organs. Conversely, a 1% WV application in a strawberry field infested with *Meloidogyne incognita* resulted in a significant 15% reduction in nematode infection and improved plant size. An in vitro seed root length bioassay on diverse plant species (*Eruca sativa, Lactuca sativa, Lens culinaris, Lolium multiflorum*, and *Solanum lycopersicum*) consistently confirmed a concentration-dependent dual effect: high concentrations exhibited marked phytotoxicity, while lower, diluted concentrations actively promoted root elongation, with an optimal biostimulant effect around 0.1%. These findings highlight WV's multifaceted bioactivity, suggesting its potential in plant disease management as a biocontrol agent against nematodes and as a plant biostimulant at precise dilutions. The study underscores the critical need for careful concentration optimization and tailored delivery systems for effective and sustainable agricultural application.

P87 Gaining a better understanding of *Colletotrichum* Species Associated with Apple Diseases in Italy through Integrated Omic Approach

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Apple Bitter Rot (ABR) and Glomerella Leaf Spot (GLS), caused by *Colletotrichum* species, represent an emerging threat to apple production in Northern Italy and globally. In recent years, the incidence of these diseases has increased, and previous studies have reported the emergence of *Colletotrichum* species that were previously absent or only rarely detected in Europe, particularly members of the Gloeosporioides and Orchidearum species complexes. Although the species diversity of *Colletotrichum* associated with apple in Italy has been described, our understanding of their pathogenicity boundaries, molecular mechanisms, and population dynamics remains limited. This study aims to gain deeper insight into these mechanisms by integrating comparative genomics, transcriptomics, and population genetics. To clarify the boundaries of pathogenicity within major *Colletotrichum* lineages and across specific apple tissues, we developed a novel inoculation protocol. Preliminary results have revealed notable correlations between genetic background and pathogenic behaviour, shedding light on the mechanisms of host penetration. Several genomes, including those of *C. chrysophilum* and related species such as *C. fructicola* and *C. nupharicola*, have been sequenced using a combination of Oxford Nanopore and Illumina technologies. This genomic dataset forms the foundation for comprehensive comparative genomics and transcriptomic analyses aimed at identifying and characterizing pathogenicity-related genes and their expression dynamics during infection. The outcomes of this ongoing research will provide valuable insights into the evolution and adaptation of *Colletotrichum* species on apple, informing future strategies for disease management and resistance breeding.

P88 Investigation on the genetic variability of *Xylella fastidiosa* subsp. *pauca* isolated from different geographical areas in Apulia.

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Since 2013, *Xylella fastidiosa* subsp. *pauca* (*Xfp*) has posed the most serious phytopathological threat to the Apulia region. Despite extensive efforts to contain its spread, the mechanisms governing host-pathogen interactions and genetic variability among *X. fastidiosa* strains remain poorly understood. This study aims to investigate the potential genetic variability among *Xfp* isolates collected from different areas of the region. Monitoring activities began in the summer of 2024 in the municipality of Alezio (Gallipoli), the site of the earliest official outbreak. Sampling followed a progressive transect approach, starting in the heavily infected Salento Peninsula and extending northward across Apulia at 10-kilometer intervals, reaching areas near Bari.
Over 100 samples were collected and analysed using a qPCR assay for molecular detection and quantification of *Xfp*. To identify the bacterium, one-year-old twigs were collected near symptomatic areas of the crown. Preliminary results led to the isolation of 30 *Xfp* strains.
Research will continue with genome sequencing of each bacterial isolate obtained from different geographic areas in Apulia to understand phylogenetic relationships and genes involved in pathogenicity and virulence in plant-pathogen interactions.

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P89 Exploring antibacterial capacity of different bacterial and fungal strains against *Xylella fastidiosa* complex

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Xylella fastidiosa (*Xf*) is a xylem-inhabiting plant pathogenic bacterium classified as a quarantine organism in Europe. It infects nearly 700 plant species across 88 families, acting either as a pathogen or an endophyte, and poses a major threat to Mediterranean agriculture. In the Apulia region of Italy three subspecies - *X. fastidiosa* subsp. *pauca* (Xfp), *multiplex* (Xfm), and *fastidiosa* (Xff) - severely affects olive, almond and grapevine crop, in the order. The lack of effective curative treatments, along with the pathogen's complex epidemiology, are critical challenges for its control. This study aimed to identify antagonistic microorganisms with potential to be biocontrol agents against *X. fastidiosa* complex. *In vitro* dual culture assays showed that 9 out of 51 bacterial isolates, belonging to the genera *Pantoea*, *Bacillus*, and *Pseudomonas*, were able to inhibit *Xfp* growth, forming clear inhibition zones ranging from 2.0 to 12 mm. Additionally, the antimicrobial activity of the culture filtrates of *Aphanocladium album*, *Clonostachys rosea*, *Trichoderma atroviride*, and *Trichoderma koningiopsis* and of a bacterial lysate obtained from *Bacillus amyloliquefaciens* strain D747, was assessed. Fungal filtrates inhibited all three subspecies, with inhibition areas ranging from 20 to 29 mm. The *Bacillus* lysate also showed strong antimicrobial activity in well diffusion assays, with halo sizes varying by subspecies. These results highlight the potential of selected microbial strains and their metabolites as components of sustainable biocontrol strategies for managing *X. fastidiosa* and other xylem-associated pathogens in key Mediterranean crops.

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P90 Use of a portable e-nose for the analysis of bread wheat kernel samples artificially infected with *Fusarium graminearum* and *Fusarium culmorum* and correlation with DON content.

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Volatile Organic Compounds (VOCs) emitted by several species of fungi are being utilized for the rapid detection of diseased samples. In this study, a portable e-nose (Smell Inspector, Smart Nanotubes Technologies GmbH, Germany) has been used to characterized wheat grain samples with DON levels ranging from 0 to >12000 ppm. Bread wheat genotypes were artificially inoculated with spores of *Fusarium graminearum* and *F. culmorum* isolates with a conidial suspension of 2×10^4 conidia mL^{-1}. at two flowering stages (25% and 75%). Artificial inoculation was performed based on flowering time to ensure that all genotypes were inoculated at two specific flowering stages: 25% and 75%. After harvesting, a total of 300 wheat samples were analyzed for DON content employing the RidaScreen® DON kit (R-Biopharm). After VOCs acquisition, the Smell Annotator was used to control, annotate and store measurements. For statistical analysis, a linear classification procedure (PLSDA) has been applied to the entire dataset: it has been divided into 2 classes (<1200 ppb and >1000 ppb) and divided into 80% for training/validation and 20% for testing. Results showed very high performances of classification either in training (89.2%) and in testing (95.5%), with Root Mean Square Error of Calibration value of 0.30184 and Root Mean Square Error of Cross-Validation of 0.33006). This data confirmed the usefulness of VOCs analysis for DON content evaluation, as already obtained using Proton Transfer Reaction Time-of-Flight Gas Chromatography Mass Spectrometry (PTR ToF).

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P91 Natural Inhibition of Aflatoxin B1 by *Pleurotus eryngii* culture filtrate and aqueous Extracts

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Aflatoxin B1, the most widespread and potent toxin, poses a serious global threat to human health. It is a powerful carcinogen produced by *Aspergillus flavus*, mainly during the storage of cereal grains. Finding biological alternatives to synthetic chemicals, which are often toxic and non-specific and are increasingly banned by governments, is therefore essential. Our results show that the mycelial culture filtrate (CF) of *Pleurotus eryngii* var. *ferulae* (PEF) reduced aflatoxin B1 production to just 5.43%, indicating an inhibition rate of approximately 94.5% at both 0.5% and 1% concentrations. In contrast, its aqueous extract (AE) showed no inhibitory effect on aflatoxin synthesis. For *Pleurotus eryngii* var. *elaeoselini* (PEEl), the mycelial filtrate reduced aflatoxin levels to 13.04% and 32.69%, corresponding to inhibition rates of 86.95% and 67.3% at concentrations of 0.5% and 1%, respectively. Its aqueous extract demonstrated an inhibition of 76% and 85%, respectively. Additionally, antioxidant activity tests showed that the PEEl variety had the strongest antioxidant potential, with IC_{50} values of 0.44 and 0.45 for the filtrate and IC_{50} values of 0.89 and 0.41 for the aqueous extract, respectively. NMR analysis showed that both AE and CF are a mixture of amino acids, organic acids, carbohydrates, alkaloids, flavonoids and other secondary metabolites. This study explores the effects of mycelial culture filtrates (CF) and aqueous extracts (AE) from two varieties of Tunisian *Pleurotus eryngii* on the growth and aflatoxin production of *Aspergillus flavus* providing valuable insight into their detoxification capacity.

This research was funded by the Ministry of Higher Education and Scientific Research and Plant, Soil and Environment Interactions Laboratory, Faculty of Sciences (Tunisia).

P92 A symptomatic caper plant revealed multiple viral infections involving old viruses and a new viral species

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In the autumn of 2019, a caper plant showing unusual symptoms consisting in chloro-necrotic veins was noticed in Catania (CT), south Italy. Virome analysis by High-Throughput Sequencing (HTS) of the RNA extracted from this symptomatic leaf sample revealed multiple infection involving cucumber mosaic virus (CMV), caper latent virus (CapLV) and a new badnavirus. The virus particles of these viruses were constantly observed together in leaf samples observed by electron microscope. Additionally, a sequence of new isolate of apple ourmia-like virus 1 was also identified, probably associate with an unidentified fungus. Near complete nucleotide sequence of RNA1 and RNA2 of a CMV isolate of the subgroup IB were *de novo* assembled, while only partial sequence of the RNA3 were obtained. Concerning CapLV, the near complete genome of three different isolates/variants were assembled. The percentage of nucleotide identity of the CP and of the replicase gene (RdRp) was always belove the 72% compared with caper carlavirus 1 and CapLV-W. Thus, following the ICTV rule concerning the specie demarcation criteria of the *Carlavirus* genus, these three viruses should be considered as CapLV isolates. The genome of the new putative species of *Badnavirus* consisted of 8103 nt showing the highest percentage of nucleotide identity (52%) with the genome of jujube associated badnavirus. This new *Badnavirus* species was tentatively named capparis spinosa badnavirus (CSpBV). Further investigations would be appropriate to verify the incidence of these mixed infections in caper, with special reference to the association and diffusion of the new species of badnavirus identified.

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P93 Preliminary Screening of Essential Oil-Based Nanoemulsions for the Control of Major Fungal Pathogens of Citrus

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Citrus is a key crop in Sicilian agriculture for its historical and economic value and fungal diseases represent a significant threat. Due to concerns over fungicide use, this study explores sustainable alternatives for managing the major fungal pathogens. Seven essential oil-based nano-emulsions (N-EOs) including clove, fennel, garlic, laurel, lavender, lemongrass and mint, were tested *in vitro* against three isolates of *Colletotrichum gloeosporioides*, *C. karstii* and *Neofusicoccum parvum.* The effect of the N-EOs was assessed through mycelial growth and conidial germination inhibition assays. IC_{50} and IC_{90} values were calculated for each N-EO–isolate combination by using non-linear regression models and implemented to categorize the treatment effectiveness as high ($IC_{50} \leq 0.7\%$ w/v; $IC_{90} \leq 1.95\%$ w/v), moderate ($0.8 < IC_{50} < 1.5\%$ w/v; $1.95 < IC_{90} < 2.5\%$ w/v) or low ($IC_{50} \geq 1.6\%$ w/v; $IC_{90} \geq 2.6\%$ w/v). According to these categories, garlic and clove showed significantly higher antifungal activity in both assays regardless the fungal species. Lavender was moderately to highly effective in both trials, while mint and lemongrass revealed moderate to high efficacy in mycelial inhibition but low in conidial germination. Laurel displayed moderate to high efficacy in mycelial growth assay against *N. parvum*, but high IC_{50} and IC_{90} against *Colletotrichum* spp. and in conidial germination assay for all species. Fennel was the least effective N-EOs across both trials, showing the highest IC_{50} and IC_{90} values. These findings support the potential of N-EOs for the integrated management of citrus pathogens, although further *in vivo* studies are needed to validate their efficacy under field conditions.

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P94 Valorizing Citrus Waste: A Fermented Bioformulation for Sustainable Control of Phytophthora Diseases

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Phytophthora species are responsible of severe plant diseases of numerous host plants. These pathogens pose a serious threat to economically important crops and the stability of natural ecosystems. More stringent regulations and concerns for human health and environment urge to seek alternative approaches to synthetic chemical fungicides for the management of Phytophthora diseases. This study evaluated a new bioformulation (bioact-LM) based on lemon peel powder fermented by a selected *Lactiplantibacillus plantarum* strain. In *in vitro* assays bioact-LM demonstrated a notable anti-oomycete activity. In agar-diffusion tests at concentration of 400.0 ± 0.1 mg/mL, mean diameter of inhibition halos exceeded 10 mm against several *Phytophthora* species, including *P.* ×*cambivora*, *P. cinnamomi*, *P. citrophthora*, *P. pseudosyringae* and *P. ramorum*. Values of minimal inhibitory concentrations (MIC) and minimal fungicidal concentration (MFC) for 11 diverse *Phytophthora* species, as determined by a standard microplate test, ranged from 18.8 to 150 mg/mL and between 37.5 and 300 mg/mL, respectively. Volatile organic compounds (VOCs) released by bioact-LM inhibited significantly the *in vitro* growth of all 11 tested *Phytophthora* species. In *in vivo* trials on artificially inoculated orange and apple fruits, the effectiveness of bioact-LM in reducing the severity of Phytophthora rot varied greatly, depending on the *Phytophthora* species and fruit type. On oranges, maximum inhibitory activity was observed in fruits inoculated with *P. pseudosyringae* and *P. parvispora*, while on apples in fruits inoculated with *P. palmivora* and *P. ramorum*. Findings demonstrate the broad-spectrum activity against *Phytophthora* of this bioactive formulation obtained by fermentation of a by-product of citrus juice industry.

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P95 Evaluating Tomato Peel-Based Growth Media for *Bacillus* and *Lactobacillus* Strains: A Sustainable Alternative to Conventional Broths

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Tomato peel waste, a major by-product of the tomato processing industry, represents a promising resource for microbial cultivation in sustainable agriculture due to its richness in polysaccharides and secondary metabolites. In this study, tomato peels were assessed as a low-cost carbon source for the growth of three bacterial strains: CAAd and SP23, which belong to *Bacillus amyloliquefaciens,* and a *Apilactobacillus kunkeei* strain, species widely employed as biocontrol agents (BCAs). The strains were cultivated in media containing Tryptic Soy Broth (TSB) or de Man–Rogosa–Sharpe Broth (MRSB), except for media prepared with glucose, and tomato peel at concentrations of 5, 10, 20, and 30 g/L, prepared in four forms: (1) fresh filtrate, (2) fresh unfiltered, (3) dried, and (4) dried supplemented with glucose. These were compared to standard media (TSB for *Bacillus*, MRSB for *Apilactobacillus*). Bacterial growth was monitored by optical density (OD600) at 24 h and 48 h (T1, T2). The results showed that SP23 showed the best and dose-dependent growth in dried peel + TSB media, outperforming the control at 30 g/L. CAAd grew moderately in all peel-based media, with performance similar to TSB, suggesting limited exploitation of peel nutrients. *A. kunkeei* strain exhibited high initial growth in fresh unfiltered peel + MRSB, but this declined at T2, likely due to nutrient depletion or inhibition. These findings demonstrate that tomato byproducts could serve as an effective, low-cost growth substrate for industrially relevant bacteria. Further optimization could enhance its scalability, opening the way for greener biotechnology solutions.

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P96 *De novo* genome sequencing of five isolates of *Plenodomus tracheiphilus*, causal agent of Mal secco disease

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"Mal secco", caused by the fungus *Plenodomus tracheiphilus* (*Pt*), is one of the most destructive plant diseases affecting lemon trees, significantly impacting on productivity. It causes a vascular infection favoured by the presence of wounds, high humidity conditions, climatic changes, and suboptimal agronomic practices. Management of the disease is still challenging, and no effective chemical treatment is available. The comprehension of the genetic factors responsible for pathogenicity and plant-pathogen interactions is necessary to identify efficient control strategies. In the framework of the AGRIVITA project, about 30 *Pt* isolates have been collected in Sicily, Calabria and Campania from affected plant materials sited in five areas where consortia for the protection of lemon cultivation (Limone Interdonato, Limone dell' Etna, Limone di Siracusa, Limone di Sorrento and Limone di Rocca Imperiale) are located. The identification of *Pt* isolates has been confirmed by analysis of colony morphology, conidial shape and molecular tests. Artificial inoculation of lemon and sour orange revealed some differences on virulence. A total of five isolates representative of the five consortia were subjected to full-length genome sequencing to assess their genomic diversity and investigate their virulence repertoire. The genomes were sequenced using Oxford Nanopore long-read sequencing platform, which resulted in very high-quality genome assemblies. The availability of *Pt* genomes together with data on morphology and virulence, will contribute to the further characterization and identification of potential virulence factors, useful for a deeper understanding of virulence mechanisms, and essential for developing efficient control strategies and advanced diagnostic tools.

This study has been funded by project AGRIVITA, "Difesa degli Agrumeti Italiani dal Malsecco" – (DM 689142, 15/12/2023)

P97 Evaluation of Italian flora biodiversity as a source of metabolites to inhibit *Pseudomonas syringae* virulence

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The extensive use of copper-based products to control plant bacterial diseases, including the bacterial canker of kiwifruit caused by *Pseudomonas syringae* pv. *actinidiae* (Psa), raises concerns due to resistance emergence and environmental persistence. An eco-friendly alternative strategy relies on attenuating bacterial virulence using natural compounds rather than killing the pathogen, reducing the risk of resistance development and promoting sustainable agriculture. Among virulence factors, the type III secretion system (T3SS) plays a pivotal role in Psa pathogenicity, making it an attractive target for antivirulence strategies. Using a reporter system, we screened 120 plant extracts, sampled all over Italy, among which a subset —particularly from *Empetrum hermaphroditum* and *Ceratonia siliqua*—were found to significantly inhibit the T3SS. These extracts were further tested on additional *P. syringae* pathovars, revealing a variable T3SS inhibition capacity, suggesting a strain-specific response to the treatments.
A transcriptomic analysis highlighted different transcriptional changes, including key regulatory and virulence-related genes, in presence of the different extracts. In parallel, an untargeted metabolomic analysis coupled with bio-guided fractionation provided valuable clues regarding the nature of the bioactive fractions, though the active compound(s) have still to be precisely identified. Finally, preliminary *in-planta* assays showed promising protective effects of these extracts, supporting their potential as sustainable antivirulence agents. Future work will focus on further validating their efficacy in plant protection and identifying the bioactive molecules involved.

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P98 Advances in the antagonistic activity of commercial *Trichoderma* based-formulations against *Plenodomus tracheiphilus*

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Citrus is one of the most economically important fruit crops worldwide. Among fungal diseases affecting citrus, Mal Secco caused by *Plenodomus tracheiphilus* is a liming factor of citrus orchards in the Mediterranean basin. Current strategies are not fully able to effectively manage the infections, and the European restriction on the use of copper make disease control challenging. This study evaluated the *in vitro* activity of four *Trichoderma*-based products, containing *Trichoderma asperellum* ICC012 + *T. gamsii* ICC080, *T. asperellum* T34, *T. atroviride* I-1237, and *T. atroviride* SC1, against eight *P. tracheiphilus* isolates through dual culture, volatile organic compounds (VOCs) and cell-free filtrate assays. All *Trichoderma* significantly inhibited pathogen isolates growth in dual culture and VOCs assays, with inhibition depending on pathogen isolate. After, their performance was evaluated on Volkamer lemon seedlings in controlled conditions and compared with copper hydroxide. Results revealed that all *Trichoderma* minimized infections, and specifically *T. asperellum* ICC012 + *T. gamsii* ICC080 mixture was the most effective since it gave similar performance to that obtained with copper compound. The efficacy of *Trichoderma* mixture was also evaluated as leaf spray and root drench and compared with copper and pyraclostrobin, a fungicide authorized on citrus in the EU. The data showed that the bioformulate always reduced foliar infections. In detail, *Trichoderma* leaf spray was similar to copper, while pyraclostrobin resulted the most effective. The noteworthy findings of this study highlighted strain-specific interactions between *Trichoderma* and pathogen isolates, involving multiple active mechanisms, and identified *T. asperellum* ICC012 + *T. gamsii* ICC080 as promising candidates for Mal Secco biocontrol.

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P99 Phytopathological assessment of lemon clones in evaluation for tolerance to mal secco disease by High Throughput Sequencing

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In the framework of the project "AGRIVITA", accessions of *Citrus* × *limon* have been selected for tolerance to mal secco disease. Part of them were subjected to shoot-tip grafting to obtain healthy mother plants maintained under screenhouse conditions. Others were generated by nucellar selection or shoot-tip grafting and are still under field evaluation at CREA experimental farms located in Acireale (Sicily), and Reggio Calabria (Calabria). The absence of systemic pathogens was confirmed by RNAseq High Throughput Sequencing (HTS) for a comprehensive phytosanitary assessment. Leaves from 13 clones were sampled. Libraries were synthesized from rRNA-depleted total RNA and sequenced as 2x150 bp paired end on an Illumina NextSeq 2000 platform, obtaining 10M reads per sample. Bioinformatic analysis (quality filter, *de novo* assembly, contigs BLAST) showed that all the plants in screenhouse were free from citrus viruses and viroids, whereas one tolerant accession from the field (Femminello Continella) revealed the presence of citrus vein enation virus (CVEV), further confirmed in other filed samples in Sicily and Calabria. The complete genome of CVEV from RNAseq shared the highest homology with an Italian (99.21%) and a Spanish isolate (99.16%). Based on HTS methods, we have assessed the phytosanitary status of lemon clones tolerant to mal secco disease. Thanks to the high diagnostic potential of HTS, the accessions free from systemic pathogens are candidates for the voluntary certification program; the detection of CVEV in a field-grown accession has prompted studies on its diffusion, also considering the presence of vectors in the area.

This study was carried out within the project "AGRIVITA - Protection of Italian citrus orchards from mal secco", financed by MASAF D.M. 689142,15/12/23.

P100 The INTEGROLIV project: a multifaceted approach to mitigate the impact of *Xylella fastidiosa* subsp. *pauca* and regenerate olive growing systems in the infected area

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Xylella fastidiosa subspecies *pauca* (*Xfp)* is a quarantine phytopathogenic bacterium with xylem localization capable of infecting several plant species, producing severe symptoms. In Europe, *Xfp* was first reported in 2013 in the Salento peninsula (Apulia Region, IT) where a new biotype of this pathogen (strain ST53) is responsible for rapid olive desiccation. To date, this bacterium has affected millions of trees, generating raising concern for Mediterranean olive growing. The disease spreading is facilitated by i) the conducive climate of the Salento Region, ii) the abundant presence of the main vector (the meadow spittlebug *Philaenus spumarius*), and iii) the widespread distribution of highly susceptible native olive cultivars (cvs). Currently, quarantine containment measures do not guarantee adequate prevention of new *Xfp* infections and replanting with resistant cvs contributes only partially to the recovery of olive growing in infected areas. The antibacterial products tested, although sometimes alleviate disease symptoms, show moderate efficacy and fail to eradicate the pathogen from infected plants. A coordinated research effort is therefore necessary to identify and implement more efficient products and strategies to manage the bacterium. In this scenario, the INTEGROLIV project, with a multidisciplinary approach which combine traditional and innovative methods, aims to select, evaluate and transfer to oliviculture new effective products and strategies to be applied through an Integrated Disease Management approach. To elucidate their direct mechanisms of action on the pathogen and their indirect responses of the plant, the most effective control products will also be monitored and studied by advanced molecular and biotechnological tools.

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P101 From Core to Control: Functional Characterization of Core Citrus Carposphere Microbiota Reveals Promising Biocontrol Agents

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The plant microbiome plays a key role in promoting plant health by performing fundamental activities such as nutrient cycling, stress tolerance, and protection against pathogens. In an agricultural context, and particularly for citrus, the fruit-associated microbiome (carposphere) is emerging as a valuable reservoir of beneficial microorganisms with potential applications in crop protection. Building upon previous research characterizing the carposphere microbiome of three citrus cultivars, this study focused on the functional assessment of core microbial members for their potential use in biocontrol consortia. We selected nine bacterial isolates, belonging to *Bacillus*, *Pseudomonas*, *Cupriavidus*, *Massilia*, *Curtobacterium*, *Pantoea*, and *Erwinia* genera, within the core microbiome shared across all cultivars, based on their ecological relevance and centrality in microbial interaction networks. These isolates were screened for both direct and volatile-mediated antagonism against different citrus fungal pathogens including *Alternaria alternata*, *Colletotrichum gloeosporioides*, *Penicillium italicum*, *Penicillium digitatum*, *Fusarium* spp., and *Botrytis cinerea*. Most strains exhibited broad-spectrum antifungal activity, with varying degrees of inhibition depending on the pathogen. To further characterize their biocontrol potential, the isolates were tested for extracellular enzymatic activities linked to antagonistic mechanisms, including urease, amylase, protease, pectinase, cellulase, and chitinase production. *Bacillus*, *Massilia*, and *Pseudomonas* isolates showed the highest enzymatic activity profiles. Future work will focus on assessing isolate compatibility and in vivo efficacy through co-culture and plant inoculation assays. The results highlight the potential of citrus-associated core microbiota as a promising source of effective biocontrol agents and pave the way for microbiome-informed approaches to manage fungal diseases and support sustainable citrus production.

P102 Both pH and Plant Signals Drive Type III Secretion in *Pseudomonas syringae* induction at the onset of Infection

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The *Pseudomonas syringae* species complex includes plant pathogenic bacteria that deploy the type III secretion system (T3SS) to disarm host defenses and establish infection. Despite its central role in virulence, the specific signals from the environment and/or the host that govern T3SS activation are not well understood, just as numerous aspects of T3SS regulation during plant infection. Here, we aimed to decipher whether *P. syringae* strains respond uniformly to plant signals and whether pH influences T3SS in combination with other environmental conditions. We used a GFP-based reporter assay to monitor the induction of the T3SS through *hrpA* promoter activity, in apoplast-like medium, at different pH, in presence or absence of leaf extracts from various plant species – to simulate the very beginning of the infection in various plant environments. Besides, the same analysis was conducted in rich medium to assess the influence of pH independently of nutrient availability, Crude leaf extracts enhanced *hrpA* promoter activity in all *P. syringae* strains, regardless of the host range. Moreover, T3SS regulation by pH variations showed strain-specificity, and the range of responsiveness was slightly enlarged in presence of plant extracts. Finally, T3SS pH-sensitivity range was also modified in rich medium, suggesting a combination effect of both pH and nutrient availability. These findings point out that fully integrating environmental variables into studies of *P. syringae* virulence is fundamental to clarify its multifactorial modulation, challenged by the broad genetic diversity of the species complex. Deciphering these regulatory dynamics and their strain-specificity may contribute to preventing pathogen outbreaks.

P103 Study on the susceptibility of some almond (*Prunus dulcis*) cultivars to the pathogen *Diaporthe amygdali*

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The ascomycete genus *Diaporthe* Nitschke (anamorph: *Phomopsis* [Sacc.] Bubák) comprises numerous phytopathogenic species of agronomic importance, characterized by a broad host range and wide geographical distribution. *Phomopsis amygdali* is the causal agent of twig canker and blight in almond (*Prunus dulcis*) and peach (*Prunus persica*), occurring wherever these hosts are cultivated. Symptomatology on almond, known as constriction canker, mirrors that observed on peach, with rapid desiccation of buds, flowers, and young leaves. Brown lesions typically develop around buds on twigs, centred at the nodes. Cankers initially appear brown, later turning tan to silvery, and mature lesions often contain pycnidia developing sub-epidermally. Shoot blight marks the final stage of disease progression. *D. amygdali* is regarded as one of the most destructive pathogens affecting almond cultivation in Europe, particularly in Mediterranean regions. Almond cultivation in the Mediterranean basin is undergoing rapid intensification, transitioning from a marginal crop to one of increasing economic significance. This shift is driven by the adoption of improved cultivars and advanced agronomic practices, resulting in a notable expansion of cultivated areas. Over the past decade, there has been growing scientific interest in assessing cultivar susceptibility to fungal pathogens. The present study aimed to: (i) collect and characterize fungal isolates from naturally infected almond samples in France through morphological and molecular analyses; (ii) evaluate the susceptibility of 18 almond cultivars (including French and Italian genotypes, with ‘Ferragnes’ as the susceptible and ‘Texas’ as the resistant control) to *D. amygdali*; and (iii) compare three field inoculation methods.

P104 *Lasiodiplodia theobromae* (Pat.) Griffon & Maubl. on *Ficus macrophylla* (Pers.) in Italy in association with *Euwallacea similis.*

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In May 2024, in Montechiarugolo (Parma), small perforations associated with a fine frass extruded from holes were observed on the main stem of *Ficus macrophylla*, known as the Moreton Bay fig or Australian banyan tree. These symptoms were attributed to the insect *Euwallacea similis*. Fungal colonies were subsequently isolated from the tissues of both the insect and the host plant. Representative monoconidial fungal isolates were identified by morphological characteristics and molecular analysis, including sequencing of the internal transcribed spacer (ITS), translation elongation factor 1-alpha (TEF-1α) and β-tubulin (TUB) genes. Multilocus phylogenetic analysis revealed that the isolates clustered with *Lasiodiplodia theobromae* strain CBS138868. Pathogenicity tests were carried out on 3-year-old potted *Ficus macrophylla* plants. A 5 mm diameter plug of the actively growing fungus was placed at the inoculation site after removing a bark disc. The inoculation site was covered with sterile moist cotton and wrapped with parafilm parafilm® (Pechney Plastic Packaging Inc., Chicago, IL USA) to avoid contamination and drying. Sterile PDA plugs were used as the negative control point on each plant. The plants were maintained under natural nursery conditions for 3 weeks, after which the length of bark necrosis was measured. Re-isolations from necrotic bark confirmed the presence of fungal colonies morphologically consistent with the original isolates. To our knowledge, this is the first report of *L. theobromae* on *Ficus macrophylla* in Italy. This result highlights a potential threat to both ornamental and forestry plants, underscoring the need for vigilant monitoring and implementation of integrated disease management strategies.

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P105 Impact of Phosphate-Solubilizing and Plant Growth-Promoting Microorganisms on Tomato (*Solanum lycopersicum* L.)

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Phosphorus (P) is essential for plant growth, but it is often a limiting nutrient in agricultural soils and is typically supplied through chemical fertilizers. However, these fertilizers are rapidly immobilized in the soil or leached away by rainwater and only a small fraction (10–30%) of the applied phosphorus is absorbed by plants. This forces farmers to apply fertilizers repeatedly, with negative impacts on the environment. Therefore, it is necessary to develop more sustainable agricultural practices. Several bacterial strains have been reported as able to promote P solubilization from organic and inorganic sources. The objective of this study was to evaluate the potential of selected P-solubilizing bacterial strains (*Bacillus megaterium*, *B. pumilus*, *Pseudomonas putida*, and *P. salmasensis*) to enhance growth, yield, and P uptake in tomato plants (*Solanum lycopersicum* L.) cultivated in low-phosphorus soils. Greenhouse experiments were conducted by inoculating plants with bacterial cell suspensions and supplying different P sources, either inorganic insoluble phosphorite or soluble KH_2PO_4. Plants inoculated with bacteria and phosphorite showed an increase in yield, total soluble sugar content compared to the uninoculated control. Specifically, root length of plants treated with *B. pumilus* in presence of phosphorite showed a 40% increase compared to the uninoculated control. Analyses of P uptake by the roots and stems of the plants are currently underway. Our results highlight the significance of utilizing microbial soil promoters as biofertilizers in sustainable crop production. These represent an eco-friendly strategy to mitigate phosphorus deficiency and enhance its uptake by plants.

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P106 Priming Tomato Plants with Bioactive Peptides and VOCs: Toward Chemical-Free Stress Resilience Strategies

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Given the intensification of environmental stressors affecting modern cropping systems, there is a pressing need to develop strategies that enhance plant productivity and resilience not based on chemical substances such as fertilizers and pesticides. There is growing interest in natural molecules capable of eliciting plant responses through a mechanism known as priming. Primed plants, following an initial stimulus, enhance their capacity to respond more rapidly and effectively to forthcoming stresses. We tested as priming compounds in *Solanum lycopersicum* (tomato) plants: bioactive peptides and volatile organic compounds (VOCs), specifically β-ionone and nonanal, selected for their demonstrated capacity to modulate defence responses against plant pathogens. Plants exposed to the priming agents were challenged subsequently with biotic stress (*Botrytis cinerea*). Advanced, non-destructive technologies were used to perform phenotyping measurements, including gas exchange, VOCs profiling, and imaging-based analyses. Our preliminary results aimed at identifying priming markers which will be then monitored, both in the presence and absence of stress. Stomatal conductance, photosynthetic efficiency, and plant height and biomass were promising phenotyping markers. Volatilome emitted by primed plants showed a very distinct profile from that of non-primed plants, suggesting that induced VOCs may serve both as priming agents and markers. These results highlight that different treatments can lead to the emission of specific VOC blends, underlining the importance of accurate identification of these compounds. A more targeted profiling approach is currently underway to define treatment-specific VOC signatures and to better understand their functional roles.

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P107 Combination of the biocontrol agent *Lysobacter capsici* AZ78 and organic amendments effectively controlled *Pythium ultimum* on tomato

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Soil disease suppressiveness has been associated with *Lysobacter* species for their antagonistic activity against soilborne plant pathogens. Organic, protein-rich materials can stimulate *Lysobacter* populations and further enhance soil suppressiveness. Building on these findings, this study assessed whether organic amendments—chitin, feather meal, fish meal, hoof meal, and yeast—could enhance *Lysobacter capsici* AZ78 (AZ78)'s biocontrol efficacy against *Pythium ultimum* in tomato seedlings under greenhouse conditions. Sandy loam soil was amended with each material (0.3% w/w), inoculated with AZ78 (1×10^6 CFU/mL), and inoculated with *P. ultimum* using colonised millet seeds (0.3% w/w). Controls received non-inoculated millet. Four treatment groups were tested under amended and unamended conditions: (1) soil only, (2) soil + AZ78, (3) soil + *P. ultimum*, and (4) soil + *P. ultimum* + AZ78. Tomato seeds were sown and grown in a greenhouse at 25 ± 1 °C. Germination rates were recorded after 14 days. Five replicates (pots) containing five tomato seeds each were used per treatment, and the experiment was repeated. *Pythium ultimum* alone strongly reduced germination, while AZ78 improved it significantly, even exceeding the untreated control, indicating potential plant growth-promoting activity. The AZ78 efficacy varied with the type of amendment: hoof, feather, and fish meal yielded the highest germination rate, chitin had a mild effect, and yeast significantly hindered seedling emergence. This study is the first to demonstrate AZ78's protective effects against *P. ultimum* in soil, highlighting the potential of combining biocontrol agents with organic amendments for sustainable plant protection.

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P108 Dissection of defense responses against viroid infection in grafted tomato plants

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Grafting, besides boosting the performance of various horticultural crops, may counteract both biotic and abiotic stresses. While the potential to increase tomato plants' tolerance to viral infections has been shown in some tomato/virus combinations, whether and how grafting may interfere with infections by potato spindle tuber viroid (PSTVd; family *Pospiviroidae*), a severe patogen eliciting stunting and leaf curling symptoms in tomato, is not known. Here, the effect of grafting on the plant responses to viroid infection has been investigated by high-throughput imaging phenotyping and transcriptome analyses. Two tomato varieties, Manduria (Ma) and UC82 (UC), tolerant and susceptible to viral infections, respectively, were studied. Quantitative data of morphological parameters were acquired at 9 time points up to 36 days post-inoculation (dpi) from non-grafted, self-grafted UC (UC/UC) and UC grafted onto Ma (UC/Ma) mechanically inoculated with PSTVd or mock-inoculated. According to PCA analysis, grafting has a global effect on the phenotype of PSTVd-infected plants, with a positive effect especially in UC/Ma compared to self-grafted tomato plants. The results of a transcriptome analyses performed on a parallel set of grafted and ungrafted plants and focusing on early responses (15 days post inoculation) showed that the number of differentially expressed genes upon PSTVd infection is higher and more variegated in ungrafted (Ma, UC) than in grafted plants (UC/UC and UC/Ma), Moreover, at both 15 and 37 dpi, the viroid titer in UC grafted onto MA plants was significatively reduced with respect to UC/UC, UC and Ma plants. These preliminary results demonstrate that phenotyping couled with transcriptomic analyses is a promising tool to evaluate tomato responses upon viroid infections and grafting.

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P109 Phytotoxic specialized metabolites produced by *Colletotrichum helleniense,* a causal agent of leaf anthracnose on highbush blueberry (*Vaccinium corymbosum* L.) in Northern Italy

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The genus *Colletotrichum* includes important plant pathogens that infect a broad range of plant hosts. A recent survey on 'Blue Ribbon' blueberry (*Vaccinium corymbosum* L.) identified *Colletotrichum helleniense* as the causal agent of leaf spots in Piedmont, northern Italy. In order to evaluate the production of phytotoxic specialized metabolites involved in the development of the disease symptoms, the fungus was grown *in vitro* with the aim to obtain a culture filtrate that was extracted using ethyl acetate at different pH. Moreover, the organic extracts were analyzed by gas chromatography mass spectrometry (GC-MS) and nuclear magnetic resonance (NMR). Phenolic compounds and organic acids were identified as the main metabolites. Furthermore, the organic extract obtained at unmodified pH (6) was fractionated by combination of column chromatography and thin layer chromatography (TLC) on silica gel to perform the chemical and biological characterization of the low molecular weight compounds produced by the fungus. Five pure metabolites were isolated and identified comparing their spectroscopic data (essentially, ^{1}H NMR and electrospray ionization mass spectrometry ESI MS data) with those reported in literature. Leaf puncture bioassays performed on the host plant at different concentrations resulted in necrotic lesions similar to those caused by the pathogen. This communication provides an overview on the work carried out on the isolation and biological characterization of secondary metabolites produced by *C. helleniense in vitro* and illustrates some structure-activity relationships. To our knowledge, this is the first report on the isolation and identification of metabolites potentially involved in the anthracnose of highbush blueberry.

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P110 Dual effect of innovative solarization in a tomato cropping system in Southern Italy: tomato soil-borne pathogens reduction and soil homeostasis promotion

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Soil solarization is a non-chemical, sustainable method to control soil-borne pathogens capturing solar radiation. Among other solarization methods, Solin® (Polyeur, Benevento, Italy) is an innovative solarization system to enhance soil temperature both at the surface and in depth through the application of a black biodegradable matrix sprayed on the soil surface before covering it by a thin polyethylene film (Polysolar®). Here we compared the effectiveness of different solarization techniques in managing soil-borne pathogens affecting tomato crop in Southern Italy. Four treatments were compared: untreated soil, standard polyethylene film, Polysolar film only, and the full Solin system. During the solarization treatment, soil temperatures were recorded using Nematool® (Bayer Crop Sciences S.r.l.) which records thermal sums. Tomato yield was assessed at the end of the cultivation cycle. Soil samples were collected before and after the solarization treatments, and 120 days after transplanting tomato seedlings, during fruit ripening. DNA-metabarcoding analysis of resident soil microbial communities revealed that solarization is an effective tool for controlling soil-borne tomato pathogens maintaining the soil microbial community. Furthermore, after tomato crop cultivation we noticed that some bacterial and fungal genera were selected as a direct consequence of solarization. To deeper investigate the microbial trends detected, bacterial and fungal species relevant for tomato cultivation and soil ecosystem are being investigated by designing species-specific primers and subsequent quantitative analysis. This work highlights by means of innovative investigation tools such as metagenomics the potential of solarization as a sustainable and effective strategy for soil-borne pathogens control without disturbing the soil homeostasis.

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P111 Anaerobic Soil Disinfestation (ASD) and soil microbiome in tomato commercial greenhouses in Sicily

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Anaerobic Soil Disinfestation (ASD) is a sustainable method for managing soilborne pathogens by inducing anaerobic conditions through incorporation of organic carbon sources and coverage with an oxygen-impermeable film. This promotes microbial fermentation and natural antimicrobial compound production, reducing pathogen presence without sterilizing the soil. This study evaluated the impact of ASD on the soil microbiome in six tomato greenhouses located in Southern Sicily, comparing it to conventional fumigation with Metam sodium (MS), a chemical biocide. Total DNA was extracted from five bulk soil samples per treatment at each site, using the DNeasy PowerSoil Pro Kit (Qiagen). Amplicon based sequencing was performed targeting the 16S rRNA gene for bacteria and the ITS region for fungi. Sequencing was carried out using the AVITI platform. Results showed that α-diversity, based on Observed and Shannon indices, did not differ significantly between ASD and MS treatments. In contrast, β-diversity analysis (Bray-Curtis dissimilarity and PCoA) revealed distinct microbial community compositions between treatments, although the main driver of variability was the farm itself, indicating a strong site-specific influence. While MS effectively suppressed certain pathogens, it also selected for stress-tolerant taxa and reduced the abundance and diversity of decomposer organisms. In contrast, ASD favored beneficial microbial groups, such as Mucorales (Mucoromycota) and Sordariales (Ascomycota), involved in organic matter decomposition, as well as anaerobic taxa linked to antimicrobial metabolite production. These findings suggest that while overall richness and evenness remained stable across treatments, the composition of microbial communities responded differently to management strategy.

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P112 Non-invasive early detection of powdery mildew in tomato using electrical signalling

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Plants are exposed to a multitude of biotic stresses caused by different pathogens, with fungal pathogens being among the most destructive. In order to safeguard plant health, especially under the influence of climate change, the necessity for developing sustainable, cost-effective, in-field and non-destructive diagnostic methods for plant pathogens is of great importance. While spectroscopic and molecular methods have made progress in plant pathology, electrical diagnostic methods are still in the beginning stages of development. In this study, electrical signals in tomato plants infected with the fungal pathogen *Oidium neolycopersici*, the causative agent of powdery mildew, were assessed. Differences in electrical responses were observed between healthy and infected plants during the 15-day infection period, and infected plants showed overall lower values of the electrical potential in comparison to healthy plants. Measurement of electrical potential allowed the successful differentiation between infected and healthy plants, 3 days before the onset of symptoms. Electrical signals differ significantly not only between infected and healthy plants but also concerning the growing substrate. The possibility of deploying the technique directly in the field followed by remote monitoring of electrical signals could provide important support for timely disease control. The results of this study suggest that measuring electrical signals may become an effective tool for the rapid, non-destructive and *in situ* diagnosis of tomato powdery mildew as well as other plant diseases.

P113 Challenging to phytosanitary surveillance of *Xylella fastidiosa* in Italy

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Xylella fastidiosa is one of the greatest phytosanitary threats to agricultural production in Europe. The habitat and climatic suitability of the Mediterranean basin have favored its spread and establishment in several countries. Surveillance is a fundamental activity for plant health, with the goal of demonstrating the absence of the pest in areas where the organism is not yet known to be present and ensuring early detection for prompt eradication. European Union countries are required to program a risk-based survey for this pathogen, using statistical tools (Regulation (EU) 2020/1201). In fact, a statistical is fundamental to improve the effectiveness and efficiency of survey activities. Habitat suitability (HS) is the main risk factor, and three levels of risk (high, medium, low) were assumed according to the impact on plant species; if the HS is high, the risk of finding the pathogen is higher. Therefore, in a GIS environment, the suitable CORINE land use classes (ISPRA, 2018) were selected to define three epidemiological units (agricultural, forest, natural, and semi-natural). Then, this land use model was interpolated with the habitat suitability model (EFSA, 2020), using zonal statistics, identifying for each polygon, area, and risk level. In the second step, the data and the defined statistical parameters were applied in RiPEST, statistical software released by EFSA, to estimate the sample size for Italy. The result shows a sample of about 8000 units, divided according to size and risk, with a design prevalence of 0.6%, achieving a confidence level of 0.99. Starting from 2024, this study has allowed for planning surveillance in free areas in a harmonized manner on a national basis in compliance with European legislation.

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P114 Potential of microbial antagonists isolated from table grape against *Phaeomoniella chlamydospora*

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Grapevine Trunk diseases represent a common issue in all major viticultural regions worldwide and *Phaeomoniella chlamydospora* is one of causal agents mostly associated with vascular infections. Here, *Trichoderma atroviride* (Tch4), *Aphanocladium album* (MX95), and *Clonostachys rosea* (GP80) isolated from grapevine plant material were tested *in vitro* and *in vivo* against *P. chlamydospora* (PCH41.2). Preliminarily, the BCAs were characterized by sequencing the ITS region and *tef1-α* gene. The inhibition activity of Tch4, MX95 and GP80 was proved through dual culture and volatile organic compounds (VOCs) assays. After, their performance was evaluated in controlled conditions on one-node vine cuttings by dipping the basal portion for 24 hours in the spore suspension of antagonist. After treatment, cuttings were inoculated with the pathogen using the same methodology. The aim was assessing the colonization ability of antagonists and their activity to minimize symptom incidence and severity on different genotypes of grapevine. Genotypes under study were 'Nero d'Avola', 'Nerello Mascalese', 'Grillo', 'Carricante', and 'Catarratto' (wine grapes), 'Italia' and 'Crimson' (table grapes), '140 Ruggeri' and '1103' Pulsen (rootstocks). Tch4 and MX95 were the most effective in reducing severity of vascular infections caused by PCH41.2. Tch4 also showed the best performances in the colonization of the cuttings. Furthermore, our data showed differences in the genotype susceptibility and revealed 'Crimson' was the less susceptible and 'Grillo' the most susceptible to PCH41.2. Further analysis are ongoing to take into account also the role of xylem morphology in grapevine susceptibility and in microbial colonization performance.

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P115 Nematicide effects of Smoke Waters Against *Aphelenchus avenae* and *Meloidogyne javanica*

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Smoke water (SW), a liquid by-product of wood pruning waste pyrogasification, was investigated for its nematicidal potential. We evaluated SW's efficacy against adult *Aphelenchus avenae* and the egg and larval stages of the root-knot nematode, *Meloidogyne javanica*, under controlled laboratory conditions. Five distinct concentrations (100%, 0.1%, 0.01%, 0.001%, 0.0001% v/v, and a sterile water control) were tested revealing potent nematicidal activity of SW. For adult *A. avenae*, a 100% SW concentration achieved near-complete mortality within 24 hours, and the 0.1% concentration resulted in 100% mortality by day four. The 0.01% concentration exhibited a gradual, yet notable, increase in mortality, exceeding 40% by day four, although not significantly higher than that observed in the control group. *M. javanica* larvae experiments revealed that 100% SW achieved 100% mortality within the first day, with the 0.1% concentration leading to complete mortality by day two. Lower concentrations also displayed substantial lethality; specifically, the 0.01% concentration induced over 50% larval mortality by day four. Furthermore, both 100% and 0.1% SW concentrations completely inhibited *M. javanica* egg hatching over the entire four-day experimental period. At 0.01%, egg hatching was entirely suppressed for the initial two days, remaining below 20% by day four. These findings indicate that SW exerts a significant nematicidal activity in a dose -dependenting manner, with efficacy particularly pronounced at higher concentrations. Future studies will focus on evaluating SW's effects under field conditions to assess its practical applicability as a natural nematicide.

P116 Sensitivity of *Stemphylium vesicarium* from Italian Pear Orchards to Fungicides: Monitoring over the Last Three Growing Seasons

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Brown spot of pear (BSP), a fungal disease caused by *Stemphylium vesicarium* (Wallr.) Simmons, has been one of the most important pear fungal pathogen in Italy since late seventies, especially in the Po Valley, a key pear-growing region. The disease can cause significant yield losses, particularly in highly susceptible cultivars such as Abate Fètel. To protect orchards, multiple fungicide applications are required from petal fall through fruit ripening.
Fungicide efficacy is increasingly compromised by the selection of *S. vesicarium* strains with reduced sensitivity or full resistance, generally driven by repeated use of the same mode of action. Recent studies show increasing variability in the sensitivity of the pathogen, stressing the need for integrated disease management and regular resistance monitoring. A three-year study was conducted over the last three growing seasons (2022-2024) to monitor pathogen sensitivity to commonly used fungicides. *S. vesicarium* isolates from symptomatic fruits were tested *in vitro* using spectrophotometric assays. The fungicides evaluated included SDHIs (boscalid, fluxapyroxad, penthiopyrad, fluopyram), DMIs (tebuconazole, difenoconazole, mefentrifluconazole), fluazinam, and captan. Results showed stable and complete sensitivity to fluazinam, Revysol, and difenoconazole. In contrast, a progressive reduction in sensitivity to tebuconazole was observed. Captan demonstrated moderately stable sensitivity, with slight declines in some isolates. Although the most part of SDHIs have been introduced in the last fifteen years, rapid development of resistance was detected; this resistance partially reverted during the study period but still requires close monitoring and incorporation into anti-resistance strategies involving mixtures and rotations. These findings highlight the importance of continuous monitoring and integrated management strategies for effective pathogen control.

P117 Comparative Genomics Reveals TE-Driven Innovation and Virulence Strategies in *Colletotrichum lupini*

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Colletotrichum lupini is an important fungal pathogen and the only species within its clade known to infect lupin plants. To gain a deeper understanding of the genetic elements associated with pathogenicity, we conducted an extended comparative genomic analysis between pathogenic and non-pathogenic closely related species. Our analyses revealed a diverse repertoire of transposable element (TE) families unevenly distributed across the genome, with a notable enrichment in lineage-specific regions (LSRs). These LSRs—genomic segments unique to *C. lupini*—represent hotspots for gene gain and loss events, underscoring their evolutionary and biological significance. Among the identified TEs, Starship elements appear to play a key role in mediating the mobilization and genomic compartmentalization of genes and gene clusters. Notably, one such cluster, encoding a hybrid polyketide synthase (PKS)–non-ribosomal peptide synthetase (NRPS), shows signatures of horizontal transfer and appears to have been acquired via a Starship element.
While genes encoding putative effector proteins were also identified in the *C. lupini* genome, the presence of a species-specific, horizontally acquired secondary metabolite cluster highlights an alternative virulence strategy based on secondary metabolism. This unique genomic compartmentalization—potentially driven by TE dynamics—may reflect novel mechanisms of genome plasticity and adaptation in this important plant pathogen.

P118 Impact of *Bacillus* sp. and natural products on *Olea europaea* L. physiology as a potential tool for *Xylella fastidiosa* sustainable management

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In Southern Italy olive trees (*Olea europaea* L.) are severely threatened by *Xylella fastidiosa* subsp. *pauca* (Xfp), the causal agent of olive quick decline syndrome (OQDS). Despite ongoing efforts in monitoring and containment, effective long-term management strategies are still needed. This study aimed to evaluate the effects of the biocontrol agent (BCA) *Bacillus gibsonii* strain RHF15 and two natural products (NPs), i.e. the fungal metabolite 6-pentyl-α-pyrone (6PP) and the cinnamon essential oil (CEO), on olive tree physiology, as potential tools for controlling Xfp. The experiment was conducted in season 2024 on 2-year-old olive trees of the susceptible cultivar Ogliarola salentina. Treatments were applied monthly by foliar spray or soil irrigation from May to July, either singly or as combinations of BCA+NP. Biochemical analyses revealed significant improvements in photosynthetic pigments (chlorophylls and carotenoids) and phenolic compounds in leaf samples, particularly with 6PP and *B. gibsonii*, either applied singly or combined. The increase in chlorophylls suggests active plant growth and efficient light absorption, while the enhancement of carotenoids and phenolic compounds may provide higher protection against oxidative stress and pathogens. A differential analysis of gene expression levels by qRT-PCR is currently in progress to evaluate the induction of plant defence mechanisms by the BCA and/or NPs. Preliminary results indicate significant differences in gene expression, providing insights into plant responses. These findings highlight the potential of NPs and BCAs in stimulating olive resistance to stress, though further investigation is needed to evaluate long-term effects and their possible role in the sustainable management of Xfp.

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P119 New insights into *Pseudomonas syringae* species complex causing leaf spots and bunch necrosis on table grape in Puglia

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Pseudomonas syringae is described as a species complex including different pathovars and the related species and acting as plant pathogens and beneficials. In 2025, fields surveys were conducted in 22 vineyards located in Bari province of cvs. Allison (1), Autumn Crisp (3), Italia (3), Ivory (1), Jack's Salute (1), Red Globe (6), Regal (1), Ruby Rush (1), Scarlotta (1), Sweet Globe (3), and Superior (1) at the phenological stages from BBCH55 (Inflorescences swelling, flowers closely pressed together) to BBCH75 (Berries pea-sized, bunches hang). Symptomatic shoots, leaves and bunches showing respectively black streak, leaf spots and bunch necrosis were sampled and bacteria were isolated on nutrient agar medium. Bacterial colonies were obtained from 'Red Globe' and 'Sweet Globe' showing leaf spots and bunch necrosis. The colonies were transferred to King B medium, and the fluorescent ones were transferred to hypersucrose medium, where two main groups of isolates were observed. One showed levaniform colonies, addressing *P. syringae* pv. *syringae* (*Pss*), and the other convex colonies with yellow mucoid material, addressing *Pseudomonas viridiflava*. All were negative to oxidase test and positive to the tobacco hypersensitivity test. Conversely to *Pss*, *P. viridiflava* isolates were also positive to potato soft rot test. All isolates were inoculated on grape leaves and wide necrotic area appeared after 48 h. 16SrDNA-BLASTn analysis confirmed the morphological and biochemical identification. In conclusion, we report that *Pss* and *P. viridiflava* are associated with leaf spots and bunch necrosis on table grapes, and their management should be considered in crop protection strategies.

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P120 *Syzygium aromaticum*: the antifungal potential of the essential oil and its main component eugenol against *Plenodomus tracheiphilus*

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Essential oils (EOs) are a group of secondary metabolites that biologically perform various functions, including plant defense against pathogens, its environment's adaptation and others. Their activity is mainly attributed to the chemical structure and stereochemistry of both oxygenated and non-oxygenate compounds. This study analyzed the chemical composition of a commercial essential oil isolated from the buds of *Syzygium aromaticum* (L. Merr. & L.M. Perry (*Myrtaceae*), commonly referred to clove oil (C); the *in vitro* activity of C and its main component eugenol (EUG) against *Plenodomus tracheiphilus* was evaluated. The C chemical composition was determined by gas chromatography-mass spectrometry (GC-MS) technique. Three components were identified: EUG as major (77.9%), β-caryophyllene and eugenyl acetate (13.4% and 1.0%, respectively) as minor ones. C was tested at concentrations of 20, 200 and 2000 mg/L, and then at 500, 1000, 1500 mg/L, to determine minimal inhibitory concentration (M.I.C.). EUG was tested, separately, at 500, 1000 and 1500 mg/L to determine M.I.C.; a copper-based fungicide [$CuSO_4 \cdot 5H_2O \cdot 3Cu(OH)_2$, expressed as Cu] and an untreated control were included for comparison. The M.I.C. values were established at 1000 mg/L for C and 750 mg/L for EUG. Complete inhibition of fungal growth was observed with C 2000, C 1500, C 1000, EUG 1500, EUG 1000 (all in mg/L). Notably, EUG 500 mg/L achieved 89.8% of inhibition surpassing the antifungal activity of the copper-based fungicide (74.7%). These findings highlight the promising antifungal potential of clove oil and eugenol, suggesting their suitability for the development of effective and environmentally friendly products to improve crop protection.

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SESSION 4

Molecular Interactions and the Plant Microbiome

FLASH TALKS FROM
“YOUNG RESEARCHERS IN TRAINING”

FT12 Seed treatment with bacterial and fungal endophytes modulates transcriptional and phenotypic responses of rice to *Fusarium fujikuroi*

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Microbial biocontrol agents (MBCAs) represent a sustainable alternative to chemical treatments for controlling *Fusarium fujikuroi*, the causal agent of bakanae disease in rice. However, detailed understanding of their molecular mechanisms of action (MOAs) is essential for regulatory approval and effective field application. This study examined the transcriptional and phenotypic responses of the susceptible rice cultivar 'Carnise' to seed treatments with three endophytic strains of *Microbacterium testaceum*, *Sphingomonas yabuuchiae* and *Epicoccum catenisporum*, under pathogen challenge. The expression of four defence-related genes (*CH1*, *GH17*, *GL8* and *MKK*), selected based on prior transcriptomic studies, was quantified by qRT-PCR at 7, 14 and 21 d post-germination (dpg). Multivariate and correlation analyses were used to explore associations between gene expression patterns and disease/biometric parameters recorded at 21 dpg, including disease severity, disease incidence, germination percentage and total fresh biomass. All MBCAs significantly reduced disease symptoms and onset, while partially restoring germination rate and biomass. Gene expression analyses revealed distinct and time-dependent induction patterns specific to each MBCA. Non-metric multidimensional scaling (NMDS) distinguished bacterial and fungal treatments by their transcriptional signatures, while Spearman correlation analyses supported coordinated regulation of cell wall-degrading enzymes and MAPK signalling genes, as well as strong positive correlations between disease parameters and three out four rice defence-related genes. These findings highlight overlapping yet strain-specific immune responses elicited by MBCAs and identify candidate molecular markers to assess their efficacy in sustainable rice disease management.

FT13 Characterization of the *MAT1* locus involved in the sexual behaviour in isolates of *Podosphaera xanthii* from South Italy

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Podosphaera xanthii, the causal agent of cucurbit powdery mildew, is one of the most common and destructive pathogens of cucurbits in all growing areas. It shows a bipolar heterothallic mating system, with both mating types usually detected in the pathogen populations. The aim of this study was to characterize the mating type (*MAT1*) locus in *P. xanthii* to gain more insight into the genetic bases of the sexual behaviour of the pathogen. RNA-Seq data and the reference genomes of strains of opposite mating type were used for structural and functional annotation of the locus. Two mating type genes (*MAT1-1-1* and *MAT1-1-3*) in the *MAT1-1* idiomorph and one gene (*MAT1-2-1*) in the *MAT1-2* idiomorph were identified. In both idiomorphs, the cytoskeleton assembly control (*SLA2*) and DNA lyase (*APN2)* genes, expected in the regions flanking the *MAT1* locus as found in many *Ascomycetes*, were found far away (121 and 7 kbp, respetively) from the *MAT1* genes. Several transposable elements classified by similarity search against Repbase using CENSOR belonging to DNA/Mariner, NonLTR/Tad1 and LTR/Gypsy classes, were identified in the regions included between *SLA2* and *APN2* gene locations including the *MAT1* genes. Re-sequencing of the whole genomes of isolates of opposite mating type of the fungus is in progress to confirm the *MAT1* locus architecture obtained by *in-silico* analysis. This study will contribute to obtain a characterization of mating type locus structure in powdery mildew fungi and a better understanding and possible factors responsible for the broad variation occurring in *P. xanthii*.

This research was funded by National Recovery and Resilience Plan, Mission 4, Component 2: "From Research to Business" – Investment 3.3. 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).

FT14 Early insights into spore germination and compatibility between *Trichoderma gamsii* and *Clonostachys rosea* under stress conditions: toward dual biocontrol of Fusarium Head Blight

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Fusarium Head Blight (FHB) poses a major threat to cereals, exacerbated by the production of mycotoxins harmful to humans and animals. Two biocontrol agents (BCAs), *Trichoderma gamsii* T6085 (*Tg*) and *Clonostachys rosea* IK726 (*Cr*), have been demonstrated individually to control the disease in wheat and oat, respectively. Recently, co-inoculation showed improved control of FHB under growth chamber conditions, reducing spike incidence by 93% and pathogen biomass in crop residues by 99%. However, *Tg* biomass production was inhibited when spores were co-inoculated in Potato Dextrose Broth (PDB), a nutrient-rich medium.
This study focuses on spore germination dynamics of both BCAs, individually and in co-culture, under varying nutritional and temperature stress conditions. A GFP-tagged *Cr* strain was used to monitor growth via spectrophotometry. In low-carbon media (1/5 PDB, 1/10 PDB and Potato Broth), the co-inoculum growth aligns with *Cr* and shows optimal growth in 1/5 PDB. In Vogel´s and Wheat Grain Broth (WGB), where carbon was extremely reduced, growth declined significantly. Interestingly, *Cr* and the co-inoculum outperformed *Tg* alone in WGB. In nitrogen limitation (Minimal Medium), we observed the lowest growth rates. Under temperature stress (16 and 30 °C in PDB), the co-inoculum showed a slight increase in growth when compared to the single inoculations.
Further microscopic analyses and qPCR are needed to reveal morphological changes, mycoparasitic interaction, and relative biomass contributions. These findings will contribute valuable insights for designing optimal treatment strategies combining the two BCAs and stabilizing their performance in more complex environments, such as field conditions.

FT15 RNAi-Based Control of *Stemphylium vesicarium* in Pear: Genomic Insights into Host Specificity

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Pear is a widely cultivated fruit, but its cultivation is facing severe challenges specially in Italy, one of the major pears producing country in Europe. Here, pear production decreased dramatically in recent years due to the exacerbation of a disease known as 'pear brown spot' caused by the fungal pathogen *Stemphylium vesicarium* (Sv). Interestingly, we found through pathogenicity experiments that *Sv* shows strong host specificity at the strain level, as only specific *Sv* strains can infect pear. This suggests that these pear pathogenic strains have unique genetic adaptations. To investigate on the molecular mechanism of the interaction between *Sv* and pears and the molecular basis of this host specificity, we conducted a comprehensive comparative genomic analysis and transcriptomic analysis. Following this, we selected a number of unique genes, produced dsRNA, and treat pear leaves to explore their protectant effects on *Sv*. Our results contribute to reveal important evolutionary relationship between different *Sv* strains pathogenic to different hosts, identify host-specific genetic elements and assess their potential as genetic target to develop RNAi-based control strategies.

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FT16 Sieve element cell wall composition and sugar transport are strictly interconnected and affect Micro-Tom tomato plant response to '*Candidatus* Phytoplasma solani'

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Phytoplasmas are phloem-limited pathogens affecting many crops of economic importance. Their presence in sieve elements (SEs) interferes with sugars upload and transport and up regulates the expression of occlusion-related genes. Sugar movement from source to sink organs is driven by hydrostatic pressure, which is mostly regulated by the SE cell wall (CW). SE CW is composed mainly of cellulose and pectin. Pectin modifications, like demethylation due to pectin methylesterases (PMEs), have crucial effects on CW mechanical properties, thus on SE transport efficiency. In Micro-Tom tomato plants infected with '*Candidatus* Phytoplasma solani', the phytoplasma associated with the stolbur disease, SE CW appears to be deeply modified, showing increased thickness and swelling. This suggests a possible different composition of SE CW upon infection. Moreover, in infected midrib tissues, two pectin methylesterase genes resulted differentially modulated and genes encoding phloematic sugar transporters resulted down regulated, while the SE occlusion-related genes were highly up regulated. This pattern suggests the attempt of the plant to maintain a functional hydrostatic pressure and phloem sap speed, allowing the movement of sugars while reducing the systemic spread of the phytoplasma.

ORAL PRESENTATIONS

OP22 Deciphering the impact of different belowground pathogens on the aboveground bacterial microbiome in tomato plants

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Plant-associated microbial communities are increasingly recognized for their role in plant resilience against biotic stressors. While several studies have described changes in the plant microbiome under pathogen pressure, the specific effects of belowground pathogens on the phyllosphere microbiome remain largely unexplored. In this study, we set up a microcosm system using tomato as a model plant (*Solanum lycopersicum* cv. 'Money Maker') to test the response of the bacterial leaf microbiome to the presence of different pathogens (*Pseudomonas syringae* pv. *tomato*, *Fusarium oxysporum* f. sp. *lycopersici*, and *Alternaria alternata*). Using 16S rRNA amplicon sequencing, we analysed microbial diversity, community composition, ecological network structure, and community assembly processes. Results show that the presence of different pathogens can lead to distinct changes in the leaf microbiome. While diversity remains unaffected, pathogens induce shifts microbial network connectivity and microbiome assembly processes. Additionally, we identified bacterial taxa associated with the presence of specific pathogens. This integrative approach provides a promising framework to investigate how leaf microbial communities respond to belowground infections and may support the development of microbiome-based tools for early pathogen detection and plant health monitoring.

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OP23 What happened to the grapevine microbiome? Spontaneous grapevines as reference standard.

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The grapevine microbiome is crucial for plant health and may play roles in grapevine trunk diseases (GTD). Endophytes are believed to help grapevines cope with biotic stress, but defining a "healthy" endophytic microbiome is challenging. Over a century of agricultural practices, including pruning, grafting, and fungicide application, have significantly altered the microbiome, with changes likely passed through clonal propagation. To identify a native microbiome, undisturbed grapevine stocks in natural environments provide an ideal model. Spontaneous grapevine populations, likely representing individuals of the crop progenitor (*Vitis vinifera* subsp. *sylvestris*), may offer these conditions. In this study, we used DNA metabarcoding, targeting the ITS gene, to investigate the microbial diversity of wood, rhizoplane and soil of spontaneous grapevines found in Portugal, Croatia, and Italy. In wood, the most abundant taxa were *Trichoderma lixii* and *Sebacina* sp., both rarely found in cultivated grapevines. Several wood pathogens were detected, with *Phaeomoniella chlamydospora*, *Phaeoacremonium* spp., *Diaporthe ampelina*, and *Neofusicoccum parvum* ranking among the 20 most abundant taxa. However, pathogens were highly abundant only in 20–30% of sampled grapevines, where they dominated the microbial community. Wood from these individuals also exhibited GTD-related symptoms, such as brown wood streaking and necrotic lesions. Comparing symptomatic and asymptomatic wood, significant differences were observed for multiple alpha diversity indices (Simpson, Shannon, Pielou's; $P < 0.05$), suggesting microbial dysbiosis. White rot symptoms were never detected, and *Fomitiporia mediterranea* was entirely absent from spontaneous grapevines trunks. This study provides insights into the microbiome composition of grapevines in the wild, contributing to future efforts of microbiome manipulation in cultivated varieties.

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OP24 Deciphering FHB infection: the metabolomics-driven quest for sustainable wheat protection

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Metabolomics provides an unprecedented window into the dynamic chemistry underlying plant-pathogen-environment interactions, allowing the untargeted detection of defense signals, stress-related metabolites, and functional biomarkers. When integrated with isotope-assisted strategies, it enables high-confidence annotation and mechanistic insight into metabolic fluxes. This study illustrates how the combination of untargeted and stable-isotope-assisted metabolomics can shed light on the biochemical responses of *Triticum aestivum* to Fusarium head blight (FHB), a globally devastating disease. In a field-based case study, two winter wheat cultivars (Bingo and Rebelde, more and less susceptible to FHB, respectively) were treated, during flowering, either with systemic agrochemicals (i.e., prochloraz and tetraconazole) or a biocontrol agent (i.e. *Trichoderma gamsii* T6085), and subsequently inoculated with a *Fusarium* spp. spore suspension. Metabolic signatures revealed cultivar-dependent patterns: Bingo exhibited an accumulation of nitrogenous compounds and terpenes, whereas Rebelde showed more rapid and integrated systemic responses (i.e., overaccumulation of defense-related secondary metabolites). In parallel, $^{13}C_9$-labeled phenylalanine (Phe) and tyrosine (Tyr) tracers were used to track aromatic amino acid metabolism in wheat spikelets under *Fusarium* mycotoxin (deoxynivalenol, DON) stress. Although Phe metabolism was quantitatively dominant, Tyr incorporation was selectively enhanced by DON and contributed to hydroxycinnamic-derived defense compounds. Collectively, these results demonstrate the complementarity of large-scale untargeted profiling and isotope-resolved analytics to uncover resistance-associated metabolic signatures and reveal hidden biochemical roles of underexplored precursors. This integrative approach offers a scalable framework to support crop protection, varietal selection and sustainable plant health strategies under increasing biotic pressure.

OP25 A dual-function metabolite from *Beauveria bassiana* shapes plant-pathogen interactions

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Organic acids (OAs) secreted by soil-borne microorganisms play pivotal roles in modulating environmental pH, nutrient availability, and microbial interactions. Despite their ecological importance, the role of OAs in shaping tritrophic interactions among plants, pathogens, and biocontrol agents remains underexplored. In this study, we investigated OAs production across multiple isolates of the endophytic biocontrol fungus *Beauveria bassiana* (*Bb*) and identified a novel metabolite, Bb1993. This compound exhibited dual, concentration-dependent functionality: at low concentrations, it inhibits germ tube formation and elongation in a pH-independent manner, whereas at high concentrations, it functions as a strong pH modulator and blocks spore germination in the fungal pathogen *Fusarium oxysporum* f. sp. *lycopersici* (*Fol*). Application of *Bb* spores or purified Bb1993 to tomato roots significantly altered the composition of root exudates (REs), making them repellent to *Fol* germ tubes, despite an observed increase in peroxidase activity—a known fungal chemoattractant. Notably, qPCR analysis revealed that both *Bb* treatment and low concentrations of Bb1993 effectively reduced fungal burden in tomato roots, demonstrating their protective efficacy against *Fol* invasion. These findings indicate that Bb1993 exerts both direct antifungal activity and indirect, plant-mediated effects by modulating spore germination, host recognition, and penetration processes. Ongoing investigations aim to isolate and characterize the bioactive constituents within REs from Bb1993-treated plants that confer repellent properties against *Fol*. Collectively, these results contribute to a deeper understanding of the chemical signalling networks governing microbe-microbe and plant-microbe interactions in the rhizosphere and underscore the potential of metabolite-based approaches in sustainable biological control strategies.

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OP26 Streptomycetes as biocontrol agents against *Fusarium oxysporum* f.sp *lycopersici* and *Fusarium graminearum* in tomato and wheat crops

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Streptomycetes have emerged as promising biocontrol and growth-promoting agents, with demonstrated efficacy in supporting plants under biotic and abiotic stresses.
In this study, we present two experiments that use proteomics and metabolomics to characterize two streptomycetes with effective positive interactions with wheat and tomato plants, respectively.
In the first experiment, an *in vitro* system coupled with a 1D GeLC-MS/MS approach identified over 300 proteins (90% of which were from wheat). These proteins were involved in the wheat response to *Fusarium graminearum* infection, either with or without a streptomycete on the seed, and in the presence or absence of mild drought stress. The fungal infection produced a significant shift in protein abundance, affecting primary and redox metabolism, transport, and defense-related proteins. Notably, seed inoculation also influenced plant responses, suggesting that *Streptomyces* sp. DEF39 modulates plant defense mechanisms against various stresses, offering insight into its mode of action.
The second experiment investigated the ability of *Streptomyces* sp. DEF17 to modulate tomato plant responses to *Fusarium oxysporum* f.sp *lycopersici*. When applied to tomato seeds, the species modulated root exudates, decreasing the attractiveness of the roots to the germinating conidia. A metabolomics study identified potential molecular players.
By integrating proteomic and metabolomic approaches, this work highlights how streptomycetes influence plant responses to biotic stresses, contributing to a deeper understanding of their functional role in plant health.

SESSION 5

Molecular Interactions and the Plant Microbiome

ORAL PRESENTATIONS

OP27 Investigations on resistance to agents of grapevine yellows in different pathosystems

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Phytoplasmas associated with Flavescence dorée (FD) disease and '*Candidatus* Phytoplasma solani', the causal agent of Bois noir (BN), are responsible for the two most significant grapevine yellows affecting viticulture in Europe. Furthermore, '*Ca*. P. solani has a much broader host range and causes the so-called 'stolbur' disease of tomato. In this study, we investigated the role of different mutants and genotypes in conferring resistance to these two diseases using distinct pathosystems under controlled inoculation conditions. FD-infected *Scaphoideus titanus*, the natural vector of FD, were forced to feed on transgenic, micropropagated grapevine plants (cv. Chardonnay and Bracat Rosa) that overexpress an ATL member of the E3-ubiquitin ligase family (VriATL156), as well as on microvines. Infection rates were evaluated eight weeks post-inoculation to assess FD resistance in comparison to wild-type plants for all genotypes. The susceptible Barbera cultivar was used as a control for microvines. For '*Ca*. P. solani', in the absence of an established laboratory model system for BN based on *Vitis vinifera* and the natural phytoplasma vector *Hyalesthes obsoletus*, we examined the impact of stolbur disease on mutant tomato plants. Sldmr6-1 tomato mutants (cv. San Marzano), which exhibit drought resistance and reduced susceptibility to *Phytophthora infestans*, were graft-inoculated with '*Ca*. P. solani' to investigate the possible role of the DMR6 susceptibility gene in this pathosystem. In this case, infection rates were evaluated four weeks after inoculation, compared to wild-type plants. None of the genotypes examined showed altered susceptibility to the disease compared to the controls.

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OP28 Decoding the Regulatory Role of PsaR3, a LuxR Solo, in *Pseudomonas syringae* pv. *actindiae* virulence

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The highly virulent biovar 3 of *Pseudomonas syring*ae pv. *actinidiae* (Psa), the eziological agent of the kiwifruit bacterial canker, harbors a plasmid-encoded LuxR solo, PsaR3. Unlike canonical LuxR proteins, PsaR3 lacks a known cognate AHL synthase, and its activation mechanism(s) and targets remain unclear.bA transcriptomic analysis performed with a strain overexpressing an inducible PsaR3 revealed the upregulation of genes related to virulence, including the type III secretion system (T3SS) and motility, as well as the plasmid-borne cluster containing *psaR3*. Within this cluster, an intergenic region (IR) located between the two opposite operons was found to act as a bidirectional promoter, regulated by PsaR3, though in absence of any exogenous inducer signal. This suggested that (i) the signal may be endogenously produced by Psa, or (ii) the overexpression of PsaR3 may lead to its spontaneous autoactivation.bTo allow a «controlled» post-translational activation of PsaR3, we designed and constitutively expressed a chimeric protein including the DNA-binding domain of PsaR3 and the AHL-responsive autoinducer-binding domain of CviR from *Chromobacterium violaceum*. Interestingly, the chimera did not respond to AHLs, thus supporting the hypothesis of an autoactivation. Moreover, the CviR-expressing strain displayed T3SS down-regulation, suggesting that the constitutive activation may generate negative feedback, likely to avoid a persistent virulence induction, or that the structure of the chimeric sensor led to a loss-of-function protein acting as a dominant negative mutant. Overall, this work provides new insights into the regulation of virulence in bacterial plant pathogens, offering potential foundations for sustainable plant disease management strategies.

OP29 Sophisticated Sabotage: How phytoplasma effectors manipulate their host plant's cell fate and metabolism

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Phytoplasmas represent a unique class of plant pathogens that pose significant challenges to agriculture due to their complex interactions with host plants and their ability to evade conventional control strategies. Understanding the molecular mechanisms by which these pathogens manipulate host biology is essential for advancing targeted plant protection efforts. Effector proteins play a pivotal role in plant-pathogen interactions by altering host cellular processes to facilitate infection and disease development. *'Candidatus* Phytoplasma mali*'* (P. mali), the pathogen associated with apple proliferation disease, utilizes different effector proteins to interfere with host physiology and disrupt essential regulatory networks. One such effector, PME2, is expressed in *Malus domestica* during phytoplasma infection and has been linked to compromised cell integrity. To investigate PME2's impact on host gene expression and its contribution to infection, we generated transgenic *Arabidopsis thaliana* lines expressing *PME2*. These *PME2*-expressing plants exhibited increased tolerance to proteotoxic stress, potentially supporting host survival and enabling pathogen dissemination. Transcriptomic analysis revealed that PME2 triggers changes in gene expression associated with stress responses, hormone signaling, and immune suppression. These results indicate that PME2 modulates host proteostasis, suppresses immune defenses and thus promotes infection. These findings enhance our understanding of P. mali's infection mechanisms. Understanding phytoplasmal disease development at the molecular level is crucial for developing targeted strategies to manage phytoplasma-related diseases in the future.

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OP30 Deciphering molecular mechanisms in the interactions of '*Candidatus* Phytoplasma solani' with its experimental herbaceous hosts

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'*Candidatus* Phytoplasma solani' (CaPsol) is associated with Bois noir (BN) of grapevine and stolbur of solanaceous plants, and is primarily transmitted by *Hyalesthes obsoletus* Signoret. CaPsol exhibits genetic variability, with the *tuf* gene serving as a marker for identifying two major CaPsol tuf-types, tuf-a and tuf-b1, present on grapevines and alternative host plants. Phytoplasmas secrete effector proteins responsible for the symptoms associated with the disease. A previous bioinformatic analysis allowed the identification of several putative effectors localized within sequence variable mosaic (SVM) regions of CaPsol genomes. This study aimed to evaluate the expression variations of CaPsol putative effector genes during infection process and between tomato and periwinkle plants used as experimental hosts. Tomato and periwinkle plants infected by different CaPsol strains were sampled in two different dates from grafting and CaPsol gene expression was analysed by qRT-PCR. Gene expression analysis allowed the identification of putative effectors which were differentially expressed in tomato and periwinkle plants in relation to date of sampling and strain. Overall, the effector genes were more expressed early in the infection process, followed by a gradual decrease as the infection progresses to a systemic stage. In addition, in plants infected with tuf-b1 strains the SAP54-like effector was highly expressed and an association between its expression and symptom intensity was observed; whereas in plants infected with tuf-a strains the SAP55-like effector was highly expressed. These results increase the knowledge of molecular mechanisms involved in CaPsol-host interactions and could facilitate deciphering the pathogenicity strategies of this successful pathogen.

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OP31 Interkingdom interactions: Transcriptional Reprogramming of Tomato by beneficial and harmful organisms

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The impact of beneficial arbuscular mycorrhizal (AM) fungi on tomato growth has been extensively studied. As components of the plant microbiota, they significantly modulate genes not only in roots but also systemically. Some AM fungi host their own bacterial microbiota including bacteria living on the hyphal surface as well as obligate endobacteria residing inside the fungal cytoplasm. Two isogenic lines of *Gigaspora margarita* one hosting a Burkholderia-related endobacterium (*Candidatus* Glomeribacter gigasporarum, *Ca*Gg), and the other cured of its endobacterium (*Ca*Gg-) were used to investigate the role of *Ca*Gg in the response of tomato plants to *Botrytis cinerea* infection. Six treatment groups were established: control plants; plants mycorrhized by either *G. margarita* CaGg or *G. margarita* CaGg- and the same groups challenged with *B. cinerea*. At the phenotypic level, no significant differences were observed among the control and mycorrhized plants in the absence of the pathogen. In contrast, plants colonized by the AM fungus *CaGg* exhibited alleviated disease symptoms upon *B. cinerea* infection.Transcriptomic analyses were performed on leaves sampled from all the treatments. Ordination analysis confirmed that both the symbiotic fungi and the pathogen were the main modulators of the transcriptomic response. AM fungi primarily triggered pathways involved in plant-cell communication, transcription regulatory activity, hormone metabolism and photosynthesis, while the pathogen induced changes in genes related to plant-pathogen interaction, glutathione metabolism and starch/sucrose metabolism. Quantitative and qualitative changes were also dependent on the presence of endobacterium both in healthy and *B. cinerea* infected plants.

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P121 *A. chinensis* var. *chinensis* on *A. macrosperma* roostock: genotype susceptibility to *Pseudomonas syringae* pv. *actinidiae*, the causal agent of kiwifruit bacterial canker

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Actinidia spp. production is mainly represented by the species *Actinidia chinensis* var. *deliciosa* and var. *chinensis* which are amongst the most recently domesticated fruit crop species commercially cultivated. Italy, with 25,000 ha, is the world's second largest kiwifruit producer, after China, with the main growing areas in the Regions of Lazio, Piemonte, Emilia Romagna, Veneto and Campania. Nutritionally, the kiwi fruits are exceptionally rich in nutrients (e.g. Vit C, Vit E, K and folate), carotenoids, dietary fiber and bioactive compounds with beneficial properties for metabolism and health. Moreover, kiwifruit is a highly profitable crop with a long shelf life suited to global trade. However, in the last 20 years, Kiwifruit Bcterial Canker (KBC) caused by *Pseudomonas syringae* pv. *actinidiae* (Psa, included in the EPPO A2 list) brought about large economic losses in the kiwifruit agri-chain and recently a reduction of 3,000 ha, about 12% of the total area cultivated with kiwifruit in Italy, occurred due to the spread of Kiwifruit Vine Decline Syndrome (KVDS). The latter was observed in different environments and often associated with waterlogging, root rotting/asphyxia. Given the relevance of kiwifruit production worldwide, to employ cultivars resistant to such stresses is the most promising control strategy. In greenhouse, the KBC disease severity was determined in three *Actinidia chinensis* var. *chinensis* genotypes on rootstock *A. macrosperma* (Bounty 71) after foliar spray inoculations with a suspension of the virulent strain Psa IPV-BO 8101, isolated in 2009 from *A. chinensis* 'Hort16A' in the first farm of Emilia-Romagna affected by KBC.

P122 Biofortified *Lycopersicon esculentum* L. plants: varietal susceptibility towards *Ralstonia pseudosolanacearum*

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Bacterial wilt of tomato caused by *Ralstonia pseudosolanacearum* (Rps) represents a serious threat to agricultural production with significant impacts on crop yield and quality. Agronomic biofortification, mostly used to increase the nutritional value of plant foods, plays a crucial role in ensuring good plant growth while maintaining plant health at optimal level. In this context, it is likely to hypothesize to adopt biofortification as a strategy to improve plant resistance to abiotic and biotic stresses. In this study, susceptibility towards Rps was evaluated in Zinc-biofortified varieties of *Lycopersicon esculentum* L. grown at two different concentrations of Zn (2 µM and 10 µM). In particular, among the Zinc-biofortified varieties, two commercial (ROSSORO and MARINER) and two non-commercial (ISI36 and LA4068), grown in coco fiber/agriperlite and subsequently inoculated with the Rps strain CFBP6424, were considered. The data suggested that, under the experimental conditions adopted, Zn supplementation did not have a decisive impact on plant resistance to Rps, but it was highlighted the need to investigate more thoroughly the role of mineral nutrition to manage this important bacterial disease. Indeed, the possibility to enhance the zinc content in tomato plants with the dual effect of increasing the food nutritional value and the plant resistance to biotic stress, might have major impacts in the food supply chain from the seed companies to the consumers. Indeed, crop biofortification is rightfully among the strategies aimed at countering pesticide use with health impacts and environmental sustainability lies at the core of the European Green Deal action plan.

P123 Development of qPCR-based diagnostic assays for *Xanthomonas arboricola* pv. *corylina* early detection in *Corylus avellana* L.

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Xanthomonas arboricola pv. *corylina* (Xac) is the causal agent of hazelnut bacterial blight, the most severe disease for coriliculture worldwide. Current Xac detection and identification methods rely on time-consuming diagnostic assays (e.g. microbiological, serological, biochemical and pathogenicity). Molecular diagnosis of Xac assay has been limited to a duplex PCR assay originally designed for *X. arboricola* pv. *pruni*, requiring modified thermal profiles to enhance sensitivity at the expense of specificity. In 2023, efforts were made to develop a series of new molecular diagnostic methods (e.g. conventional PCR, qPCR and LAMP) based on the "region 2.4" specific to pathovar *corylina*. Despite that, to detect latent infections in asymptomatic tissues, the PCR assay typically used, although rapid, is not sufficiently specific. Furthermore, for the identification of *X. arboricola*, highly pathovar-specific and sensitive methods are not yet available except for pathogenicity testing on host plants. The study aimed to development and validated a reliable qPCR-based diagnostic protocol for the early and rapid detection of Xac in asymptomatic halzenut tissues, thereby improving disease prevention and management. Primers were designed based on *fts*X and *xop*H genes, both specific for pv. *corylina*. Samples from symptomatic and asymptomatic hazelnut plant material were preliminarily tested. The qPCR assays demonstrated high sensitivity and specify, enabling consistent detection allowed to achieve encouraging results for Xac identification in asymptomatic and symptomatic plant material. However, it is necessary to deepen the genetic aspects on Xac virulence and to broaden the choice and type of molecular targets to prevent and control the disease.

P124 Endophytic bacterial communities of tomato seeds produced in organic and conventional systems

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Seeds carry vertically transmitted microbes that shape the plant microbiome and influence plant health and resilience. Understanding seed-associated bacterial communities is key to developing microbiome-based strategies for crop improvement. We analyzed the endophytic bacterial communities in seeds, endosphere and spermosphere of four tomato cultivars produced under organic and conventional system by amplicon-based metagenomics. Alpha-diversity metrics revealed that seeds from organically cultivated genotypes exhibited greater richness and microbial diversity in both compartments. Notably, diversity remained stable across compartments in organic seeds, whereas conventional seeds showed a marked decline in richness and diversity from endosphere to spermosphere. Principal component analysis based on ASV abundances indicated a significant separation between the two compartments, independent of farming practice. Although cultivation system exerted a moderate but non-significant effect on overall community composition, differences in phyla were observed between compartments within the same system. The seed microbiota was primarily dominated by Pseudomonadota, Actinomycetota, and Bacillota (up to 90%), with organic spermospheres exhibiting a notable reduction in Actinomycetota. At finer taxonomic resolution, dominant families included Burkholderiaceae, Microbacteriaceae, Sphingomonadaceae, Staphylococcaceae, and Pseudomonadaceae, known for their plant-associated functional traits. Core microbiome analysis identified 25 core bacterial genera, with seven exhibiting high relative abundance, suggesting ecological dominance and potential functional relevance in tomato seed microbiomes. These findings offer a comprehensive snapshot of seed-associated bacterial communities under different cultivation regimes, laying the groundwork for isolating functionally beneficial strains. Future efforts will focus on the cultivation and characterization of promising taxa for use as bioinoculants in sustainable tomato production.

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P125 Investigating the efficacy and side effects of a new sustainable fungicide against grapevine downy mildew and powdery mildew

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Downy mildew (caused by *Plasmopara viticola*) and powdery mildew (caused by *Erysiphe necator*) can negatively impact grapevine health and production. Current disease management relies on the use of conventional fungicides, raising concerns about environmental sustainability and potential side effects on non-target microbial communities. This study aimed to evaluate the efficacy of a new sustainable fungicide, based on choline pelargonate (CP), against *P. viticola* and *E. necator* and to assess potential side effects on phyllosphere microorganisms under field conditions. Field trials demonstrated the efficacy of CP against grapevine downy mildew and powdery mildew in two locations in Northern Italy and seasons (2024 and 2025), with particularly high efficacy observed against powdery mildew. Phyllosphere microbial communities were isolated in 2024 from grapevine leaves and bunches of control plants and plants treated with CP or with a strategy of copper and sulfur as reference fungicides. Results showed that the composition of bacterial and fungal communities of grapevine leaves and bunches varied according to vineyard location and phenological stage. Thus, the effect of CP on microbial communities was influenced by vineyard- and season-specific differences in the microbiome composition of the grapevine phyllosphere. This study demonstrated that CP is an effective fungicide to manage grapevine diseases, for further development as an alternative product to conventional fungicides.

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P126 Valorization of traditional olive tree genetic resources in Southern Italy

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The present research aimed to assess the incidence of major pathogenic agents affecting plants of the local olive cultivar 'Bambina' from Apulia (Southern Italy), with the goal of promoting sustainable cultural management strategies and enhancing the value of marginal areas. Over a two-year period, field surveys were conducted in an experimental plot hosting several local olive cultivars. Disease assessments were based on visual inspections of foliar symptoms, complemented by laboratory diagnostics using polymerase chain reaction (PCR) to quantify pathogen presence in infected tissues. The study focused on evaluating the phytosanitary status of the test plants in relation to key olive diseases, including olive leaf spot (OLS) caused by *Venturia oleaginea*, olive knot caused by *Pseudomonas savastanoi* pv. *savastanoi*, Olive Quick Decline Syndrome (OQDS) caused by *Xylella fastidiosa* subsp. *pauca* ST53, anthracnose caused by *Colletotrichum* spp., cercosporiosis caused by *Pseudocercospora cladosporioides*, and verticillium wilt caused by *Verticillium dahliae*. The evaluation of disease susceptibility provided valuable insights into the response of the 'Bambina' cultivar to the most common pathogens affecting olive trees. The results revealed differential susceptibility patterns depending on the pathogen, leading to the development of a phytosanitary profile for this cultivar. This profile may be of interest to growers currently cultivating or considering the cultivation of 'Bambina', particularly in the context of biodiversity conservation and varietal valorization in marginal agricultural areas.

This work was partially carried out in the framework of the projects 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).

P127 Carposphere microbiome of pear harbours potential microbial biocontrol agents against *Stemphylium vesicarium*

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Stemphylium vesicarium, the causal agent of brown spot of pear (BSP), is responsible for important economic losses in the main pear-producing areas of Italy, particularly in Emilia Romagna, where the highly susceptible cultivar *Abbé Fétel* is widely cultivated. The pear microbiome is a rich reservoir of microorganisms, offering a valuable source of potential microbial biocontrol agents (*m*BCAs) against major diseases. Using a culturomics approach, eight isolates, selected over 1000 initial bacteria and yeasts isolated from the pear carposphere in orchards located in Emilia Romagna provinces, were tested for their antagonistic activity *in vitro*, using dual-culture assays, against a set of *S. vesicarium* strains. A bioassay on detached leaves was then conducted to assess their biocontrol potential *in vivo*. The candidate yeasts and bacteria were identified by sequencing the ITS regions and 16S rRNA gene, respectively. Antagonistic yeasts were identified as *Aureobasidium pullulans*, *Metschnikowia* sp., *Rhodotorula babjevae*, and *Rhodotorula* sp.; bacterial isolates belonged to the genera *Bacillus*, *Pseudomonas*, and *Pantoea*. *In vitro* antagonistic activity of the selected isolates was slightly variable, depending on the *S. vesicarium* strains tested. On detached leaves, both bacterial and yeast isolates significantly reduced BSP severity. Interestingly, results from *in vitro* assays were not always consistent with those from pear leaf bioassays, suggesting different biocontrol mechanisms. Further investigations are needed to identify the mechanisms of action of these *m*BCA candidates against *S. vesicarium*. Finally, *in planta* assays are currently ongoing to assess their ecological behaviour and potential for effective BSP control.

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P128 Impact of biological formulations on non-target bacterial and fungal communities in *Citrus volkameriana*

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The efficacy of two microbial-based products one containing *Trichoderma gamsii* ICC 080 and *T. harzianum* ICC 012 and the other *Bacillus amyloliquefaciens* QST 713 against *Plenodomus tracheiphilus*, the causal agent of citrus Mal secco disease, was demonstrated on the citrus rootstock Volkamer lemon (*Citrus volkameriana*). To assess the impact of the biological products on non-target citrus microbial communities, an amplicon-based metagenomic analysis was carried out. Microbial communities were collected from either the rhizosphere or the phyllosphere of Volkamer lemon treated with the two products, using distinct and specific protocols for each compartment. Amplicon-based metagenomics targeting the V3–V4 region of the 16S rRNA gene for prokaryotes and the ITS1 region of the fungal rRNA operon was performed on the AVITI platform. Application of the *Trichoderma*-based formulation did not significantly affect the bacterial composition and diversity of the rhizosphere, but led in the fungal communities to an increase in the abundance of Basidiomycota phylum. At the genus level, *Penicillium*, *Gymnopilus*, and *Leucocoprinus* were predominant in treated plants, which also showed a higher relative abundance of *Trichoderma* compared to controls. Foliar *Bacillus* application reduced bacterial and fungal diversity in the phyllosphere, with treated samples dominated by *Bacillus* and an increase of beneficial genera such as *Sphingomonas* and *Burkholderia–Caballeronia–Paraburkholderia*. Fungal phyla abundances remained stable, with *Cladosporium* and *Symmetrospora* prevailing post-treatment. The observed shifts in the microbiome indicate that the biocontrol agents can modulate microbial communities, an effect worth exploring for its potential contribution to plant health and disease suppression.

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P129 Exploring the potential of beneficial bacteria and synthetic consortia for sustainable alternatives to control fungal tomato diseases

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Biological control offers a sustainable and eco-friendly alternative to chemical input for managing plant diseases. In this study, 62 bacterial strains, isolated from natural and forest soils, were screened *in vitro* for their activity as biocontrol agents (BCAs) against four fungal tomato pathogens (*Fusarium oxysporum* f. sp. *lycopersici*, *Rhizoctonia solani*, *Phytophthora nicotianae* and *Alternaria alternata*) using dual-culture assays. Strains were further evaluated *in vivo*, under greenhouse conditions, for their plant growth-promoting (PGP) effects on tomato plants (*Solanum lycopersicum* cv. 'Money Maker'). Comparative analysis of *in vitro* and *in vivo* results identified seven promising strains exhibiting strong antifungal activity (inhibition rates >60% of mycelium growth) and significantly enhanced shoot and root biomass. These strains were identified by whole genome sequencing as *Burkholderia gladioli, Pseudomonas spelaei*, *Pseudomonas lactis, Pseudomonas* sp. and *Serratia plymuthica*, each represented by two distinct strains. We then assembled three synthetic microbial communities (SynComs), each composed of four strains from those identified above, and assessed their PGP activity and biocontrol efficacy against *R. solani* and *P. nicotianae*. Our findings highlight the potential of these bacterial isolates and their consortia as effective BCAs and PGPB, offering a promising tool for integrated disease management in sustainable tomato cultivation.

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P130 From research to practice: monitoring oxathiapiprolin and zoxamide sensitivity in *Plasmopara viticola* populations in Friuli Venezia Giulia (2021–2024)

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From 2021 to 2024, a monitoring programme was conducted in Friuli Venezia Giulia (Italy) to assess the sensitivity of *Plasmopara viticola* populations towards two key fungicides used against grapevine downy mildew: oxathiapiprolin and zoxamide. *P.viticola* samples were regularly collected from commercial vineyards and subjected to *in vivo* sensitivity tests. Over the four-year period, the majority of the populations maintained high sensitivity to both active substances. However, shifts in sensitivity thresholds were observed, particularly under high pathogen pressure or suboptimal application strategies. The results were integrated with vineyard management data and climatic conditions, allowing us to identify key risk factors and to develop tailored recommendations for local growers. Practical guidelines were disseminated through technical bulletins from ERSA which served as an effective tool to directly reach growers and technicians, and promote best practices for fungicide application. This long-term monitoring activity highlights the importance of systematic fungicide sensitivity assessments to preserve the effectiveness of key active ingredients.The results demonstrate how applied research can be translated into practical recommendations, improving decision-making in vineyard protection and contributing to integrated plant health management.

P131 Sniffing Out Powdery Mildew: Can Dogs Detect Early Symptoms of *Erysiphe necator*?

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Erysiphe necator is an obligate parasite on genera within the Vitaceae, including *Vitis*, *Cissus*, *Parthenocissus* and *Ampelopsis*. The most economically important host is grapevine (*Vitis*), particularly the European grape, *V. vinifera*, which is highly susceptible to powdery mildew. The biological characteristics of the fungus, combined with the destructive nature of infections and the difficulty in detecting early symptoms, pose significant challenges to the implementation of rational and timely disease management strategies. As a result, control approaches are often based on fungicide preventive treatments. Within the framework of integrated and sustainable disease management, we trained two dogs for the early detection of *E. necator* symptoms. Thanks to their extraordinary sense of smell, dogs are already employed in diverse fields such as security, hazardous substance detection, and biodiversity conservation, and they can also play a role in plant health. We developed a protocol using two experienced detection dogs; the training sessions were conducted from March to June 2025 in controlled conditions. Remarkably, both dogs were able to detect the presence of the pathogen with as little as 2% of the leaf tissue showing active sporulation. This promising result suggests that trained dogs could effectively complement traditional monitoring methods, enabling field activities, reducing the need for intensive chemical treatments, lowering environmental impact, and promoting a more sustainable viticulture aligned with the principles of integrated pest management.

P132 Integrated Surveillance and Molecular Diagnostics of *Xylella fastidiosa* and *Flavescence Dorée* in Campania region (Italy)

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The detection of *Xylella fastidiosa* subsp. *pauca* in the Apulia region in 2013, and the first report of the phytoplasma associated with *Flavescence Dorée* on the island of Ischia in 2011, highlighted the need for systematic surveillance at the regional and national level. Both pathogens fall under the scope of Regulation (EU) 2016/2031 on protective measures against plant pests, as well as Regulation (EU) 2019/2072, which sets uniform conditions for the application of phytosanitary measures. In the Campania region, thanks to the URCoFi project (Regional Phytosanitary Coordination Unit), CNR-IPSP and Plant Protection Service with the Phytopathological Laboratory "Fitolab" has been actively engaged in extensive monitoring activities. A dedicated network has been established to carry out field monitoring, sample collection, and molecular diagnostics aimed at detecting the presence of these quarantine organisms. All diagnostic activities were conducted in accordance with Regulation (EU) 2020/1201 or official EPPO standards. Pathogen detection and identification relied on molecular methods, including Real-Time PCR and LAMP (Loop-Mediated Isothermal Amplification) assays. From 2020 to May 2025, approximately 8,700 samples of host plant species were collected and analysed for the presence of *Xylella fastidiosa*. In the case of *Flavescence Dorée*, 670 samples of *Vitis spp*. were collected and molecularly analysed. All samples tested negative for the bacterial pathogen *Xylella fastidiosa*, while 13 samples, all collected on Ischia Island resulted positive for the associated phytoplasma. For the monitoring and diagnosis of these pathogens, both the collected samples and the analysis reports are entered into the SIMFito and SIMFitoLab digital platforms.

P133 Plant health from the source: diagnosis of fungi in strawberry seeds and *in vitro* propagation as a sustainable solution

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Mexico is the fifth-largest producer of strawberries (*Fragaria x ananassa*) globally. However, strawberry production faces significant phytosanitary challenges due to fungal diseases, mainly because of a shortage of disease-free planting material. For this reason, several companies are working to develop disease-resistant varieties and *in vitro* propagation protocols to sanitize their parental materials. Within strawberry plant breeding programs, increasing genetic diversity depends on seed germination, making it essential to understand the pathogens that can persist in them. In this study, the fungal diversity affecting strawberry seeds was determined by analyzing 170 seeds that were disinfected and plated on potato dextrose agar and on blotting paper for the freezing blotter test. Based on the morphological features observed in pure colonies, the genera *Cladosporium*, *Colletotrichum*, *Alternaria*, and *Rhizoctonia* were identified. Based on these results, a disinfection protocol and *in vitro* development of axenic lines from seeds were implemented to produce disease-free mother plants. This involved washing the seeds with running water for 5 minutes, then rinsing them with 5% sodium hypochlorite for 1 minute, followed by a wash with 70% ethanol. Three rinses with sterile distilled water were performed after each step. The seeds were sown in magenta boxes containing MS medium, then subcultured with the addition of IBA (5µM) and BAP (10µM), resulting in direct organogenesis and the development of healthy, complete plants within 100 days. Our results offer an initial insight into the diversity of fungi present in seeds, which can impede the *in vitro* propagation of strawberry parent materials.

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P134 Transcriptomic Insights into the Priming Effect of a Bacterial SynCom Against *Xanthomonas euvesicatoria* pv. *perforans* in Tomato

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A six-strain bacterial consortium (MIX2), previously shown to support plant growth and reduce water stress *in vivo*, was tested for its ability to protect tomato plants against the foliar bacterial pathogen *Xanthomonas euvesicatoria* pv. *perforans* (Xep). This pathosystem was chosen to investigate plant-mediated effects of a soil-applied microbial consortium under spatial separation. MIX2 treatment led to a significant reduction in disease incidence and severity, resulting in fewer infections and smaller leaf lesions. The molecular responses involved were investigated through RNA-Seq analysis of tomato leaves collected at 12 hours post-inoculation (hpi), and at 3- and 6-days post-inoculation (dpi). Four treatment groups were analyzed: Control (water), MIX2, Xep, and MIX2+Xep. Based on differential gene expression analysis, MIX2 alone caused only mild transcriptional changes, while Xep triggered a strong early response. Notably, the MIX2+Xep combination induced the most pronounced shifts in gene expression, consistent with a priming effect. KEGG pathway analysis showed enrichment of several pathways compared to untreated controls. At 12 hpi, MIX2 upregulated genes linked to pattern-triggered immunity (PTI), and by 6 dpi, it boosted expression of genes involved in reinforcing leaf surface barriers. In the MIX2+Xep treatment at 12 hpi, PTI was enhanced and brassinosteroid signaling was activated, while auxin pathways were strongly suppressed pointing to a more effective balance between growth and defense compared to plants inoculated with Xep alone. By 3 dpi, Xep-infected plants showed strong downregulation of photosynthesis and energy metabolism genes. Meanwhile, MIX2+Xep plants exhibited enrichment in phenylpropanoid biosynthesis pathways, potentially explaining their reduced disease symptoms and smaller lesion size.

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P135 Microbial biocontrol agents modulate interactions between *Fusarium oxysporum* f.sp. *radicis-lycopersici* and tomato rhizosphere communities

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Understanding the interactions between microbial biocontrol agents (mBCAs), resident microbiota, and plant pathogens is essential for developing sustainable disease management strategies. In this study, we investigated the rhizosphere microbiome response of tomato cv. Moneymaker to *Fusarium oxysporum* f. sp. *radicis-lycopersici* (Forl), and how individual mBCAs (*Bacillus velezensis* PSE31B, *Pseudomonas salmasensis* POE54, *Lysobacter capsici* AZ78, *Trichoderma asperellum* C1 and C2) and a consortium of all strains modulate these interactions. Rhizosphere microbial communities were profiled one-month post-treatment using Next-generation sequencing (NGS)-based ITS and 16S rRNA gene sequencing and analyzed via the Amplicon Sequence Variant (ASV) approach to assess diversity, structure, and complexity of the communities. Forl inoculation reduced bacterial and fungal community richness and diversity (α-diversity) also altering community composition (β-diversity). Microbial inoculants had a greater impact on the microbiome in the absence of the pathogen, with distinct effects observed depending on the specific mBCA applied. Notably, treatments with *B. velezensis* PSE31B and *P. salmasensis* POE54 induced pronounced shifts in bacterial communities in both inoculated and non-inoculated plants, forming clusters distinct from any other treatment. Among the unique changes triggered by these two strains was the enrichment of nitrogen-cycling bacterial taxa, such as *Nitrosomonas* and *Nitrosospira*, which are responsible for the oxidation of ammonium (NH_4^+) to nitrite (NO_2^-), and *Nitrobacter*, which converts nitrite to nitrate (NO_3^-) in soil. Notably, these taxa were otherwise depleted in the presence of Forl. Pathogen challenge also promoted enrichment of putative antagonistic genera, including *Microbacterium* and *Pseudomonas*, that could be further exploited for pathogen suppression.

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P136 From nature to laboratory: carvacrol and thymol helping mal secco disease

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Carvacrol (2-methyl-5-propan-2-ylphenol) and thymol (5-methyl-2-propan-2-ylphenol) are phenolic isomers constituents most of essential oils from the *Lamiaceae* family, such as oregano and thyme. This chemical group of natural compounds exhibit notable antifungal activity against plant pathogens, making them candidates for crop protection application. The activities of carvacrol (CARV) and thymol (THY) were tested, separately, by *in vitro* experiments against *Plenodomus tracheiphilus*. The tested concentrations (100, 300 and 500 mg/L) were selected based on previously *in vitro* experiments (published data) performed with oregano and thyme essential oils (separately), in which they are main components. A copper-based fungicide [$CuSO_4 \cdot 5H_2O \cdot 3Cu(OH)_2$] and an untreated control were included for comparison. All tested concentrations inhibited the fungal growth to different degrees. By the statistical analysis, CARV 300, CARV 500, THY 300, THY 500 (all in mg/L) were the most effectives showing almost total inhibition of the mycelial growth (96%) followed by THY 100 mg/L with 88% of inhibition than by CARV 100 mg/L and fungicide with 74%. Their structure activity relationship (SAR) highlights the presence of a free hydroxyl group and the phenol ring that can be responsible of their antimicrobial properties. In general, their mode of action (MOA), is associated with cellular membrane damage. Hence, further *in vivo* trials studies are necessary to confirm the antifungal activity and the modes of action of the studied compounds.

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P137 Development of a Droplet Digital PCR protocol for the detection of *Stemphylium vesicarium* in pear orchard grass

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Stemphylium vesicarium (Wallr.) E. Simmons, the causal agent of Brown Spot of Pear (BSP), is a fungal pathogen of *Pyrus communis* L. that causes significant economic losses in European orchards. The pathogen survives and persists in weedy grasses and in infected fallen leaves and fruits on the soil surface, which serve as important sources of inoculum during the growing season. To manage BSP, chemical control is applied together with agronomic practices, such as orchard grass sanitation, application of biocontrol agents, and leaf removal. Furthermore, mechanical treatments (e.g., disruption and burial of vegetation) and physical methods (e.g., flame weeding) are also applied. However, evaluating the effectiveness of these interventions requires sensitive and specific monitoring tools. To this end, a droplet digital PCR (ddPCR) assay targeting the mitochondrial *cytochrome b* gene of *S. vesicarium* was developed. Forty-one environmental samples, including grasses and fallen pear leaves, were collected during the 2023 - 2024 seasons from orchards across the Emilia-Romagna region. The DNA of the samples was extracted enabling absolute quantification and distinguishing from a closely related species. This molecular diagnostic tool allowed accurate detection and quantification of *S. vesicarium* from both aboveground and soil-associated sources, making it a valuable resource for assessing the effectiveness of agronomic and chemical control measures. Furthermore, routine early-season quantification of inoculum in grasses and leaf debris could help to predict disease dynamics, supporting timely and sustainable orchard management decisions.

P138 First report of crown and foot rot on durum wheat caused by *Fusarium algeriense* in Europe

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Crown and Root Rot (FCR; FRR) is an economically important disease on durum wheat (*Triticum turgidum* ssp. *durum*) in Italy, particularly in the Mediterranean region. Several fungi may cause FCR or FRR leading to significant yield and quality losses. The most common causal agent in Italy is *Fusarium culmorum* (W.G. Smith). During an extensive survey on fields affected by FCR or FRR in Southern Italy, in 2024, besides confirming the presence of *F. culmorum* and *Fusarium pseudograminearum*, *Fusarium*-like colonies were also isolated from symptomatic plants sampled in 4 regions: Apulia, Basilicata, Campania and Sicily. After 6 days of incubation at 25°C, the developing colonies were removed, and single-spore cultures were obtained. On PDA, the pigmentation varied from light orange to yellowish-white. Morphological characteristics observed under microscope matched the first description of *Fusarium algeriense* made by Laraba et al. (2017). Sequence analyses were performed for four genes (*tef1-α*, *ITS*, *CaM*, *βT*), showing high identity with sequences available in GenBank for the *Fusarium algeriense* type strain, isolate NRRL 66647 (Laraba & O'Donnell): *tef1-α* showed 99.68–99.82% and *ITS* showed 99.81–100% identity. A pathogenicity assay was carried out in greenhouse conditions using the susceptible durum wheat *cv* Iride. The tested isolates of *F. algeriense* varied in virulence and generally proved weak pathogens, causing a disease index ranging from a 4.4% to 38.0% with an average of 15.0% compared to 100% scored for a highly virulent isolate of *F. culmorum. F. algeriense* was successfully reisolated from the symptomatic tissues of the inoculated seedlings, thereby fulfilling Koch's postulates. To the best of our knowledge, this is the first report of FRR or FCR caused by *F. algeriense* in Europe.

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P139 Elimination of viruses in Maletto Strawberry through In Vitro Regeneration from Floral Explants

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Strawberry (Fragaria × ananassa) is a high-value horticultural crop worldwide, with particular regional significance in Sicily, where the Maletto Strawberry—cultivated on the slopes of Mount Etna—is celebrated for its distinctive sensory attributes and cultural heritage. Like many strawberry cultivars, it is susceptible to the accumulation of systemic pathogens, notably viruses, which can lead to severe yield losses and diminished fruit quality. In May 2023, virus-like symptoms were observed in approximately 50% of plants in a 0.5-hectare field of the local "Etna ecotype." A comprehensive etiology study based on High-Throughput Sequencing (HTS) identified *Polerovirus SPV* alongside a complex infection involving *Sadwavirus fragariae*, *Potexvirus fragariae* and *Cytorhabdovirus fragariarugosus*. To address this critical phytosanitary issue, the study explored in vitro regeneration from floral tissues as a novel alternative to conventional meristem tip culture for plant sanitation. This approach leverages the morphogenetic capacity of floral explants to regenerate whole, pathogen-free plants under sterile conditions. A factorial experiment tested four explant types (anthers, petals, pistils, and pseudocarps) and five combinations of plant growth regulators (PGRs). The highest regeneration rates were achieved on media containing NOA (β-naphthoxyacetic acid) and TDZ (N-phenyl-N'-1,2,3-thiadiazol-5-ylurea), with no significant differences among explant types. Acclimatized, asymptomatic plants were successfully obtained, and molecular diagnostics are currently underway to confirm the elimination of targeted viruses. This work highlights the potential of floral regeneration as an effective tool for the sanitary recovery of valuable strawberry germplasm.

**These authors contributed equally to this work and share first authorship.*

P140 Preliminary evaluation of the resistance against *Plasmopara viticola* in HIGS grapevine plants

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Grapevine downy mildew caused by the oomycete *Plasmopara viticola* represents a constant threat for viticulture causing severe losses and costly management. The limitations to pesticide use make urgent the need of resistant or tolerant varieties. With this respect, the use of RNAi technology can provide convincing alternatives to conventional agrochemicals. In particular, the Host Induced Gene Silencing (HIGS) can be applied to grapevine rootstocks for inducing stable gene silencing in the scion through the movement of the RNA signals across the plant. This leads to durable protection from the infection of targeted pathogens. In this work, different hairpin gene constructs targeting *Dicer-like genes 1* (*DCL1*) and *2* (*DCL2*) of *Plasmopara viticola*, were used to achieve stable expression in grapevine cv. Thompson Seedless and 140 Ruggeri rootstocks. The expression of the gene constructs in the transformed plants was validated by PCR amplification with specific primers. The susceptibility to *P. viticola* infections was investigated both in HIGS self-rooted Thompson Seedless plants and in HIGS plants grafted on 140 Ruggeri wild-type. Disease incidence and severity were compared to those shown by wild-type in order to evaluate the resistance level of transformed plants and preliminary results are reported. Next, the uptake of siRNA by the pathogen during the infection of HIGS plants will be assessed by isolation of nucleic acids and qRT-PCR will be applied to assay the gene silencing.

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P141 Volatilome-mediated control of soilborne pathogens by *Papiliotrema terrestris*

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The control of soilborne fungal pathogens such as *Fusarium oxysporum* and *Rhizoctonia solani* is a major challenge in sustainable agriculture. In this study, we investigated the biocontrol potential of the basidiomycetous yeast *Papiliotrema terrestris* strain PT22AV applied as a soil treatment and demonstrated the release of its Volatile Organic Compounds (VOCs) as an important mode of action. *In vitro* double plate assays revealed that *P. terrestris* VOCs significantly inhibited the mycelial growth of both pathogens, with growth reductions exceeding 60%. *In vivo* tests confirmed a marked reduction in disease incidence in tomato and lettuce seedlings grown in soils treated with *P. terrestris* and simultaneously contaminated with *F. oxysporum* or *R. solani*. Evaluation of VOCs activity revealed a strong inhibitory effect on fungal pathogens conidial germination and mycelial development, effectively disrupting the early stages of the infection process. To explore the ecological impact of *P. terrestris* application, a metagenomic approach based on whole-genome shotgun sequencing was applied to analyse the soil microbiome in treated versus untreated soils. Results showed a significant decrease in the relative abundance of DNA of fungal phytopathogens in soils treated with *P. terrestris*, suggesting a suppressive effect on pathogenic fungal communities operated by this biocontrol yeast. These findings demonstrate the biocontrol activity of *P. terrestris* strain PT22AV against two major soilborne pathogens and its potential to modulate rhizosphere microbial communities, thus promoting the plant health. This study supports the potential exploitation use of VOCs-mediated biocontrol as a sustainable tool for integrated disease management in horticultural systems.

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P142 Non-invasive Raman spectroscopy for monitoring metabolite changes in tomato plants infected by stolbur phytoplasma

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Phytoplasmas, wall-less bacterial pathogens transmitted by phloem-feeding insects to plants, are expanding their global host-range and threaten agriculture worldwide. In particular, '*Candidatus* Phytoplasma solani' infects a wide range of weeds and cultivated plants. It is associated with stolbur disease in *Solanaceae* plants and with Bois noir disease in grapevines, compromising crop yields and quality. Early detection is critical for disease management, yet conventional molecular diagnostics such as the polymerase chain reaction (PCR) often lack sensitivity during the initial stages of infection due to the low titer and erratic distribution of the phytoplasmas within the infected plant. This study evaluates the use of Raman spectroscopy as a rapid, non-invasive technique for detecting early metabolic changes in tomato plants infected with '*Ca.* P. solani'. Tomato plants were grafted with infected scions (stolbur strain maintained *in vivo* at the IPSP collection) and with healthy ones as negative controls. Raman spectra were collected at different time intervals post-infection. Raman spectroscopy could detect metabolic changes, specifically in chlorophyll, carotenoids, and polyphenols, as early as two weeks post-infection, before the pathogen could be detected by molecular methods. These findings demonstrate the potential of Raman spectroscopy to identify early biochemical responses in plants during phytoplasma infection and provide a valuable tool for timely intervention and precision agriculture. To the best of our knowledge, this is the first application of Raman spectroscopy to characterize the effects of phytoplasma infection in plants.

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P143 Evaluating *Metschnikowia* strains as biocontrol agents against *Botrytis cinerea* in tomato fruit

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Tomato (*Solanum lycopersicum*), one of the most widely cultivated and consumed vegetables worldwide, is highly valued for its nutritional properties, distinctive flavour, and adaptability to different climatic conditions. During storage, however, tomato is particularly vulnerable to various pathogenic fungi, which can compromise its quality and safety. Among them, ***Botrytis cinerea***, the causal agent of grey mold, is particularly destructive, leading to significant economic losses. The present work evaluates the efficacy of two antagonistic strains, *Metschnikowia pulcherrima* MPR3 and *Metschnikowia fructicola* NRRL Y-27328 (commercial formulation NOLI), both alone and in mixture, in reducing *B. cinerea* development *in vitro* and on tomato fruit. Their efficacy was benchmarked against two commercial basic substances based on chitosan hydrochloride (Chitosano Biorend) and *Equisetum arvense* L. (Naturdai Equibasic), applying different procedures (wound- and dip-treatments) and varying the time intervals between treatments and pathogen inoculation. Both yeast strains exhibited strong antagonistic activity, attributable to direct mechanisms of action, including the production of volatile organic compounds (VOCs) and lytic enzymes, as confirmed *in vitro* by the activity of their culture filtrates and VOC emission. On tomato fruits, both yeast strains reduced disease incidence and severity by over 70% when applied three days before pathogen inoculation, in both wound- and dip-treatments, showing performance similar to or better than the tested basic substances. Notably, they showed persistent protective effects over time, remaining effective even when applied ten days before pathogen challenge, thus highlighting their potential for use in preventive disease management strategies.

P144 Involvement of *Phytophthora plurivora* in the decline of English walnut (*Juglans regia*) in Tuscany, central Italy

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A severe dieback of English walnut (*Juglans regia*) has recently been documented in several walnut plantations throughout Tuscany, central Italy. Affected trees exhibited symptoms such as bleeding cankers, with production of tarry exudates on the lower stem; bark lesions; root and collar rot; and progressive canopy transparency. Micro-morphological and molecular characterisation of isolates recovered from symptomatic tree tissues and the rhizosphere led to the identification of *Phytophthora plurivora* as the aetiological agent responsible for the disease. The fulfilment of Koch's postulates proved the virulence of this oomycete and its critical role in the development of the disease. This study thus provides the first evidence of the involvement of *P. plurivora* in the dieback of English walnut in Tuscany. The prominent role of *P. plurivora* in walnut groves seems to be related to anthropogenic factors, primarily the introduction of infected planting material and inappropriate agronomic practices. In addition, the climate anomalies of recent years, with rising temperatures on the one hand and heavy downpours and flooding on the other, may have exacerbated the problem by weakening walnut trees and favouring the spread of the pathogen. This study highlights the emerging threat posed by this invasive *Phytophthora* species, which is of concern for the important economic value of English walnut cultivation in Italy, with numerous plantations distributed along the Peninsula. An integrated approach to managing the disease is therefore necessary in order to reduce its damaging effects on walnut cultivation.

P145 Fast detection of *Penicillium* rot and the conservation status of packaged citrus fruit using an optical array sensor

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This study introduces a novel optical array sensor for the fast and non-destructive detection of *Penicillium digitatum*-induced rot and the monitoring of the conservation status of packaged citrus fruits. The sensor consists of 20 fluorescent organic probes (BODIPYs, naphthalimides, and rhodamines) capable of multiple non-covalent interactions with volatile organic compounds (VOCs) released by citrus fruits during ripening and spoilage. Each probe exhibits unique fluorescence changes upon VOC exposure, enabling pattern-based recognition of fruit health status. The sensor was tested using oranges either inoculated with *P. digitatum* or treated with sterile water as controls. Probes were deposited on a polyamide support and exposed to VOCs in closed packaging, with fluorescence measurements recorded over four days. Partial Least Squares (PLS) regression and Principal Component Analysis (PCA) were used to correlate spectral changes with ripening progression and fungal contamination. Results show that the sensor array can accurately predict the degree of ripeness of healthy fruits ($R^2 = 0.9997$) and detect infection-induced deviations in VOC profiles. PCA revealed distinct clustering of contaminated samples, particularly on day four, suggesting sensitivity to early-stage rot. Specific probes (especially probe 18, BDPy-Ar) were found to be highly responsive to fungal VOCs through π–π interactions, providing insight into the selectivity mechanism. Compared to conventional analytical techniques (e.g., gas chromatography), this optical system offers a low-cost, portable, and user-friendly alternative suitable for real-time monitoring in industrial settings. It allows quality assessment without opening the packaging, thus reducing waste and enhancing food safety. The sensor also shows potential for broader applications in the post-harvest monitoring of other agricultural products.

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P146 Fighting plant diseases with ozone: a clean and sustainable strategy for plant health?

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Climate change is one of the most serious threats to today's agriculture, posing a significant risk to global food security. A major challenge for the agricultural sector is the development of innovative farming practices that protect plant health, given the adverse effects of traditional pesticides and fertilizers on both human health and the environment. Among these alternatives, the application of ozone (O_3) appears to be a promising approach. As a strong oxidizing agent, O_3 degrades rapidly without leaving harmful residues. Despite its potential, the molecular mechanisms underlying O_3 bioactivity in enhancing plant defenses remain poorly understood. This study aimed to investigate the impact of O_3 on plant growth, development, and defense responses, by using a multidisciplinary approach. Open-field experiments were carried out with various plant species, including the model plant *Nicotiana tabacum* and economically important crops such as tomato, lettuce, and bean. Ozone was applied in the form of ozonated water to the soil. Additionally, gaseous O_3 was introduced directly into the nutrient solution of hydroponically grown lettuce plants. Assessments of physiological parameters, including biomass, chlorophyll content, and stomatal conductance, revealed species-specific responses to O_3 treatment. Furthermore, gene expression analyses demonstrated that O_3 significantly modulates defense-related signaling pathways, particularly those involving pathogenesis-related (PR) proteins. These findings suggest that O_3 can trigger plant immune responses by mimicking a pathogen attack, offering a sustainable and promising strategy for crop protection.

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P147 Cultivar-dependent biochemical responses to *Xylella fastidiosa* subsp. *pauca* infection in olive Trees from a Salento grove

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The olive tree (*Olea europaea* L.), a key crop in the Apulian region of Southern Italy, has been severely threatened for over a decade due to *Xylella fastidiosa* subsp. *pauca* (*Xfp*), the causal agent of Olive Quick Decline Syndrome. This devastating disease has primarily affected susceptible cultivars such as Ogliarola Salentina and Cellina di Nardò. In 2024, a naturally infected 25-year-old olive grove in Torre Vado (Morciano di Leuca, Lecce, Apulia) was selected for investigation. The grove included five olive cultivars, Cima di Melfi, Frantoio, Leccino, Nociara, and Pendolino, all exhibiting mild canopy desiccation. Five infected trees per cultivar were sampled for biochemical analyses aimed at assessing specific responses to *Xfp*. The results revealed significant differences among cultivars. Leccino displayed notable response to *Xfp*, characterized by lower oxidative stress and sustained metabolic function, suggesting an effective defense strategy. Cima di Melfi also maintained photosynthetic performance and antioxidant capacity, indicating resilience to infection. Pendolino, although experiencing high oxidative stress, showed increased accumulation of antioxidants and metabolites, implying an active compensatory mechanism and maintenance of photosynthetic functionality. In contrast, Frantoio and Nociara exhibited elevated oxidative damage with reduced capacity to counteract infection; however, Frantoio activated a broader range of metabolic pathways in an attempt to respond to stress. Overall, Leccino and Cima di Melfi appeared to be the most responsive cultivars to *Xfp*, while Pendolino demonstrated an intermediate response based on metabolic compensation. Frantoio and Nociara seemed to be the most vulnerable, highlighting the necessity for strategic cultivar selection in *Xfp*-endemic regions.

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P148 The grapevine, the insect and the phytoplasma: a study on Flavescence dorée in South Tyrol

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Flavescence dorée (FD) is one of the most severe grapevine yellows diseases and poses a serious threat to European viticulture. In recent years, an increase in disease incidence has been observed in South Tyrol, leading to significant crop losses. Flavescence dorée phytoplasma (FDp) is acquired and transmitted by the leafhopper *Scaphoideus titanus* by feeding on the phloem sap of grapevine leaves. To date, control strategies have focused exclusively on limiting *S. titanus* populations, with no available solutions focused on plant defense mechanisms. This project aims at investigating FD from multiple perspectives. First, we will monitor five local grapevine cultivars (Chardonnay, Pinot gris, Pinot blanc, Lagrein, and Schiava) over a three-year period in several vineyards located in different areas of South Tyrol, using a multiplex qPCR assay to quantify FDp in both roots and leaves. This approach will allow to detect the presence of asymptomatic infected plants, which may act as hidden reservoirs of FDp, thereby facilitating the spread of FD. FDp strains will be also characterized using *16S rRNA* gene sequencing. Second, a metabarcoding technique will be employed to identify FDp and other phytopathogens associated with the vineyard's insect population. Furthermore, insect species other than *S. titanus* will be analyzed regarding their potential to act as vectors in this context. Third, we will test endophytic microorganisms isolated from asymptomatic plants to evaluate their potential biocontrol activity against FDp. This integrated strategy will provide new insights into FD epidemiology and contribute to the development of more sustainable management strategies.

P149 Development of a qPCR assay for early detection and quantification of *Anthostoma decipiens*, causal agent of "mal dello stacco" disease on hazelnut.

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"Mal dello stacco" is one of the most important fungal trunk diseases of hazelnut characterized by cankers, internal necrotic lesions and reddish conidia masses on bark. Historically, *Cytospora corylicola* and further *Cytospora* species were known as the pathogens associated with "mal dello stacco", however, recent studies conducted in Italy and Spain revealed *Anthostoma decipiens* as the causal agent. In recent years, the disease incidence has spread in the main hazelnut growing areas causing important losses due to the plant death and reduced production. However, management strategies are limited due to the lack of knowledge about the pathogen epidemiology and a limited number of active ingredients registered for hazelnut. Early diagnosis in the field alongside the reduction of contaminated materials in nursery and field represents an effective preventive control strategy. Thus, a qPCR assay for an early detection and quantification of *A. decipiens* was developed with SYBR Green method. The nuclear ribosomal internal transcribed spacer (ITS) region was targeted for the design of primers. The specificity of the diagnostic tool was evaluated with 32 *A. decipiens* strains isolated from different countries and hazelnut cultivars and 30 off-target fungal species phylogenetically close to *A. decipiens* or commonly associated with hazelnut wood. Preliminary results suggest that the qPCR assay developed is sensitive and specific to target *A. decipiens*. Further trials are ongoing to test the diagnostic tool using hazelnut wood as matrix, under both naturally and artificially infected conditions.

This research was co-funded by the Hazelnut Company division of Ferrero.

P150 Development of a qPCR assay for *Phythophthora citrophthora* identification in citrus

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Citrus production worldwide is significantly affected by several *Phytophthora* species. In regions with a Mediterranean climate, *Phytophthora citrophthora* Leonian and *Phytophthora nicotianae* Breda de Haan are the primary pathogens associated with foot rot disease, also known as gummosis. *P. citrophthora* can also infect aerial parts of the plant, such as twigs, leaves, and fruit, in addition to the roots and collar. These pathogens cause substantial yield losses globally, particularly in susceptible rootstocks. Therefore, effective management of foot rot disease in citrus urgently requires molecular tools for early and accurate diagnosis. To date, no updated quantitative real-time PCR (qPCR) assay is available for the detection of *P. citrophthora*. In this study, we developed a new qPCR assay for the specific and reliable identification of *P. citrophthora*. Novel primers and a species-specific probe were designed based on the Ras-related protein (Ypt1) gene. The non-coding regions of this gene exhibited sufficient interspecific variation while maintaining intraspecific stability, making it a suitable target for the development of molecular markers across nearly all *Phytophthora* species. Assay specificity was evaluated against a range of *Phytophthora* species spanning different clades and subclades: the primers and probe successfully discriminated *P. citrophthora* from closely related and newly described species, both in silico and in vitro. This qPCR assay represents a significant advancement in the molecular detection of *P. citrophthora* in citrus samples. It can be employed independently or in duplex with a specific *P. nicotianae* assay to accurately identify the causal agents of foot rot disease in citrus crops.

This study was carried out within the project "AGRIVITA - Protection of Italian citrus orchards from mal secco", financed by MASAF D.M. 689142,15/12/23.

P151 Ozone application as a useful tool against crop diseases in pre- and post-harvest

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The application of ozone (O_3), which is a powerful oxidizing agent with zero residual, represents a promising technology in the management of pre- and post-harvest diseases of crops. Ozone can be dissolved in water (ozonated water; OW) and applied through irrigation, which was shown to stimulate the synthesis of bioactive compounds involved in plant resistance, or can be directly used in its gaseous form (e.g., controlled atmosphere), which appeared effective in fungal decontamination. Here, two examples of O_3 application are reported: (i) OW (400 ppb, 100 mL pot^{-1}, every two days for four weeks) was tested in *Dianthus chinensis*/*Erysiphe buhrii* pathosystem by investigating the plant signalling/antioxidant molecules and the disease severity for three weeks post inoculation (wpi); and (ii) gaseous O_3 (500 ppb, for 30, 60 or 90 minutes) was used for the disinfection of *Cicer arietinum* grains from mycotoxigenic fungi and their metabolites (i.e., aflatoxins and patulin). Immediately after the inoculation, leaves of OW-treated plants showed a salicylic/abscisic acid-mediated response (+70 and +80% respectively, in comparison to controls), whereas flowers showed an ascorbic acid and α-tocopherol accumulation starting from 1 wpi (+50 and +20%, respectively). After 3 wpi, the disease severity decreased in OW treated plants (-45%). Gaseous O_3 significantly decreased the incidence of *Penicillium* spp. (-50%, independently to the time of exposure) and reduced the patulin and aflatoxin contents after 30 minutes (-85 and -100%, respectively). Overall, these results confirm the potential of O_3 application as a useful tool in plant disease management and conservation of crop products.

P152 Isolation and molecular characterization of citrus-associated fungi with potential antagonistic activity against *Plenodomus tracheiphilus*

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Plenodomus tracheiphilus is the fungus responsible for Citrus Mal secco disease, which is widely spreading in citrus groves of southern Italy, with a great economic impact, especially on lemon production. The aim of this study was to determine the presence of *P. tracheiphilus* in the Rocca Imperiale consortium (Cosenza, Calabria, Italy), where the Calabrian IGP lemon is produced. Fungi were isolated from symptomatic lemon twigs, which showed leaf wilting, fruit drying and browning. Pure cultures were obtained and maintained under controlled conditions. Morphological analyses, based on the microscopic study of fungal colonies, and molecular characterization were performed to identify each isolate. Genomic DNA was extracted from mycelium and the internal transcribed spacer (ITS) regions of the rDNA were amplified and sequenced. NCBI-BLAST confirmed the presence of *P. tracheiphilus* in the samples, along with other likely non-pathogenic fungal species. The next phase of the work will involve dual culture assays between *P. tracheiphilus* and other isolated fungi to evaluate potential antagonistic interactions. This approach aims to investigate whether, among the fungi naturally associated with damaged tissues, there could be an inhibitory effect on the growth of the pathogen. The study sets preliminary conditions for monitoring the spread of Mal secco caused by *P. tracheiphilus* and evaluating its potential interaction with other fungi presents on infected plants.

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P153 *Xylella fastidiosa* and olive suckers: resistance and variability among cultivars

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Xylella fastidiosa (*Xf*) is a Gram-negative bacterium responsible for the infection of numerous plant species including olive trees, where it causes Olive Quick Decline Syndrome (OQDS). It colonizes the xylem vessels and blocks the flow of water and nutrients, leading to progressive desiccation of the crown and death of the plant. Despite this, it is common to observe the appearance of suckers at the base of the trunk, often without apparent symptoms as described by farmers. Their formation can be due to various factors including the abandonment of agronomic management, but it can also represent a survival strategy: the olive tree reacts by trying to regenerate after damage to the crown. This study analyzed suckers of different ages belonging to the Cellina di Nardò, Ogliarola and Leccino cultivars to evaluate whether they activate more effective defense mechanisms. Preliminary results indicate that only 10% of Ogliarola suckers older than five years were *Xf*-negative, while among the younger ones (< 5 years) over two thirds were negative; in *Xf*-positives the bacterial load ranges from 10^3 to 10^7 CFU/mL. In Cellina di Nardò, about 70% of younger shoots were found to be free of *Xf* while the positive samples showed bacterial concentrations between 10^3 and 10^6 CFU/mL. In Leccino only younger shoots were negative while the older ones showed concentrations between 10^4 and 10^6 CFU/mL, a rather high value in a cv considered resistant. This suggests that their resistance to *Xf* is linked to age rather than cv.

P154 Soil biosolarization is a sustainable tool to manage onion white rot with little impact on the plant microbiome

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Sclerotium cepivorum, the causal agent of white rot, poses a serious threat to onion production. Chemical control is inefficient against this soil-borne pathogen, thus, in this study, our goal is to understand whether alternative control methods – solarization and biosolarization – can be effective in managing *S. cepivorum*. In addition, we tested whether our treatments alter the soil microbiome, and the sclerotia-associated microbiome, with the goal of identifying microbial taxa that might improve the efficacy of our control treatments. We conducted a field trial in 2023, which included three farms and, within each, three treatments plots (control, solarization and biosolarization) replicated three times. Plots were cropped with "Rossa di Tropea" onion, and treatments lasted about 50 days. At the end of the trial, we estimated the disease incidence and severity within each plot, measured the plant biomass, and collected roots and sclerotia (placed in bags at the beginning of the trial) for metagenomics analyses. Our results show that the biosolarization method, while having little impact on the root microbiome, reduce the disease incidence and increase plant biomass. This suggests that biosolarization can be a sustainable tool for managing *S. cepivorum* in the field, aiding the transition towards an environmental-friendly agricultural production.

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P155 Occurrence and characterization of fungal species from Brassicaceae in southern Italy and novel host associations

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During the 2022-2023 growing seasons, symptomatic cultivated Brassica plants, collected from the Apulia, Abruzzo and Campania regions (southern Italy) were analysed in order to ascertain the mycoflora associated. Twenty-two samples from *Brassica oleracea* var. *botrytis*, *B. oleracea* var. *italica*, and *B. rapa* var. *cymosa,* exhibiting disease symptoms such as stunting and wilting, leaf yellowing and necrotic concentric spots, irregular dark spots and water-soaked lesions on corymb were collected and subjected to fungal isolation. From these, 259 fungal isolates were obtained, of which 126 were preliminarily attributed to four main genera: *Alternaria*, *Fusarium, Plectosphaerella* and *Sclerotinia*. *Alternaria* and *Plectophaerella* genera exhibiting the most higher isolation frequencies. Molecular identification by MSP-PCR and multigenic analyses revealed nine fungal species: *Alternaria alternata* (21), *A. brassicicola* (8), *A. japonica* (1)*, Fusarium solani* (25), *Plectosphaerella cucumerina* (20), *P. pauciseptata* (18), *P. plurivora* (9), *Sclerotinia sclerotiorum* (17) and *Stemphylium vesicarium* (7). *Alternaria*, *Fusarium* and *Sclerotinia* species are known as pathogens on several Brassicaceae worldwide, while *P. pauciseptata*, *P. plurivora* and *S. vesicarium* are reported for first time. These findings highlight a considerable intraspecific diversity able to enhance the adaptability of hemibiotrophs and weak pathogens becoming more virulent and expanding their host range within the Brassicaceae family. In particular, due to the hemibiotrophic nature of the genus *Plectosphaerella*, which can become pathogenic under pre-existing biotic stress conditions, some species as *P. paucisectata* and *P. plurivora* should deserve a major consideration as they have already been reported as pathogens on numerous other cultivated crops.

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P156 Landscape epidemiology of almond anthracnose in intensive production systems

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Almond anthracnose, caused by *Colletotrichum* spp. fungi, is a major disease affecting intensive almond orchards in Portugal, and its rapid spread is a direct threat to almond production. *Colletotrichum* is a genus of predominantly polyphagous pathogens capable of spreading among diverse crops such as strawberries, blueberries, peaches, quinces, and olives. This study aimed to assess how landscape, agronomic, soil and climatic conditions may affect disease incidence. For this purpose, several intensive and super-intensive almond orchards in Alentejo were visited to assess the incidence of the disease between 2022 and 2024. Meteorological and geographical land use data were collected and analyzed using a robust regression model, considering data from 100m, 1km, and 10km buffers around sampling points. The statistical model confirmed field observations and showed that older almond trees, super-intensive production systems and the 'Soleta' cultivar are associated with a higher disease incidence. The approach followed shows that larger areas of almonds contribute to the increase in incidence, while fig and citrus areas are associated with lower incidence levels in almond orchards. No significant association between almond and olive orchards, despite the phytosanitary proximity of the two pathosystems. Soils with a higher degree of texture (clay, silt, and sand content) are associated with a lower occurrence within a 1km buffer. Higher summer ombrothermic index and rainfall were associated with increased disease incidence, highlighting the role of humidity in its development. Understanding the epidemiology of anthracnose is key to improving protection strategies and promoting sustainable intensification of almond production.

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P157 Development of resistance in *Capsicum annuum* towards resistance breaking CMV isolates

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Cucumber mosaic virus (CMV; genus *Cucumovirus*, family *Bromoviridae*) is one of the most important viral diseases in pepper worldwide. The CMV outbreak management, especially in the vegetables-production areas, is difficult due the broad virus host range (more than 1200 plant species) and for its fast transmission by many aphid species.
Development of disease resistant pepper varieties can give a competitive advantage. In many commercial pepper varieties, disease resistance towards CMV is based on the presence of a dominant gene, known as "*Cmr1*". During the last decade, incidences of *Cmr1* breaking CMV isolates are frequently reported, like 2019 outbreak we identified in pepper commercial fields in Extremadura (Spain), thus stressing the need to have genetic resistance alternatives.
BASF-Nunhems developed a phenotyping protocol in pepper seedlings able to differentiate CMV resistant versus susceptible materials. New CMV resistant sources towards *Cmr1* breaking isolates, were identified through high-throughput phenotyping a core collection of proprietary BASF-Nunhems germplasm.
Two promising resistant sources have been identified and additional tests on adult plants also confirmed their effectiveness both at the phenotypic level and in the low amount of virus detected by RT-PCR in the plant tissues.
A bi-parental segregating population was developed, and consecutive QTL fine-mapping rounds lead to the discovery of the putative genomic regions involved in the resistance. Molecular markers finally evolved in order to support and facilitate the breeding marker assisted selection.

P158 UHPLC-Q-TOF-MS metabolomic fingerprinting reveals cultivar-dependent mycotoxin profiles of pomegranate fruit affected by heart rot incited by *Alternaria alternata*

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High-Performance Liquid Chromatography Quadrupole Time-of-Flight Mass Spectrometry (UHPLC-Q-TOF-MS) metabolomic profiling was used to characterize secondary metabolites of *Alternaria alternata* in juice from Alternaria heart rot-affected and asymptomatic pomegranate fruits of the cultivars Acco and Wonderful. A total of 22 *A. alternata* metabolites were identified, including tenuazonic acid (TeA), alternariol (AOH), alternariol monomethyl ether (AME), altenuene (ALT), and tentoxin (TEN). Heart rot-affected fruits showed a marked increase in mycotoxin content, with TeA reaching 737.6 µg L^{-1} in 'Acco' and 1 442.7 µg L^{-1} in 'Wonderful' fruit. Alternarlactone A and AME also accumulated to higher levels in symptomatic fruits. AAL toxin TB2 was detected only in juice from infected fruits of 'Wonderful'. In contrast, punicic acid, a major nutraceutical component of pomegranate juice, showed a substantial reduction in juice from symptomatic fruits of both cultivars: from 293.4 to 13.7 µg L^{-1} in 'Acco', and from 146.1 to 64.9 µg L^{-1} in 'Wonderful'. Principal Component Analysis explained 92.8 % of the total variance and separated the four sample groups (symptomatic and asymptomatic fruits of 'Acco' and symptomatic and asymptomatic fruits of 'Wonderful'). Random Forest analysis (OOB error 0.0833) identified punicic acid, AME and alternarlactone A among the top discriminants. The accumulation of specific fungal toxins and depletion of punicic acid define a cultivar-dependent metabolic fingerprint associated with Alternaria heart rot. These results provide new evidence on the effects of *A. alternata* infection on pomegranate juice quality and suggest the possibility of using biochemical markers for early detection and selection of infected fruits.

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P159 Development and optimisation of a portable DNA amplification system for the discrimination of aflatoxigenic and non-aflatoxigenic isolates of *Aspergillus* sect. *Flavi* from maize and hazelnuts

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Aflatoxins are mycotoxins produced by strains of *Aspergillus* sect. *Flavi* representing a major concern for food safety worldwide. These mycotoxins are carcinogenic and teratogenic to humans and livestock. As not all the strains of these species are capable to produce aflatoxins, an early discrimination between toxigenic and non-toxigenic strains at field level is essential for setting up an effective prevention strategy: it is known that non-tox strains can limit the growth of tox ones. To obtain a rapid, easy and on-field applicable system to monitor the presence of tox and non-tox strains in maize and hazelnut, a Lab-on-a-Chip (LoC) system constituted by DNA extraction module and a microfluidic platform for DNA amplification (LAMP/Real Time PCR) was proposed. The first module performs a DNA extraction from heat shocked fungal spores in water solution, followed by the DNA amplification optimised for specific recognition of the tox/non-tox discriminant *aflT* gene. Well-characterized reference strains were employed to set up the system: the aflatoxigenic *A. flavus* NRRL 3357 and the non-aflatoxigenic strain NRRL 9643. LoC system showed a good capacity for amplifying hence discriminating tox from non-tox *A. flavus*. These preliminary results laying the bases for future transfer to portable platforms and for field application of rapid, sustainable and low-cost diagnostic methodologies.

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P160 Sustainable Management of *Botrytis cinerea* on Tomato Using Compost from Food by-products

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Botrytis cinerea is a necrotrophic fungal pathogen causing significant economic losses in tomato, particularly by infecting flowers and stems following defoliation practices. Current control strategies rely mainly on chemical fungicides and, in greenhouse production, on climate regulation. Among sustainable alternatives, the use of compost incorporated into the soil remains poorly investigated. This study evaluated the potential of three composts—derived from cocoa husk, brewer's spent grains, and grape pomace—to reduce disease severity under controlled climate chamber conditions. Three independent trials were conducted on potted tomato plants. Composts were incorporated at 10% v/v into the substrate in nursery trays prior to sowing. After one week, seedlings were transplanted into 1.5 L pots filled with peat. Each pot contained two tomato plants, with five replicates per treatment. An untreated inoculated control and a healthy non-inoculated control were included for comparison. Four weeks after transplanting, two leaves were removed from the stem, and 10 µL of a *B. cinerea* conidial suspension (1×10^6 conidia/mL) were applied to each wound site. After one week, the length of stem necrosis was measured to assess disease progression. All three composts significantly reduced necrosis length, displaying intermediate efficacy between the inoculated untreated control and the healthy control. Among them, the compost derived from cocoa husk showed the most pronounced protective effect.

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P161 Transcriptomic responses of strawberry fruits exposed to postharvest treatments with Plasma-Activated Fog

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Plasma-Activated Fog (PAF) is a new promising technology for fruit decontamination against postharvest fungal pathogens. It consists of an aerosol made by droplets of water, nebulized by the effluent gases of a plasma discharge. In this work, PAF was generated via dielectric barrier volume discharge in a jet-like configuration and used in postharvest applications on strawberry fruits reducing significantly the incidence of rots. To study the effects of treatments on fruits, transcriptomic changes induced by PAF were investigated through RNA-Seq analysis. Total RNA was extracted from strawberries exposed to 10 min of PAF treatment and from the untreated control fruits, at 6 h and 24 h after treatment, and used for Illumina sequencing. A total of 524,3 Gb of sequencing data (2x150 bp reads) from twelve cDNA libraries were generated. By comparing the expression values in treated versus untreated samples, a total of 1,611 differentially expressed genes (DEGs) were identified as significantly modulated (FC≥ |2| and FDR≤ 0.05) after PAF treatment. Genes involved in the ethylene biosynthetic process (e.g., 1-aminocyclopropane-1-carboxylate oxidase), fruit ripening and sweetness (e.g, genes coding for miraculin-like proteins which are glycoproteins with taste-modifying activity that converts sourness into sweetness), plant responses to biotic and abiotic stresses (e.g., L-type lectin-domain containing receptor kinase, and PR-4-like genes), and auxin homeostasis and signalling were significantly up-regulated in treated versus untreated fruits. These findings demonstrate that PAF treatments activated fruit defence responses suggesting an increased resilience in the treated fruits that may affect their shelf-life and quality.

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P162 Characterization and subcellular localization of the putative RNA-dependent RNA polymerase of Tulasnella ambivirus 4 in *Saccharomyces cerevisiae*

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Ambiviruses are infectious agents merging characteristics of viroids and RNA viruses. Like viroids, they have a circular single-stranded RNA genome folding in a compact secondary structure and with paired self-cleaving ribozymes, which replicates through a rolling circle mechanism; like viruses, they contain two open reading frames (ORFs; ORFA and ORFB) coding for one protein in each polarity strand. Whereas ORFB encodes a protein with unknown function, ORFA potentially codes for an RNA-dependent RNA polymerase (RdRP), based on structural similarity to viral RdRPs. Nevertheless, its role remains to be elucidated. We investigated the function of ORFA gene product, using Tulasnella ambivirus 4 (TuAmV4) which infects *Tulasnella* sp., mycorrhizal fungi of orchid roots, and the budding yeast *Saccharomyces cerevisiae* as model virus and host, respectively. TuAmV4 ORFA fused to the Myc epitope was cloned under the control of a constitutive or of an inducible promoter in appropriate yeast expression vectors and transformed into *S. cerevisiae* YPH499 cells. The optimal culture conditions for ORFA expression were determined. TuAmV4 ORFA was correctly expressed either constitutively or transiently, as shown by western blot analysis. The ectopic expression of ORFA did not affect yeast cell growth as a function of time. By differential centrifugation of protein extracts it was shown that ORFA expressed protein sedimented in a membrane-enriched fraction and showed to be resistant to alkaline, urea or salt extraction, a property of integral membrane proteins. Immunofluorescence analysis showed that TuAmV4 ORFA was not dispersed in the cytosol, but it localized to cell membranes.

P163 Emergent and re-emergent citrus rootstock diseases: experience and perspectives

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The management of Tristeza quick decline relies on rootstocks tolerant or resistant to *Closterovirus tristezae* (Citrus tristeza virus - CTV). Over the past decades, thousands of hectares of sweet orange trees grafted onto citranges, citrumelo, Volkameriana lemon, and Macrophylla have been planted. However, various disorders have emerged in Sicily, although their etiology remains unclear, and some plantings aged 8 to 10 years have been uprooted**.** This contribution reports cases of decline and disorder observed in citrus plantings, based on field and laboratory findings collected in recent years. The most widespread disorders were observed in Navelina and Newhall sweet oranges grafted onto citranges, characterized by uneven growth between scion and rootstock at the bud union line, with an inner bark ridge constricting the xylem. Other declines, associated with gumming of xylem vessels and branch browning, were reported in 6–8-year-old Moro and Tarocco oranges on citrange. Severe bark cracking, gumming, and irregular overgrowth were seen in eight-year-old Tarocco Lempso grafted onto Volkameriana lemon. These symptoms appear to interfere with nutrient uptake from the roots and compromise resilience in calcareous, heavy, and/or saline soils, leading to reduced growth and impaired renewal. Fibrous roots become soft and water-soaked, with easily sloughing cortex tissue. Laboratory analyses detected mixtures of viroids alongside CTV, *Phytophthora* spp. and *Fusarium* spp. The symptoms raise questions that may foster research into pathogen–rootstock interactions and the rhizosphere microbiome, a key factor in citrus health.

P164 Role of essential oils from Mediterranean officinalis plants in control of post-harvest diseases

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Essential oils (EOs) from Mediterranean officinalis plants are receiving considerable interest in their antimicrobial activity. Here, antifungal activity of volatile compounds of EOs extracted from *Rosmarinus officinalis, Origanum vulgare, Salvia officinalis, Thymus officinalis* and *Laurus nobilis* was assessed against post-harvest pathogens *Botrytis cinerea, Aspergillus niger, Aspergillus carbonarius, Monilia laxa*, *Monilia polystroma* and *Monilia fructicola.* Antimicrobial activity on conidia germination was evaluated *in vitro*, in 2 mL tube inoculated with 10 µL conidial suspension ($1x10^6$ conidia/mL). In presence of 22 mg/mL of EO (50 µL of EO on cap of tube to evaluate exclusively the volatile phase), all EOs inhibited completely the germination of conidia of all strains. The activity on mycelia growth was evaluated by adding 0.75 or 0.37 mg/mL of EO (10 µL undiluted or 1:1 v:v) on filter paper placed on media, at the center of 60 mm diameter Petri dishes. *O. compactum* and *T. officinalis* EOs completely inhibited the growth of all the pathogens at 0.75 mg/mL. *L. nobilis* EO showed high effectiveness against the three *Monilia* species, ranging from 97 to 100% inhibition, while lower effectiveness against *B. cinerea, A. niger* and *A. carbonarius* (73, 63 and 93%, respectively). EO from *R. officinalis* showed efficacy only against *M. laxa* and *M. polystroma* (97% for both), while *S. officinalis* inhibited the growth of all the pathogens in the range 37-100%. These results show remarkable antimicrobial activity of the EOs against important pathogens. Evaluation of antimicrobial activity *in vivo* on grape and cherry berries are ongoing.

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P165 *Lasiodiplodia exigua*: a source of biologically active secondary metabolites

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Lasiodiplodia exigua (fam. *Botryosphaeriaceae*) was originally isolated from broom bush (*Retama raetam*) in Tunisia in 2012, but it was later identified as an aggressive pathogen of grapevine (*Vitis vinifera*) in Mexico and Turkey, cork oak (*Quercus suber*) in Algeria and pistachio (*Pistacia vera*) in Arizona (USA). Symptoms caused by *L. exigua* include leaf chlorosis, shoot blight and chiefly sunken cankers with characteristic wedge-shaped wood necrosis visible in cross section. The appearance of symptoms caused by this emerging pathogen suggest the potential involvement of phytotoxic metabolites (PMs) in the host–pathogen interaction. Studies on PMs produced by *Botryosphaeriaceae* species have increased due to growing impacts of the diseases caused by these pathogens worldwide. In the present communication, the *in vitro* production of secondary metabolites by the ex-type culture of *L. exigua* has been described for the first time. In this respect, several metabolites were purified from the crude extracts of culture filtrate and mycelium using chromatographic techniques. Chemical structures were elucidated by NMR spectroscopy, GC-MS, mass spectrometry and optical methods. Interestingly, *L. exigua* produces metabolites with huge structural diversity belonging to different classes of natural products, including lactones, melleins and the palmarumycins. The latter are characterized by an unsaturated decalin unit connected with a 1,8-dioxynaphthalene ring. In addition, the ability of the isolated compounds to inhibit seed germination was evaluated.

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P166 Fusarium-resistant tomato cultivars show root exudate-mediated pathogen deterrence

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Plant-pathogen interactions in the rhizosphere are mediated by chemical signals released through root exudation, which can either facilitate or inhibit microbial colonization. While genetic resistance to *Fusarium oxysporum* (*Fo*) in tomato cultivars is established, the role of root exudates in determining cultivar-specific pathogen responses has received limited attention. Understanding whether resistance genes influence the composition and bioactivity of root exudates could reveal novel mechanisms underlying plant immunity. In this study, root exudates from susceptible (Moneymaker) and multiple resistant tomato cultivars (Motelle, B2, B4 and C10) carrying two *Fo* resistance genes (e.g. I1 and/or I2), were used in chemotropic assays to evaluate their ability to attract fungal germ tubes of the vascular pathogen *Fusarium oxysporum* f. sp. *lycopersici* (4287) race 2 (*Fol*). Root exudates from the susceptible cultivar Moneymaker exhibited strong attractive effects on *Fol* race 2 germ tubes, while all resistant cultivars showed significantly reduced attraction, despite having significant peroxidase enzymatic activity (i.e. the major chemoattractant from plant roots). NMR analysis of root exudates showed distinct metabolic profiles between susceptible and resistant cultivars, while all resistant lines displayed similar chemical fingerprints. To further investigate the molecular nature of root exudate compounds involved in neutralizing peroxidase-dependent chemoattractivity on *Fol* germ tubes, activity-guided fractionation experiments were performed. Interestingly, an ethyl acetate soluble fraction was able to inhibit peroxidase dependent chemoattraction in *Fol*. These findings suggest that resistant cultivars constitutively produce root exudates that block the attraction of soil fungal pathogens, representing a novel pre-infection resistance mechanism that influences plant-pathogen interactions at the rhizosphere level.

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P167 Evaluation of the efficacy of biological control agents in managing olive anthracnose caused by *Colletotrichum* spp. in Italy and Spain

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Olive anthracnose, caused by *Colletotrichum* species, represents a major threat to the olive tree (*Olea europaea*) cultivation worldwide, particularly within the Mediterranean Basin. This study investigated the effect of six potential biological control agents (BCAs; *Aureobasidium pullulans* PV-1033; *Bacillus amyloliquefaciens* PV-700; *Epicoccum nigrum* RB4C; *Phoma* sp. PV-375; *Trichoderma asperellum* IMI393899; *T. atroviride* TRICH-S) against representative isolates of the main *Colletotrichum* species causing the disease in Italy and Spain: *Colletotrichum acutatum* C9D2C and UWS149, *C. godetiae* OLP12, OLP16, Col-508, Col-511 and *C. nymphaeae* Col-151 and Col-466. Copper sulfate (2 g/L) and *Bacillus subtilis* (Serenade ASO®, 8 mL/L) were used for comparison. *In vitro* assays assessed the inhibition of mycelial growth and volatile organic compound (VOC) production by the BCAs. All tested BCAs significantly inhibited mycelial growth in dual cultures and produced VOCs that suppressed *Colletotrichum* species growth. TRICH-S and IMI393899 showed the strongest inhibitory effects in both assays. Detached fruit assays using 'Arbequina' olives confirmed the pathogenicity of all fungal isolates, with disease incidence ranging from 41.67% to 98.33%. The most virulent isolates (C9D2C, OLP12, Col-511, and Col-151) were selected for *in vivo* efficacy in detached fruits. For this, BCAs were applied by spraying 96 h and 24 h before pathogen inoculation. Among the BCAs, IMI393899 was the most effective against C9D2C and OLP12; PV-700 against Col-511; and RB4C and PV-700 against Col-151. These findings highlight promising BCAs for subsequent *in planta* evaluation and exploration of their mechanisms of action.

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P168 Orchestrating *Xylella fastidiosa* Lifestyle: The Adhesin and Oxylipin Connection

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Lipids play a pivotal role in dictating the lifestyle of *Xylella fastidiosa*, a pathogen confined to the xylem. This adaptable bacterium can seamlessly transition between planktonic, twitching, and biofilm states. A key player in this regulation is Diffusible Signalling Factors (DSF), specifically cis-2-enoic fatty acids. The severe symptoms *X. fastidiosa* inflicts on various hosts are thought to stem from its ability to form biofilms within the xylem vessels, a process critically dependent on the pathogen's adhesion to xylem cell walls. Our recent findings highlight the significance of 7,10-DiHOME, an oxylipin derived from oleic acid, as a crucial signaling molecule. It promotes biofilm formation and twitching motility. The synthesis of 7,10-DiHOME appears to be linked to a signal transduction pathway that requires the presence of the afimbrial adhesin XadA2; without this protein, the process is impaired. While previous research offered insights into the in vitro mechanisms controlling these essential lifestyle switches, the question of what transpires within the host remained. Considering the context of Olive Quick Decline Syndrome (OQDS), it appears that plant oxylipins, particularly those from the 13-lipoxygenase (13-LOX) pathway, might collaborate with bacterial oxylipins in orchestrating *X. fastidiosa* lifestyle transitions. In the model plant Arabidopsis, the silencing of the LOX2 gene (that codify a 13-LOX involved in jasmonate synthesis) led to a reduction in 13-oxylipins, thereby facilitating the pathogen's growth and movement within the plant. This observation has been further ascertained in olive trees under natural infection conditions. Interestingly, 13-HODE, an oxylipin synthesized by plant 13-LOX, accumulates in olive varieties susceptible to X. fastidiosa but not in resistant ones. Collectively, these findings suggest a complex interplay between oxylipins and adhesins in governing the lifestyle transitions of X. fastidiosa. Deciphering this intricate relationship is paramount for developing targeted strategies to control this devastating pathogen.

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P169 Lipidome of resilient and *Xylella fastidiosa* subsp. *pauca* infected olive trees differs from healthy trees: a potential infection marker?

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In previous studies, lipid profile alterations were characterized in plant samples collected from olive trees infected by *Xylella fastidiosa* subsp. *pauca* (Xfp+), compared to healthy ones (Xfp-) and we identified lipid-based classifiers capable of distinguishing between Xfp+ and Xfp- olive trees. Resilience to OQDS was assessed and quantified using Normalized Difference Vegetation Index (NDVI) analyses carried on between 2018 and 2022 by satellite imagery of Xfp+ olive trees in the Salento region. In this work, we investigate whether specific lipid entities can serve as predictors capable of distinguishing Xfp- from Xfp+ symptomatic and Xfp+ resilient samples. Targeted lipidomic and plant hormone analysis was performed using HPLC-MS/MS on 36 olive trees of the cultivars Cellina di Nardò and Ogliarola Salentina. Principal Component Analysis (PCA) was applied to the combined dataset to evaluate how healthy status influences lipid profiles. The resulting score plots showed a clear separation between Xfp- and Xfp+ trees, whether symptomatic or resilient, notwithstanding the minor differences among these latter. This differentiation was primarily driven by the 13-oxylipins produced through the oxidation of linoleic and linolenic acids by lipoxygenases (LOX), along with the diffusible signalling factor 1 (DSF1, C14:1) and the plant hormone salicylic acid (SA). Interestingly, the bacterial load was similar in Xfp+ symptomatic and Xfp+ resilient trees, suggesting that lipid markers rely upon the sanitary status of the trees (Xfp+ vs Xfp-) notwithstanding their phenotype (symptomatic/resprouting). The identification of lipid biomarkers associated with infection could represent a valuable and innovative tool for Xfp diagnosis.

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P170 Exploiting the growth-defense tradeoff for crop protection: plant immune stimulation to fight herbicide resistant weeds

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A plant induced to defend itself sustains metabolic expenditure and antagonistic hormonal cross-talks that can negatively affect its growth and fitness ("growth-defense tradeoff"). With this study, we aimed to exploit this phenomenon to provide a new mechanism of herbicidal action. The study was carried out by using cerato-platanin (CP), a fungal protein elicitor known to activate PAMP-triggered immunity in *Arabidopsis thaliana* and *Platanus acerifolia*. Sensitivity to CP was assessed in important arable weeds by seedling-growth inhibition assays. CP-treated seeds from *Lolium multiflorum*, *Digitaria sanguinalis* and *Amaranthus hybridus* showed stunted seedling growth, revealing sensitivity to the protein. The dose-response assay performed in *L. multiflorum* with BSA as a control protein pointed to specific concentration-dependent activity by CP. Interestingly, CP reduced growth of *Lolium* spp. populations resistant to the herbicide pinoxaden, an acetyl-coenzyme A carboxylase (ACCase) inhibitor. In contrast, *A. palmeri*, *A. tuberculatus* and *Avena fatua* seedlings were not affected by the eliciting activity of the protein. Western-blot analyses showed absorption of CP by *L. multiflorum*, while gene expression results showed activation of defense responses. Wheat was used to assess off target effects on a crop: CP did not affect the growth of *Triticum aestivum* seedlings in our plate assays, and the Western-blot result suggested degradation of the protein by wheat seed proteases. Ongoing research aims to identify the epitope(s) of CP responsible for the eliciting activity. Preliminary results obtained with a series of CP-derived peptides suggest that *L. multiflorum* and *A. thaliana* perceive different (adjacent) regions of the protein.

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P171 Basalt dust for sustainable control of tomato bacterial speck disease.

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Copper is an active ingredient highly effective in controlling many plant pathogens, including bacteria. However, its ecotoxicological characteristics (persistence, toxicity and bioaccumulation) have prompted the European Commission to list them as candidates for substitution and reduce its use in agriculture. In addition, bacteria tolerance and resistance to copper has been documented. These evidences highlight the urgent need for sustainable alternatives. Basalt dust has shown promising effect in crop nutrition and plant protection. In this context, we investigated the effect of foliar application of the basal dust (Farina di Basalto® XF"; Basalti Orvieto s.r.l.) in controlling tomato bacterial speck disease caused by *Pseudomonas syringae* pv. tomato. The treatment significantly reduced disease symptom severity, encouraging further investigation to deepen the protection mechanisms. *In vitro* experiments, also performed by using confocal microscopy, suggested that basal dust exerts bacteriostatic effect. Moreover, *in planta* histochemical experiments demonstrated a strong callose apposition in the cell walls of treated tomato leaves. Since callose apposition is a marker of induced plant resistance common to different defence pathways, transcriptomic analyses are currently underway to identify the defence pathways activated by basalt treatment.

P172 Modelling and mapping the effects of seasonality and climate on the risk of infection by *Heterobasidion* spp. in conifer stands of Latvia

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Latvian conifer stands are threatened by *Heterobasidion* spp., fungal pathogens causing root rot and wood decay in association with relevant economic losses. Since *Heterobasidion* spp. infect their hosts via airborne basidiospores landing on the surface of freshly cut stumps, felling is a crucial step, eventually triggering the onset of infection foci. Indeed, the spread of *Heterobasidion* spp. via mycelial colonization of wood tissues is prompted by root contacts and grafts occurring among infected stumps and neighboring uninfected standing trees. Based on this premise, an effective strategy to reduce the risk of infection could be planning forest cuttings when/where the spore release by fruiting bodies of *Heterobasidion* spp. is expected to be low. Hence, the goal of this study was to build a spatial and temporal-explicit model to assess the risk of infection by *Heterobasidion* spp. in Latvia. A previously validated model predicting the sporulation levels of *Heterobasidion* spp. based on average temperatures and relative humidity was fed with the georeferred matrices of such climatic variables gathered/interpolated from the WorldClim dataset. A series of output maps predicting the risk of infection by *Heterobasidion* spp. were obtained. For each month of the year and season, the maps display with a spatial resolution of approximately 1km^2 the risk of infection rated from class 1 (low risk) to class 5 (critical risk). These maps provide Latvian forest managers with a practical tool to plan silvicultural operations and reduce the impact of *Heterobasidion* spp., as well as the related economic losses.

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P173 Beneficial *Bacillus-Trichoderma* consortium improves tomato resistance against fungal pathogens and drought stress

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Beneficial microbes (BM), including *Bacillus*, *Pseudomonas,* and *Trichoderma* spp., have emerged as sustainable solutions for disease management strategies in agriculture. Of particular interest is the potential of microbial consortia, which can offer synergistic benefits beyond those of individual strains. In this study, we tested several bacterial and fungal strains – either singly or in combination – previously selected for their biocontrol efficacy or growth-promoting effects on tomato plants (*Solanum lycopersicum* L. cv. Moneymaker). The most effective treatments in reducing plant mortality caused by fungal pathogens *Rhizoctonia solani* and *Fusarium oxysporum* f. sp. *lycopersici* (Fol) included the bacterium *Bacillus velezensis* PSE31B and the fungus *Trichoderma asperellum.* Moreover, PSE31B alone or in combination with *T. asperellum*, significantly enhanced tomato plant growth, chlorophyll content, and tolerance to water stress. Further experiments are currently in progress to elucidate the underlying mechanisms of biocontrol and water stress mitigation. Preliminary evidence revealed that PSE31B impairs fungal virulence by limiting Fol invasive growth *in vitro*, although this inhibitory effect was not associated with extracellular acidification. Ongoing metabolomic analyses of the BM liquid cultures aim to identify the main metabolites produced, putatively involved in biocontrol activity. Additionally, chemotropic assays using root exudates from inoculated plants are being conducted to assess whether these BMs may induce repellence towards fungal pathogens. Overall, this study underscores the potential of combining beneficial bacteria and fungi to mitigate both biotic and abiotic stresses in crops, while contributing to a deeper understanding of the mechanisms involved in the plant-microbe interaction.

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P174 Epidemiology of Fusarium Crown Rot on Durum Wheat in Southern Italy

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Fusarium Crown Rot (FCR) is an important worldwide wheat disease caused by a wide complex of *Fusarium* species, mainly the mycotoxigenic *F. culmorum*, and *F. pseudograminearum*, able to produce type B trichothecenes and zearalenone. The FCR is often underestimated, since its symptoms overlap with other fungal diseases. In addition, the fungal species distribution undergoes a continuous evolution influenced by the environmental factors, with the current climate crisis triggering modifications of usual profile of *Fusarium* species involved in FCR, in different geographical areas. This study aimed to investigate FCR epidemiology and distribution of FCR-causing *Fusarium* species in durum wheat, in the Southern Italy and the mycotoxigenic risk associated. A monitoring of FCR symptoms in 30 wheat fields located in 3 different regions of Southern Italy (Apulia, Basilicata and Campania) has been carried out in 2024. Sixty wheat plants in each field investigated, randomly selected following the W experimental design, were considered to assess FCR incidence and severity. FCR was observed in all monitored fields of Apulia (8-35%), Basilicata (2-18%) and Campania (12-22%) regions. However, disease severity was very low, with the highest value (20%) detected in a single field of Apulia region. In order to evaluate the *Fusarium* species distribution occurring on durum wheat in Southern Italy, 647 *Fusarium* strains isolated from crowns (313), stems (140) and heads (194) were molecularly identified. A great biodiversity of *Fusarium* species was observed with 20 species identified: *F. culmorum*, members of *Fusarium incarnatum-equiseti* species complex and *F. avenaceum* were the most occurring, counting for 63, 10 and 6% of the total identified species, respectively. Some of the less frequent *Fusarium* species detected were isolated from FCR symptoms for the first time, in Italy. A second year of field survey is ongoing to increase the set of data available.

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P175 A versatile all-rounder: unraveling the pangenome of *Bacillus velezensis* species

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Bacillus velezensis is an ubiquitous bacterial species composed of strains displaying various beneficial properties, ranging from the biological control of plant and animal pathogens to plant growth promotion and probiotic activities. Described first 20 years ago, recent genome-to-genome comparisons allowed to reclassify *B. methylotrophicus*, *B. amyloliquefaciens* subsp. *plantarum* and *B. oryzicola* as later heterotypic synonyms of *B. velezensis, thus* increasing the number of available genomes belonging to this species. To better understand the genomic background of the different strains of *B. velezensis*, we performed a pangenome analysis on 860 genomes using both publicly available and genomes isolated and sequenced in our laboratory. A total of 28801 orthologous gene families were found to compose the pangenome, with 2188 core genes. Interestingly, the use of ANI (Average Nucleotide Identity) & Mash distance allowed to predict 10 phylogroups within the species based on whole genome alignment. Principal coordinate analysis (PCoA) on gene presence/absence matrix further highlighted differences among *B. velenzensis* phylogroups. The in-depth characterization of the genomic clusters involved in the production of secondary metabolites revealed the presence of a core of clusters for the biosynthesis of bacillaene, bacillibactin, bacilysin, butirosin, difficidin, fengycin, macrolactin H and surfactin. Furthermore, we noticed differences among phylogroups, with phylogroup I displaying the lowest number of genomic clusters for secondary metabolite production, while plantazolicin- and bacillothiazol-related genes appeared as phylogroup-specific clusters. Altogether, this work provides a classification of *B. velezensis* strains, displaying common and specific features, associated with different functions, to target a specific category within the *B. velezensis* species for different aims, like biocontrol, plant-growth promotion or the production of probiotics.

P176 Metabolomic Profiling of Olive Leaves and Biofilms Formed by *Xylella fastidiosa* subsp. *Pauca*

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Xylella fastidiosa, a Gram-negative, xylem-limited bacterium, poses a severe threat to agriculture, causing significant economic damage worldwide, especially to olive trees in the Mediterranean region. This study investigated metabolomic differences in several olive genotypes that are susceptible/tolerant/resistant to *Xylella fastidiosa* subsp. *pauca* ST53. In addition, the characterization of biofilms produced by *X. fastidiosa* subsp. *pauca* is ongoing, aiming to define the structure of this self-produced matrix that adheres to inert or living surfaces.
Liquid and gas chromatography coupled to mass spectrometry (LC-MS and GC-MS) were employed to analyze metabolites extracted from olive leaves and *X. fastidiosa* biofilms. Biofilm composition and morphology were also analysed using Scanning Electron Microscopy with Energy Dispersive X-ray Spectroscopy (SEM-EDS), while Micro-Computed Tomography (Micro-CT) will be used to compare cultivars with varying susceptibility and resistance.
Leaf metabolomic analysis revealed significant differences across cultivars in fatty acids, carbohydrates, terpenes, flavonoids and their derivatives. Notably, the tolerant FS17 (Favolosa) cultivar showed 20 upregulated and 33 downregulated metabolites compared to the susceptible Ogliarola Salentina. Among the upregulated molecules was quinic acid, a precursor of ROS-scavenging compounds that protect plants from oxidative stress.
Biofilm analysis by GC-MS revealed differential abundance of fatty acids, carbohydrates, and diketopiperazines (DKPs), cyclic dipeptides known for their diverse biological activities and role in interactions with other microbes and plants.
These findings provide valuable insights into the *X. fastidiosa*-olive interaction and contribute to the development of targeted control strategies against this devastating pathogen.

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P177 Adaptive response of fitness-related traits under thermal stress in *Hymenoscyphus fraxineus* populations from the Italian peninsula

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The spread and establishment of non-native invasive species, including forest pathogens, are a consequence of global change. Among these, the invasive fungal pathogen *Hymenoscyphus fraxineus* is threatening native ash species (*Fraxinus* sp.) across Europe. In Italy, *H. fraxineus* was recently detected on *Fraxinus excelsior* along the Apennines, showing the ability to colonize Mediterranean habitats previously considered outside its optimal growth range. There is a knowledge gap regarding the adaptability and distribution of *H. fraxineus* in Italy, due to the fragmented presence of the host, especially in the south. The aim of this work is to characterize the population-level adaptive traits of *H. fraxineus* along the Italian peninsula, to study the phenotypic variability and the plastic response to different thermal conditions. Samples were collected from symptomatic *F. excelsior* along the distribution of ash populations and fungal strains were identified by nuclear and mitochondrial loci sequencing. The phenotypic responses were studied to assess optimal range and thermal stress tolerance by testing the mycelial growth of strains under heat and cold treatments. The results show a high variability of response under thermal stress conditions, highlighting the possibility of a greater expansion of the pathogen in the Mediterranean area. This study contributes to the understanding of possible adaptive responses of invasive fungal pathogens in the context of temperature fluctuations and could be useful for the development of prevention and forest management strategies, helping to conserve the richness of ash biodiversity at the southern edge of the natural distribution of the species.

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P178 Use of alfalfa extracts as sustainable biopesticides against tomato diseases

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The concept of sustainability in agriculture supports farming approaches able to ensure food security, without compromising long-term environmental health. The EU Directive 2009/128/EC aims to a sustainable use of pesticides by promoting the Integrated Pest Management with non-chemical alternatives. Phytochemicals from plants are increasingly appealing because of their potential as eco-friendly biopesticides. In this work, we describe the use of three alfalfa extracts, characterized for their bioactive compounds, that were tested for the control of some fungal and viral pathogens of tomato as well as for their potential nontarget effects on beneficial predatory mites. Flavonoids, saponins and prosapogenins were obtained from the aerial parts of alfalfa. Apigenin and chrysoeriol glycosides were the most abundant components of the flavonoid extract. The saponin fraction mainly contained bidesmosides of medicagenic and zanhic acids, whereas, upon alkaline hydrolysis, the prosapogenins were composed only of the relevant monodesmosidic compounds. In biological activity assays, *Alternaria alternata* and *Botrytis cinerea* cultures *in vitro*, whose medium was supplemented with prosapogenins, were effectively inhibited in the mycelial growth and conidia germination. The same mixture also showed *in vivo* control of alternariosis and grey mold in tomato: the dose-dependent trend indicated an antifungal activity exceeding the nutritional effect. The flavonoid mixture decreased the tomato spotted wilt orthotospovirus titer by 10^{-3}-fold one month post-inoculation. Toxic effects were not observed on two beneficial mites used as biological control agents, i.e., *Phytoseiulus persimilis* and *Amblyseius swirskii*. These results support the application of flavonoids and prosapogenins from alfalfa in biopesticide development programs.

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P179 *Phytophthora inundata*: a new report in commercial citrus orchards of the Mediterranean region

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Phytophthora diseases are a serious concern of citrus industry worldwide and resistance to Phytophthora root and foot rot has been an objective of most breeding programs of citrus rootstocks. In the Mediterranean region, *Phytophthora nicotianae* is the most common species responsible for this disease. Here, we report for the first time the detection of *P. inundata* on citrus in the Mediterranean region. This oomycete species was consistently isolated alongside with *P. nicotianae* from fine roots and soil of declining mature citrus trees in a commercial orchard in Sicily. The two species were identified on the basis of both morphological traits and multilocus phylogenetic analysis (ITS, β-tubulin, and COI). Pathogenicity tests on citrus saplings grafted on 'Carrizo' citrange rootstock and with the soil infestation method showed *P. nicotianae* was more virulent than *P. inundata*. The mean root damage class, as determined according to a scale from 4 to 0 (healthy control: 4; dead plant: 0) in saplings inoculated with *P. nicotianae* was 1.9 ± 0.5, while it was 2.1 ± 0 in saplings inoculated with *P. inundata*. Notably, co-inoculation of both species caused a more severe damage (1.2 ± 0.09), suggesting an additive interaction. Optimum temperature for mycelium growth of *P. inundata* was 25 °C while it was 30 °C for *P. nicotianae*. However the range of temperatures for active growth of both species largely overlapped. Overall, findings indicate *P. inundata* is a weak, opportunistic pathogen but under favorable environmental conditions, such as soil saturation, it may exacerbate root rot caused by the more virulent congeneric species *P. nicotianae*.

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P180 Evaluation of diagnostic sensitivity for *Xylella fastidiosa* detection in *Vitis vinifera* and *Prunus dulcis* across different seasonal sampling periods

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The spread of *Xylella fastidiosa* (Xf) in Europe has raised increasing concern not only for olive cultivation but also for other economically and environmentally relevant hosts. In recent years, the bacterium was detected in Tuscany and Lazio affecting *Prunus dulcis*, and more recently in Apulia, where *X. fastidiosa* subsp. *fastidiosa* (Xff) ST1 in grapevine and subsp. *multiplex* (Xfm) ST26 were detected on grapevine and almond, respectively. As molecular diagnostics play a central role in the surveillance and containment of Xf, there is an increasing need—particularly in asymptomatic plant—to assess their reliability across various plant host under different seasonal conditions. In this study, we evaluated the analytical sensitivity of four molecular methods, real-time PCR-Harper, digital droplet PCR (ddPCR-Dupas), tetraplex qPCR-Dupas, and qPCR-Hodgetts, for the detection and subspecies identification of Xff in grapevine and Xfm in almond. Plant matrices were spiked and collected across four seasonal time points. ddPCR demonstrated the highest sensitivity, consistently detecting Xf at concentrations as low as 10^2 cfu/g of plant tissue, regardless of matrix or sampling periods, with the exception of grape in July (10^3 cfu/g). qPCR methods showed greater variability (10^2-10^3 cfu/g) based on the test (Harper and Hodgetts better than Dupas) and on the sampling-period (May-July better than November-February). In conclusion, ddPCR emerges as the most robust and reliable diagnostic tool across all sampling periods and host matrices, accordingly with its resistance to PCR inhibitors that makes ddPCR particularly suitable for surveillance of plant host with low bacterial loads.

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P181 Virome analysis of 'old' citrus diseases using high-throughput sequencing

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Recent studies have identified novel viruses associated with "old" citrus virus diseases that have largely faded due to sanitation and certification programs initiated in Italy in the late 1970s, particularly those related to the psorosis complex. *Coguvirus citri*, linked to gummy bark concavity, and *Coguvirus eburi*, also detected in plants affected by impietratura, were only recently described. In this study, we performed a high-throughput sequencing (HTS)-based virome analysis in an old citrus orchard, predominantly grafted onto sour orange rootstock. Trees showed symptoms consistent with cristacortis (CRIS pool), psorosis (PSO pool), and exocortis (EXO pool). Although infection with *Closterovirus tristezae* had been previously documented, no symptoms specifically attributable to this virus were observed. Phylogenetic analysis of the assembled viral genomes revealed the presence of 'mild' isolates of *C. tristezae* across all three pools. Notably, to the best of our knowledge, this study reports for the first time the presence of *C. citri* (CRIS pool) and *C. eburi* (PSO pool) in Sicily. The detection of mild *C. tristezae* variants supports the hypothesis of a natural evolution of virus populations since the early 2000s, possibly involving natural cross-protection phenomena in groves still grafted on sour orange. These findings confirm the value of HTS as a powerful approach to unravel viral complexity and gain insights into virome evolution in perennial crop systems.

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P182 Multifunctional bacteria with biocontrol activity against *Phytophthora infestans* and PGP traits

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Abiotic stresses, including salinity, drought, and pH fluctuations, along with the increasing spread of phytopathogens, pose serious threats to plant health and crop productivity. In this scenario, microbial fertilizers containing plant growth-promoting bacteria (PGPB) play a crucial role in enhancing plant resilience and achieving higher yields, by influencing soil fertility through decomposition, mineralization, and nutrient storage/release mechanisms. In this study, the potential of straw digestate, mycorrhized *Quercus ilex* roots, and a peperino stone fountain, as sources of bacteria were investigated. The 21 bacterial isolates obtained belonged to eight genera: *Bacillus*, *Pseudomonas*, *Stenotrophomonas*, *Burkholderia*, *Acinetobacter*, *Aeromonas*, *Exiguobacterium*, and *Sphingobacterium*. The isolates were assessed for plant growth-promoting traits, biocontrol activity against *Phytophthora infestans*, and tolerance to abiotic stressors. Functional assays showed that 38% of strains produced indole compounds and solubilized phosphorus and/or potassium, key factors in stress adaptation. Over 80% produced lytic enzymes, with many also synthesizing siderophores and tolerating wide pH ranges. Notably, strains FONT1B, FONT3B, FONT5, and M3 exhibited multiple plant growth-promoting properties and strong anti-*P. infestans* activity. Functional differentiation among isolates from different environments suggests adaptive specialization and highlights their potential application as biofertilizers or biocontrol agents in sustainable agriculture.

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P183 Essential oils as a natural alternative to control post-harvest gray mold in kiwifruit: Efficacy and Mode of Action.

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Kiwifruit (*Actinidia chinensis spp.*) is a fruit highly demanded in the global market due to its nutritional and sensory properties, with a wide range of varieties now available to meet consumer preferences. However, its susceptibility to various postharvest pathogens poses a major challenge for its conservation and commercialization. Among them, *Botrytis cinerea*, the primary causal agent of gray mold, is responsible for significant losses during storage and transport. In this study, the *in vitro* antifungal activity of essential oils (EO) from oregano, cinnamon bark and clove buds was evaluated against *B. cinerea* through radial growth inhibition, spore germination, germ tube elongation, and fungicidal effect assays. For all but clove bud EO, a dose-dependent inhibition of radial growth was observed, as well as a fungicidal activity. To reduce EO effective concentrations, EO combinations were evaluated at various concentrations, identifying oregano/cinnamon bark as the most active in both radial growth inhibition and fungicidal capacity. Further, three formulations containing each EO were developed and applied in combination to kiwifruit berries, to evaluate their protective effect. Mechanistic studies were also conducted to explore EO mode(s) of action, assessing membrane permeability, cell viability and relative ion leakage. Finally, different parameters were assessed to ensure that EO-treatment does not affect fruit quality. Based on the results, it is possible to demonstrate that EOs could be an effective alternative strategy for the treatment of kiwifruit against *Botrytis cinerea*, with the goal of reducing postharvest economic losses but maintaining high fruit quality.

P184 *In vivo* interspecific competition among the main Fusarium head blight causal agents and the role of enniatins and deoxynivalenol in the interaction

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Fusarium head blight (FHB) is a damaging disease of wheat, caused by several *Fusarium* species. Multiple species can coexist within the same spike resulting in competitive dynamics. Their ability to produce secondary metabolites may influence these interactions. Due to the wide distribution of *Fusarium graminearum* (FG) and *Fusarium avenaceum* (FA), their main secondary metabolites, deoxynivalenol (DON) and enniatins (ENNs) respectively, commonly co-occur in grains. *Fusarium culmorum* (FC) and *Fusarium poae* (FP) are also frequently associated with FHB. This study investigated the interspecific competition among the main FHB agents and whether DON and ENNs influence their interactions. Three FA and two FG strains, either producers or non-producers of ENNs and DON respectively, along with one FP and one FC strain, were inoculated either singularly or in pairwise combinations on common wheat spikes. *Fusarium* spp. DNA was quantified by qPCR at 21 days post-inoculation, showing that the moderately aggressive FC strain reduced the abundance of FG, the most aggressive species. FC abundance was reduced by FG but also by the weaker FA strain. This last species abundance was reduced by FG and FC but increased by the co-presence of the weakest FP. Finally, the occurrence of ENNs or DON did not affect spike colonization by *Fusarium* species that co-existed with FA or FG. In conclusion, a competition was observed when two species coexisted and, in general, the species aggressiveness determined which species had advantage. ENNs and DON were not found to contribute to the competition among the different *Fusarium* strains tested.

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P185 *Bacillus velezensis* N3.2 as a potential biocontrol agent against *Xylella fastidiosa* subsp. *pauca* ST53

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Xylella fastidiosa subsp. *pauca* (*Xfp*) strain ST53 is a pathogenic bacterium responsible for Olive Quick Decline Syndrome, a serious threat to olive cultivation in the Mediterranean region. The lack of effective and sustainable control strategies makes the development of new biocontrol products urgent. Our study aimed to characterize for its activity against *Xfp* the biocontrol bacteria *Bacillus velezensis* strain N3.2, previously selected through *in vitro* screening. The antagonistic activity of *B. velezensis* N3.2 against *Xfp* was demonstrated in co-culture assays, along with the antimicrobial effects of its cell-free supernatants. Genome analysis on several biosynthetic gene clusters, to gain comprehensive insights on the biocontrol potential of strain N3.2, showed high similarity to known gene clusters associated with antimicrobial activity, induction of plant immunity, resistance to pathogens, plant growth promotion, and biofilm formation. Comparative genomics with other *B. velezensis* strains (i.e., FZB42, QST713 and D474), known for antagonistic activities against pathogenic fungi and bacteria, revealed that most biocontrol-related genes are conserved across all *B. velezensis* strains. However, some genes were found to be strain-specific. Notably, N3.2 strain appears capable of producing secondary metabolites with specific antimicrobial properties. Finally, to evaluate the effects of strain N3.2 on olive plant growth and its persistence within the plant, additional experiments in controlled conditions are underway. Preliminary results have demonstrated the endophytic behaviour of strain N3.2 and its persistence in the plant up to one year after inoculation. Our findings clearly indicate that *B. velezensis* N3.2 is a promising candidate for the control of *Xfp*.

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P186 *Colletotrichum perseae* and *C. gloeosporioides sensu stricto* Causing Stem lesion, Dieback and Fruit Rot on Avocado in Italy

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In the last decade, avocado production was increasing in Italy due to fruit high nutritional quality and high economic value. During 2024, new symptoms occurring on young plants after grafting in nursery and 2–3 months after transplanting were observed in eastern Sicily (Southern Italy). Disease incidence exceeded 45%, and symptoms included stem lesion, wood discoloration and dieback, often starting at the grafting point. *Colletotrichum*-like colonies were frequently isolated from symptomatic tissues. A total of 46 single-spore isolates were obtained and identified as belonging to the *C. gloeosporioides* species complex. Multi-locus phylogenetic analysis (loci: *gapdh*, *chs*, *act*, *tub*, *cal*, *gs* and ApMat) was conducted on 11 representative isolates, identifying 6 as *C. perseae* and 5 as *C. gloeosporioides sensu stricto (s.s.)*. Two isolates representative for *C. perseae* (APIN16) and *C. gloeosporioides s.s.* (APIN3), were selected for pathogenicity tests performed on wounded stem of 2-year-old avocado plants cultivated in greenhouse. After two months, both species induced necrotic lesions, wood discoloration and reddish-brown streaking at the inoculation point. Additional inoculations were carried out on wounded avocado fruit to demonstrate the ability of both species to cause symptoms on fruit. Both *C. gloeosporioides* and *C. perseae* caused fruit rot after 5 days. All inoculated fungi were successfully re-isolated and identified, completing Koch's postulates. This is the first report of stem lesion and dieback caused by *Colletotrichum* species and the first occurrence of *C. perseae* on avocado plants in Europe. The results highlight the importance of early detection especially in nursery during the propagation process.

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P187 Rapid detection of *Clavibacter michiganensis* subsp. *michiganensis* using LAMP in tomato seeds and plant tissues

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Clavibacter michiganensis subsp. *michiganensis* (Cmm), the causal agent of bacterial canker of tomato, is a major concern for seed and transplant production due to its ability to be seedborne and to establish latent infections that may persist for months without symptoms. The bacterium systemically colonizes the plant's vascular tissues, leading to progressive wilting and eventual plant death. In this study, we developed and validated a LAMP (Loop-mediated Isothermal Amplification) assay for the rapid and specific detection of Cmm in both tomato seed and fresh plant tissue. Furthermore, the amplification of an endogenous internal control ensures the success of the extraction and the reliability of the amplification step. Inclusivity and exclusivity were confirmed through testing on a broad panel of target and non-target bacterial species, respectively. For seed matrices, we compared DNA extraction protocols and assessed the assay's sensitivity using artificially contaminated seed lots with known percentages of infected seeds (0.1%, 1%, 10%). The assay was also validated on naturally contaminated field samples, demonstrating its applicability to routine testing scenarios. For plant tissue, an easy and rapid membrane-based sampling and extraction method was used, suitable for both laboratory and on-site diagnostics. The LAMP assay proved to be highly sensitive and specific in both matrices, enabling the detection of low pathogen loads in heterogeneous samples. These results support its potential use for phytosanitary surveillance, seed quality control, and rapid response in case of disease outbreaks.

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P188 Multifactorial Decline of Mediterranean Oaks in Southern Italy: Insights into Pathogen Interactions and Environmental Stress

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The decline of Mediterranean oaks, particularly *Quercus ilex* and *Quercus coccifera*, in the Salento area of Southern Italy has become a growing ecological concern. Affected trees exhibit leaf browning, canopy thinning, dieback, and branch loss. Two distinct syndromes have been identified: Chronic Oak Decline (COD), which is predominant in urban environments, and Acute Oak Decline (AOD), which is more frequent in rural areas. Environmental stressors—especially prolonged drought, increased temperatures, and soil imbalances—appear to play a critical role in exacerbating tree vulnerability and decline symptoms. Field and laboratory investigations, including qPCR and 16S rRNA sequencing, revealed the widespread presence of fungal pathogens such as *Diplodia seriata* across all study sites. More notably, bacteria associated with AOD, including *Brenneria goodwinii* and *Gibbsiella quercinecans*, were identified in symptomatic tissues of both *Q. ilex* and *Q. coccifera*. Pathogenicity tests confirmed their ability to induce wood necrosis and exudate formation, consistent with field symptoms, thereby validating their role in the decline process. These results strengthen the hypothesis that oak decline in Mediterranean environment is a multifactorial phenomenon involving the synergistic action of opportunistic fungi and emerging bacterial pathogens acting under climate-induced stress conditions. The detection of AOD-associated bacteria in new host species and a previously unreported geographic area highlights the urgency for proactive surveillance and integrated forest management strategies. Diagnostic approaches are crucial for mitigating the decline and preserving health and resilience of Mediterranean oak forests in the face of ongoing environmental changes.

P189 Monitoring *Erwinia amylovora* spread in apple orchards: development of a detection protocol from corbicular pollen

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Fire blight, a severe disease triggered by *Erwinia amylovora*, poses a substantial threat to apple production worldwide. As honeybees are key vectors of *E. amylovora*, we have developed a qPCR-based method for the early detection of the bacterium in corbicular pollen. Sterile pollen was artificially contaminated using a suspension of *E. amylovora* Ea21, a rifampicin-resistant strain, at concentrations ranging from 1×10^8 to 1 CFU/mL. Non-contaminated pollen served as the negative control. One gram of each inoculated sample underwent serial dilution and plating on Nutrient Agar supplemented with rifampicin to determine CFU counts. Simultaneously, 30 g of inoculated pollen was homogenised in 120 mL of 0.85% (w/v) NaCl with 0.001% (v/v) TWEEN®80 and kept on ice under orbital shaking (140 rpm). After one hour, samples were centrifuged to remove debris, and the supernatants were recovered and further centrifuged. Resulting pellets were resuspended in Tris-HCl buffer (pH 8) and subjected to thermal lysis. DNA was extracted using the DNeasy® mericon® Food Kit (QIAGEN) and analysed via qPCR, following EPPO Standard PM 7/20. To assess robustness, the method was applied to more than 200 corbicular pollen samples collected in 2022 and 2023 from Valsugana and Val di Non, two apple-growing locations in Trentino. Overall, the results showed that the developed detection protocol was significantly reliable. This protocol represents a promising early warning tool for the presence of *E. amylovora*, potentially enabling proactive fire blight management in apple orchards.

P190 Multispecies microbial consortia for improving growth and protection of tomato crops

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Biological control of plant diseases is a valuable strategy to reduce fungicide uses in agriculture. As innovation bioinspired by natural microbiomes, single microorganisms can be assembled into consortia to achieve synergistic effects in protecting plants against both biotic and abiotic stressors. This work presents pipelines for assembling microbial consortia by plant phenomics to characterize their performances on plants using a Plant Eye multispectral scanner. Tomato was used as the target crop of the study, which was conducted under both biotic and abiotic stress conditions, specifically infections caused by *Fusarium oxysporum* f.sp. *lycopersici* and *Sclerotium rolfsii*, as well as nitrogen and water deficiency. Three microbial multispecies consortia, each composed of a bacterial core, *Peribacillus* sp. C6, *Neobacillus* sp. TR12 and *Microbacterium* sp. TR9 combined respectively with *Trichoderma rifaii* PB1 (C1), PB3 (C2) and *T. harzianum* T2 (C3), were assayed for their ability to improve the fitness of potted tomato plants. The experiment followed a block design with 4 treatments per bench, each replicated five times across plots containing seven pots, totaling 140 potted plants per bench. Phenomics analysis indicated that C2 and C3 were effective in controlling, tracheofusariosis and Southern blight, respectively, while C1 showed a general efficacy against infections and nitrogen deficiency. The most positively correlated parameters with improved plant phenotypes were Digital Biomass, 3D Leaf Area, and Plant Height. On the contrary, PSRI and NPCI values were lower in effective treatments compared to the stressed control plants. Plant phenomics has the potential to innovate the assembly of microbial consortia.

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P191 Exploring Molecular Responses to Flavescence Dorée in Grapevine Cultivars and Rootstocks

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Flavescence dorée (FD) is a serious phytoplasma disease affecting grapevines, with different impact depending on cultivar susceptibility. Current management relies almost exclusively on chemical control of the insect vector, raising environmental concerns and highlighting the need for more sustainable and targeted strategies. A deeper understanding of the molecular responses activated in the plant upon infection could support the development of new approaches that reduce pesticide dependence. In this study, we investigated gene expression profiles in grapevine cultivars and rootstocks with different susceptibility to FD. Plants were infected under controlled greenhouse conditions, and transcriptional responses were analyzed to identify patterns associated with disease tolerance. Our findings revealed distinct activation signatures of genes encoding sugar transporters between more and less susceptible varieties, suggesting that the timing and intensity of defense-related responses play a key role in shaping disease progression. Notably, transcriptional changes related to sugar transporters were observed even before visible symptoms emerged, indicating that tolerant genotypes initiate key signaling and metabolic adjustments that may contribute to limiting infection. These insights advance our understanding of how grapevines respond to FD and point to potential molecular targets for breeding or biotechnological interventions aimed at enhancing resilience in viticulture.

P192 Survey of rotten hazelnut: an increasing phenomenon affecting kernel quality.

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Italian hazelnut production is mainly spread in the following regions: Piedmont (47%), Campania (36%), Lazio (30%) and Sicily (13%) (ISTAT 2021). A low incidence of kernel defects is one of the key characteristics used to evaluate hazelnut nut and kernel quality. In the last years a survey was conducted in a total of 9 hazelnut orchards in Campania and 7 orchards located in Piedmont. Sampling began at the end of March and covered several phenological stages: bud break/initial fruit formation (March–April), nut development (May–June), embryo and kernel development (late June–July), ripening nuts-harvest phase (August–September), and post-harvest sampling (September–October). A total of 23.460 hazelnuts were analyzed both from Campania (15.760 hazelnuts) and Piedmont (7.700 hazelnuts). The analysis carried out included fungal isolations from parts of hazelnuts on potato dextrose agar (PDA) plates and morphological and molecular analyzes to identify the fungal colonies present in the hazelnuts. Despite a limited incidence of rotten hazelnut several genera fungi such as *Alternaria alternata* complex., *Colletotrichum* spp., *Botryosphaeria* spp. and *Diaporthe*/*Phomopsis* spp. were isolated during this 4-year study. Moreover, during this survey *Eremothecium coryli*, causal agent of dry rot was isolated from nut damaged by the bug from both Piedmont (2017) and Campania (2019). In addition, a new fungus *Didymella corylicola* was consistently collected in early stage (March-April) in Campania orchards. Artificial inoculation tests with both individual fungal isolates and a mixture of fungi have not defined which is the primary pathogen of this rotten hazelnut.

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P193 Effects of forest fires on the stability of the soil microbiome: a network analysis approach.

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Forest soils host diverse microbial communities responsible for many essential ecosystem functions. However, their balance is increasingly threatened by forest fires, the frequency and intensity of which are increasing due to climate change. Indeed, fire has a profound impact on soil microbial communities, modifying their structure, reducing their diversity and compromising their ecological functions. In this study, through network analysis, we performed a comparative analysis of the stability of microbial networks between burnt and unburnt soils, identifying the key microorganisms for maintaining their stability. The ecological networks of burnt soils were found to be more vulnerable and subject to more rapid collapse than those of unburnt soils, reflecting a lower ecological stability of the post-fire communities; in contrast, the microbial networks of unburnt soils were found to be more resilient due to their more diverse composition. The results of this study contribute to our understanding of post-fire soil microbiomes, directly supporting soil management and conservation in fire-prone forest environments.

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P194 Preliminary evaluation of the tolerance of Italian and foreign olive cultivars to *Venturia oleaginea*

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Olive peacock spot is a common and significant problem in olive cultivation. Infection is usually associated with high humidity and winter conditions. In severe cases, infected trees show leaf defoliation, resulting in poor shoot growth and fruit setting, resulting in severe yield losses. This study evaluated the response to infection of different olive cultivars from the five countries involved in the international GEN4OLIVE project: Italy, Greece, Morocco, Spain and Turkey. The early diagnosis method, based on the observation of round black spots after immersion of adult leaves in a sodium or potassium hydroxide solution, was performed for two years, before spring, collecting asymptomatic leaves and quantifying the latent infection through an arbitrary scale expressed as a percentage. Based on the mean values obtained, the cultivars were grouped into four resistance classes: Highly Resistant (HR), Resistant (R), Moderately Susceptible (MS) and Susceptible (S). Cultivars such as Moraiolo and Coratina showed the lowest infection levels (HR class). Verdale and Gordal Sevillana were considered resistant (R), while Frantoio and Grappolo were classified as moderately susceptible (MS). On the contrary, Pendolino and Carolea showed high susceptibility and were assigned to the S class. ANOVA and post hoc tests confirmed significant differences between the classes. Although this diagnostic method detects the disease only if the pathogen is in an advanced stage of colonization, the results obtained contribute to the identification and selection of cultivars with higher levels of resistance to *Venturia oleaginea* and allow to optimize control strategies with targeted treatments before the onset of symptoms.

This work was supported by the european project "Mobilization of Olive GenRes through pre-breeding activities to face the future challenges and development of an intelligent interface to ensure a friendly information availability for end users"- GEN4OLIVE gen4olive.eu/it

P195 Isolation and molecular characterization of epiphytic fungi from olive trees in Calabria: preliminary results

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Olive phylloplane and carpoplane are characterized by a vast diversity of epiphytic fungi, some of which can positively affect plant physiology by promoting stress tolerance or inhibiting/suppressing pathogens. In this study, the epiphytic fungi from leaves and drupes of different cultivars grown in the world olive germplasm bank (WOGB) of CREA-OFA in Mirto-Crosia and Rende (Calabria region, Italy) have been isolated and molecularly characterized. Fungi were isolated from asymptomatic olive tissues, indicating their possible non-pathogenic nature. The plant samples were processed under sterile conditions and plated on Potato-Dextrose-Agar (PDA) and Nutrient Agar (NA) media. Morphologically different fungal colonies were isolated and purified, and microscopical characterization of fungal mycelia was carried out. Genomic DNA was extracted from each isolate and the internal transcribed spacer (ITS) regions of the rDNA were amplified and sequenced. Preliminary results showed that the composition and distribution of the fungal isolates differed markedly between the two sites, even within the same cultivar, suggesting that local climatic and geographical characteristics may strongly influence epiphytic fungal communities. The greatest number of fungi were isolated from the leaves, most of which were different from those found on the drupes. This preliminary work could contribute to the identification of epiphytic fungal strains and to evaluate their potential role in different applications areas, such as in the containment of phytopathogenic fungi.

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P196 First report of Grapevine Pinot Gris Virus in Sicily and rapid real-time reverse transcription loop-mediated isothermal amplification for its detection

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Grapevine Pinot gris virus (GPGV) is an emerging pathogen associated with grapevine leaf mottling and deformation, increasingly reported in major grape-growing regions worldwide, including Sicily (Italy). Although symptoms can be mild or absent, GPGV affects plant vigor, yield, and fruit quality. Its transmission through infected propagation material and possible presence in several non-Vitis hosts raise concerns about virus spread via asymptomatic plants. During spring 2024-2025, a total of 150 grapevine samples were collected from 5 vineyards in Trapani and Agrigento provinces and analyzed by RT-PCR developed by Bianchi and coworkers (2015). Seventy-eight samples (52.0%) resulted positive to GPGV. Moreover, it was developed and validated a real-time reverse transcription loop-mediated isothermal amplification assay, targeting a 130 bp fragment within the GPGV coat protein gene, coupled with a rapid and simple RNA extraction protocol. The assay's sensitivity and specificity were evaluated and compared with conventional and quantitative RT-PCR. To our knowledge, this study represents the first report of GPGV in Sicily. Moreover, the developed assay, associated with the rapid sample extraction method, offers a specific and efficient tool for a rapid on-site GPGV detection within 20 minutes, with no cross-reactivity to other grapevine viruses, supporting vineyard monitoring and management. In conclusion, this study provides a novel contribution to grapevine virus diagnostics in the Mediterranean basin, underlying the urgent need for official regulations to limit GPGV spread, particularly given its wide host range and asymptomatic infections.

P197 Optimization of laccase from *Trametes versicolor* for improving the aflatoxin B1 detoxification

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Laccase is an enzyme of general interest in biotechnology with potential in aflatoxin decontamination; however, the most active natural isoforms cannot provide the necessary efficiency to substantially benefit the industry. Previous research has focused on optimizing laccase through rational design or directed evolution. In the context of aflatoxin degradation, molecular docking has provided mechanistic insights, 3D structures analysis of different isoforms assessed interaction with aflatoxins, and mutational analysis explored beneficial changes. We employ laccase from *T. versicolor*, a fungal species whose ecological niche is tailored around laccase-mediated lignin degradation. Previous data from our lab indicates that performance improvement cannot be achieved by specializing laccase towards general categories of compounds (e.g. hydrocarbons, aromatic nonphenolic structures, or even aflatoxins as a category). We therefore performed an extensive, full quantum mechanical (QM) characterization on the entire isoform 2 of *T. versicolor* laccase (Uniprot accession number Q12718) structure bound to aflatoxin B1 (~7,000 atoms). We mechanistically characterized the role of single amino acid residues in interacting with aflatoxin B1 and identify theoretical variants expected to have better performance on aflatoxin B1. These laccase variants were then cloned and transformed into *Pichia pastoris*, expressed, purified, and tested for aflatoxin B1 detoxification. Results indicate that laccase affinity for the substrate was enhanced by replacing specific amino acids as predicted by the model's simulations. These findings confirm the prediction that π-π interactions are important for substrate binding, and corroborates the use of full QM models as an effective decision-making tool in designing laccase variants targeted at efficient aflatoxin detoxification.

P198 Investigating functional conservation of D effectors in soil-borne fungal pathogens

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Fungal pathogens secrete effector proteins to interfere with host immunity and enable colonisation. *Verticillium dahliae* (Vd) and *Fusarium oxysporum* (Fo) are soil-borne fungi with similar infection strategies but distinct host ranges. While Vd can infect numerous plant species, Fo strains are typically host-specific and classified into *formae speciales*. Some effector genes are conserved across these plant pathogens and contribute to virulence. One of them is the D effector, originally identified in defoliating Vd strains infecting cotton. Homologous genes have also been found in Fo, including *F. oxysporum* f. sp. *vasinfectum* (Fov) and *F. oxysporum* f. sp. *radicis-cucumerinum* (Forc), as well as in non-defoliating Vd strains. Previous functional assays using purified D protein homologs from these strains showed their ability to induce wilting symptoms in cotton, suggesting a conserved functionality. The D gene has been previously described as encoding a protein involved in mRNA processing, named TRADE. We investigated whether *Fusarium oxysporum* and *Verticillium dahliae* TRADE homologs induce similar effects on *Arabidopsis thaliana* as previously observed in cotton. To this end, we performed protein assays in 96-well plates, where *Arabidopsis* seedlings were grown on semisolid medium supplemented with purified effector proteins. This assay enabled the evaluation of protein-induced phenotypic changes during early seedling development. The observed effects were quantitatively measured and statistically analysed to assess their significance. Interestingly, while the TRADE effector from non-defoliating *V. dahliae* strains did not induce symptoms in cotton, it triggered a distinct phenotypic response in *Arabidopsis thaliana*, suggesting a potential host-dependent functionality of this conserved effector.

SESSION 6

Emerging Plant Pathogens and Epidemiological Trends

FLASH TALKS FROM "YOUNG RESEARCHERS IN TRAINING"

FT17 From observations to forecast: advancing aflatoxin risk prediction with seasonal climate projections

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Aflatoxin contamination in maize (*Zea mays*), primarily caused by *Aspergillus flavus*, is strongly influenced by environmental conditions. Predictive models have been developed to support contamination risk assessment and management strategies, typically relying on meteorological data from local weather stations. While these inputs offer high accuracy, their limited spatial coverage and lack of forecasting capability reduce their applicability for early warning systems and in-season decision support. This study investigates the integration of seasonal weather forecasts into AFLA-maize, a mechanistic model for predicting aflatoxin B1 contamination, with the aim of extending its temporal and spatial applicability. Forecast data, initialized at various points during the growing season, were evaluated for their influence on AFLA-maize performance and reliability. Bias correction techniques were applied to improve the accuracy of key input variables and align forecasts with observed trends. Preliminary results indicate that forecast-based simulations can provide contamination risk estimates 3-8 weeks before harvest, with reasonable alignment to historical patterns depending on the timing of forecast initialization. This refers to the point in the growing season when weather predictions are first generated. Early initializations offer extended lead time for decision-making but are associated with greater uncertainty, while later initializations improve forecast accuracy but limit the time available for intervention. Incorporating forecast ensemble members enables the representation of multiple plausible climate trajectories, accounting for uncertainty and improving the reliability of early warning outputs. This approach offers a promising advancement in aflatoxin warning systems, with potential application as decision-support tool for farmers to enhance climate resilient agricultural planning.

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FT18 Twig Canker and Shoot Blight of peach in Italy: the role of *Diaporthe amygdali* and a cultivars tolerance screening

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Prunus persica (peach) is a major fruit crop globally, with Spain and Italy leading production in the European Union. As environmental and regulatory pressures push to reduce synthetic plant protection products, managing diseases like twig canker and shoot blight (TCSB) becomes increasingly important. TCSB, caused by *Diaporthe amygdali*, leads to severe dieback of shoots, flowers, leaves, and branches, typically observed in late winter or early spring. Despite its damaging impact, comprehensive knowledge about the pathogen's biology and the susceptibility of different peach cultivars remains limited. This study aimed to improve understanding of *D. amygdali* by characterizing isolates collected from symptomatic peach trees in a key production area of Emilia-Romagna. Morphological and molecular analyses were conducted to confirm species identity, followed by *in vitro* evaluations of mycelial growth and conidial germination at various temperatures to define optimal growth conditions. To assess varietal susceptibility, 95 commercial and experimental peach genotypes were artificially inoculated with *D. amygdali*. Disease development was monitored, and lesion lengths were measured to compare genotypic responses. The findings offer insights into the thermal biology of *D. amygdali*, supporting future development of predictive models for improved disease management. Moreover, the susceptibility tests revealed significant variation among genotypes, with some showing promising tolerance traits. These initial results lay the foundation for further genetic and physiological studies aimed at identifying mechanisms of disease resistance. Such knowledge can contribute to breeding programs focused on developing new peach cultivars with improved resilience to TCSB, supporting more sustainable orchard management.

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FT19 The Role of EFSA Commodity Risk Assessments in Identifying High-Risk Plant Pathogens

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Under Regulation (EU) 2016/2031, the European Union (EU) established the concept of 'High-Risk Plants' in plant trade to regulate import of plants, plants products, and objects that could threaten plant health. The European Food Safety Authority (EFSA) conducts Commodity Risk Assessments (CRA) to evaluate the risk of introducing pests associated with these 'high-risk' commodities. Since 2019, EFSA has published 56 Scientific Opinions assessing over 53 plant species across agricultural, forestry, and ornamental sectors. Of 447 total pests selected, 36.7% were plant pathogens, resulting in 164 actionable pathogens (i.e., fungi, oomycetes, bacteria, viruses, viroids, and phytoplasmas), with fungi being the predominant group (52 different species). Notably, EU-regulated pathogens such as *Phytophthora ramorum* (EU quarantine pest), *Erwinia amylovora* (PZQP), and *Nepovirus lycopersici* (RNQP) were selected across multiple commodities. Several unregulated pests were also flagged as potential quarantine pests due to restricted EU distribution and likely impact. These include *Colespotium eupatorii* (never reported in the EU to date), five species belonging to the *Colletotrichum gloeosporioides* species complex, *Diplodia bulgarica*, *Lasidiplodia pseudotheobromae*, *Neoscytalidium dimidiatum*, *Pestalotiopsis microspora* and *Pyrrhoderma noxium*. Interesting, the recently identified *Phytophthora siskiyouensis* and *P. kernoviae* emerged as potential threats and deserve further assessments. EFSA's CRA plays a key role in supporting EU policy and identifying potential future risks for plant health. Additionally, by highlighting emerging threats and knowledge gaps, CRA fosters new research opportunities into the epidemiology, symptomatology, diagnostics and control of poorly understood potential quarantines pest, thereby advancing plant health science on a broader scale.

FT20 Unraveling the pathogenicity of *Pseudomonas syringae* pv. syringae Italian strains causing severe wilting in eggplants

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The present study is 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 DAPP-PG 773 strain to systemically infect this plant species as well.

ORAL PRESENTATIONS

OP32 *Trichoderma afroharzianum*, an emerging pathogen of maize in Europe: identification and early diagnosis

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Trichoderma afroharzianum, a fungal species traditionally used as a biocontrol agent (BCA) and plant growth promoter, was recently identified as an emerging causal agent of ear rot on maize (*Zea mays* L.), a key crop in Europe. It was first reported in Germany in 2018 and subsequently detected in France and Italy in 2020, where it was isolated from symptomatic maize ears and seeds. Laboratory inoculation trials confirmed its pathogenicity, demonstrating that infections can occur even in the absence of visible kernel injury. This is the first time a *Trichoderma* species was directly associated to a maize disease in Europe, leading to its inclusion in the EPPO (European and Mediterranean Plant Protection Organization) Alert List. Given the widespread cultivation of maize across EPPO-regulated regions, the emergence of *T. afroharzianum* poses significant concerns regarding the safe use of *Trichoderma*-based products in agriculture. Despite these findings, the epidemiology of *T. afroharzianum* remains poorly understood. Critical factors such as infection pathways, inoculum sources, and possible alternative hosts under field conditions must be studied. To support early detection and monitoring, we developed a species-specific real-time PCR assay targeting the *tef1-α* gene. This molecular tool enables rapid and sensitive identification of *T. afroharzianum* in both symptomatic and asymptomatic maize seed samples, facilitating early diagnosis, disease surveillance, and seed health certification. These findings highlight the ecological complexity of microbial interactions in agroecosystems and emphasize the importance of rigorous risk assessment protocols for microbial products in crop management.

OP33 Survey of *Neofabraea vagabunda* in Friuli Venezia Giulia Region: causal agent of apple bull's eye rot

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Neofabraea vagabunda is the causal agent of bull's eye rot symptoms in pome fruits. *Neofabraea* can infect fruits from petal fall to harvest time, with susceptibility gradually increasing during fruit ripening. However, bull's eye rot symptoms only manifest at the postharvest stage, thus posing a particularly challenging threat to postharvest management. However, there is considerable variation between and within fungal strains in the hosts colonization as well as the mycelial growth and sporulation, often connected to the optimal temperature, water activity (a_w) and the biochemical composition of the substrate. For all these reasons, we aimed to isolate, identify, and characterize a population of *N. vagabunda* strains currently found in Friuli Venezia Giulia Region. While all the 31 isolates were identified as *N. vagabunda*, these strains exhibited distinct morphological characteristics, indicating the presence of genetic variation within the species, influenced by environmental factors or host specificity. The most representative strains of the *N. vagabunda* population were characterised using *in vitro* and *in vivo* assays, together with genomic analysis. The biological response of *N. vagabunda* to different a_w conditions on different apple cultivars and at different incubation temperatures was investigated. Different a_w values and temperatures influenced the mycelial growth and conidial production of the strains. Furthermore, strains virulence on different apple cultivars at two storage temperatures was verified. The results obtained provided a general overview of the pathogenicity of the strains under varying storage conditions and apple varieties.

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OP34 Several *Phytophthora* species are associated with chestnut ink disease in Tuscany, central Italy

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A resurgence of ink disease is being observed in chestnut stands, with diffuse mortality of trees in both fruit orchards and coppice stands. Symptoms like stunted growth of branches and shoots, canopy desiccation, immature burrs and fruit development, and small-sized and yellowish foliage are often associated with root and collar rot and abundant production of a bluish-brown exudate from the basal portions of the trunk, suggestive of the disease long ascribed to *Phytophthora cambivora*. To better clarify the aetiology of the disease, a survey was conducted in various chestnut-growing areas in Tuscany characterised by different microclimates. The study included coastal areas, with a dry and arid climate for most of the year, inland hilly areas, with a mild climate, where chestnut stands are less exposed to thermal and drought stress, and Apennine foothill areas, cooler and with rainfall regimes distributed more evenly throughout the year. A total of 128 samples were collected from necrotic wood/root tissue and soil at the base of symptomatic chestnut trees, with specimens taken from 60 trees. Laboratory isolations revealed the occurrence of several *Phytophthora* morphotypes. Representative isolates were ascribed to *P. cambivora*, *P. plurivora*, *P. cinnamomi*, *P. pseudosyringae*, *P. castanetorum* and *P. gonapodiydes* on the basis of colony phenotypes, micro-morphological characteristics and DNA sequence data (rDNA-ITS and mtCoxI regions). Investigations into physiological parameters (minimum, maximum and optimal growth temperatures) and pathogenicity tests are underway to clarify the role of each of these oomycetes in the decline of chestnut stands.

OP35 Emergence of Acute Oak Decline in Mediterranean holm and kermes oaks: detection of bacterial pathogens and ecological considerations

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The decline of holm oak (*Quercus ilex* L.) in the Mediterranean region is emerging as a critical concern due to the increasing incidence of Acute Oak Decline (AOD). A distinct variation in symptom expression was observed between urban and rural habitats: urban trees showed mostly crown decay and insect infestations, in particular by *Kermes* spp. and *Nidularia* spp., while rural trees showed typical AOD symptoms, such as longitudinal bark fissures oozing dark exudates, insect emergence holes and larval galleries attributable to Buprestidae beetles. Molecular analyses confirmed the presence of three bacterial species associated with AOD, but only in rural tree samples, such as: *Brenneria goodwinii*, *Gibbsiella quercinecans* and *Rahnella victoriana*. *B. goodwinii* and *G. quercinecan* were also found in symptomatic *Quercus coccifera* L. (kermes oak) plants, highlighting the potentially at-risk health status of the oaks in the Apulian territory. Phylogenetic comparisons revealed a high genetic similarity between the isolated strains and those previously identified in Europe and Iran, supporting the hypothesis of transregional spread via vector insects or infected plant material. These results underline the importance of biotic and abiotic factors, such as water stress and soil degradation, in determining disease dynamics. Continuous monitoring and comprehensive ecological assessment are essential to manage the progression of AOD in Mediterranean forest systems.

OP36 Advances in understanding genomic diversity and adaptive evolution of the plant pathogenic model system Colletotrichum.

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The genus *Colletotrichum* includes a diverse group of organisms, ranging from plant pathogens and epiphytes to saprobes and opportunistic human pathogens. One of the major challenges in studying *Colletotrichum* lies in the reliability of historical taxonomic classifications. In recent decades, the genus has undergone significant revisions based on morphological characteristics and molecular approaches, including single-locus analysis and multi-locus sequence typing (MLST). Despite these efforts, several lineages remain unresolved, and standard BLAST searches against public databases such as nr/nt often fail to accurately assign taxonomic identities to newly isolated strains. By integrating whole-genome sequencing and bioinformatic tools, this study aims to: (1) clarify and update the taxonomy of *Colletotrichum* spp. according to current criteria; (2) develop a curated secondary database combining MLST and WGS data to enable accurate characterization of newly isolated *Colletotrichum* strains; and (3) establish a user-friendly, cost-effective protocol for reliable species identification. Leveraging metadata - such as host species, geographic location, and date of isolation - from both our curated database and European culture collections, we will also generate a comprehensive overview of the geographical and temporal distribution of *Colletotrichum* spp. in crop and non-crop hosts across the EU. In doing so, we aim to re-evaluate and reassign historical records under the updated taxonomic framework. Overall, this study will facilitate a much-needed taxonomic revision of the genus *Colletotrichum* and provide key insights into its occurrence, distribution, and host association patterns through the lens of genomic diversity and adaptive evolution.

OP37 Apple Bitter Rot and Glomerella Leaf Spot: Diversity and Tissue-Specific Behavior of *Colletotrichum* spp. in Northern Italian Orchards

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Apple bitter rot and Glomerella leaf spot are major pre- and post-harvest apple diseases caused by *Colletotrichum* spp. In Europe, bitter rot has normally been associated with species from the Acutatum complex; however, members of the Gloeosporioides complex have recently been increasingly linked to fruit decay and defoliation. This study aimed to investigate the diversity, pathogenicity, and tissue-specific behavior of *Colletotrichum* spp. Around 700 isolates were collected from symptomatic fruits and leaves in orchards across Italian regions Emilia-Romagna, Veneto and Trentino-Alto Adige, identified within the Acutatum, Gloeosporioides, and Orchidearum complexes through multi-locus sequencing. *C. chrysophilum* was the most prevalent, followed by *C. fioriniae*, *C. siamense*, *C. grossum* and *C. sojae*. Pathogenicity tests on 'Gala' apple fruits and leaves revealed *C. siamense* as the most aggressive species, followed by *C. grossum*. *C. sojae* was non-pathogenic on fruits and caused lesions only on wounded leaves. Conidial germination and appressorium formation were evaluated on different tissues and cultivars at room temperature and under thermal gradients. *C. chrysophilum* showed the highest germination overall and appressoria rate on leaves. In contrast, *C. siamense*, *C. grossum*, and *C. fioriniae* exhibited higher germination and appressoria rate on fruits, with *C. siamense* as the most aggressive. Temperature trials revealed optima at 30–35 °C for *C. siamense* and *C. grossum* and around 15 °C for *C. fioriniae*, while *C. chrysophilum* maintained high germination across all temperatures. These findings enhance understanding of *Colletotrichum* composition and epidemiology, supporting improved disease management strategies under changing climatic conditions.

OP38 Drought is a key factor exacerbating the virulence of emerging pathogens of London plane trees (*Platanus x hispanica*)

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Sudden diebacks and mortality of London plane (*Platanus* × *hispanica*) were observed and monitored at two sites in Northern Italy over multiple years. This study aimed at assessing: I) if the observed decline was associated with putatively emerging fungal trunk pathogens; and II) whether their virulence could be enhanced under drought stress. A total of 76 plane trees were inspected for decline symptoms. Fungi were isolated from symptomatic tissues and identified through morphological and molecular diagnostic assays. In total, 1352 fungal isolates were obtained and assigned to 24 species. *Botryosphaeriaceae* was the most represented family (51% of isolates), followed by *Diaporthaceae* (11%). The most frequently isolated fungal species was *Neofusicoccum parvum*. Interestingly, the causal agent of canker stain of plane trees *Ceratocystis platani* was never detected. Pathogenicity tests on healthy London planes revealed that 60% of *Neofusicoccum parvum* isolates induced necrotic lesions of varying size ($P < 0.05$). Additional tests were conducted under two irrigation regimes for five *Botryosphaeriaceae* (including *N. parvum*) and *Seiridium aquaticum*. *Diplodia mutila*, *Lasiodiplodia theobromae*, and virulent *N. parvum* isolates were pathogenic regardless of irrigation regime. However, average lesion areas on inoculated stems were significantly and up to 200-fold larger (P>0.05) on drought-stressed trees than on those regularly irrigated. Results highlight the role of emerging fungal trunk pathogens in the onset of decline in plane trees, with drought acting as a key factor exacerbating their virulence. Such pathogens, affecting also a plane cultivar resistant to *C. platani*, may pose a serious threat to plane trees under climate change scenarios.

OP39 New insights on the role of oospores in primary infections and seasonal dynamics of downy mildew

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In the last seasons, severe outbreaks of *Plasmopara viticola* have been observed in early season, leading to significant yield losses; this renewed the focus on the role of oospores and the resulting primary infections. Moreover, the increasing trend toward a reduction of fungicide use, induce growers to stop the downy mildew (DM) control early in the season, leaving new leaves from lateral shoots poorly protected, with a consequent abundant production of oospores. Recent research has demonstrated that the season-after-season production of oospores form an oospore pool in the vineyard ground, which consists of three components: leaf litter above the soil (from the affected leaves of the season); fragmented and decomposed leaf residue into the soil; and the soil. Depending on the component, the oospores may vary in numbers, age, and viability, and experience different environmental conditions that influence their germination dynamics. A clear relationship was found between the proportion of affected leaves in fall, the number of oospores into the vineyard pool, and the severity of primary infections, demonstrating that the concept of epi-season is valid for DM, with a legacy from the previous and the current season epidemics. The oospores' pool maturation and germination follow a progressive seasonal dynamic, modulated by environmental conditions, and these processes occur in synchrony with grapevine phenology. These findings have been integrated into a new mathematical model that makes it possible to estimate the role of oospores in DM epidemics under different scenarios, which provides a valuable tool to inform disease management strategies.

OP40 New insights on mycotoxigenic *Aspergillus* species on peach fruits in Southern Italy

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Peach fruits are largely cultivated in Southern-Italy, with part of them intended to produce fruit-based products for infants. Recently, climate change is driving the spread of xerophilic *Aspergillus* species in many crops in Southern Europe and the maximum limits of Aflatoxins (Afs), the most dangerous carcinogenic compounds produced by *Aspergillus* species, have been established also in fruit products intended for baby diet. This study aimed to monitor the presence of *Aspergillus* species and AFs on peach in field and in post-harvest conditions. Twenty commercial orchards, located in Southern-Italy were monitored at blossom, veraison and ripening stages, and environmental data were also monitored. Several fungal species, including *Aspergillus*, *Alternaria*, *Penicillium*, *Cladosporium, Aureobasidium* and *Pichia* species were detected. A very few *Aspergillus* strains were isolated from flowers, while a higher frequency was observed on fruits (more than 50% of sampled fruits), with an increasing occurrence when warmer climatic conditions occurred. Sixty-seven *Aspergillus* strains were considered for molecular and chemical characterization. Based on ITS and Betatubulin sequence analyses, the strains were grouped in *Flavi*, *Terrei*, *Circumdati* and *Versicolores* Sections. The capability of these strains to produce Afs was investigated by HPLC. Thirty-two out of 67 strains produced AFs, with values ranging from 2 to 7895 µg/kg. Furthermore, to assess the natural Afs contamination of peach fruits and the potential toxicological risk, 40 samples of peach-puree, obtained from sampled fruits, were analysed. Only three samples showed Afs contamination with values of 2, 13 and 17 µg/kg, respectively. This is the first report of the occurrence of different aflatoxigenic *Aspergillus* species and AFs on peach fruits in Southern-Italy.

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