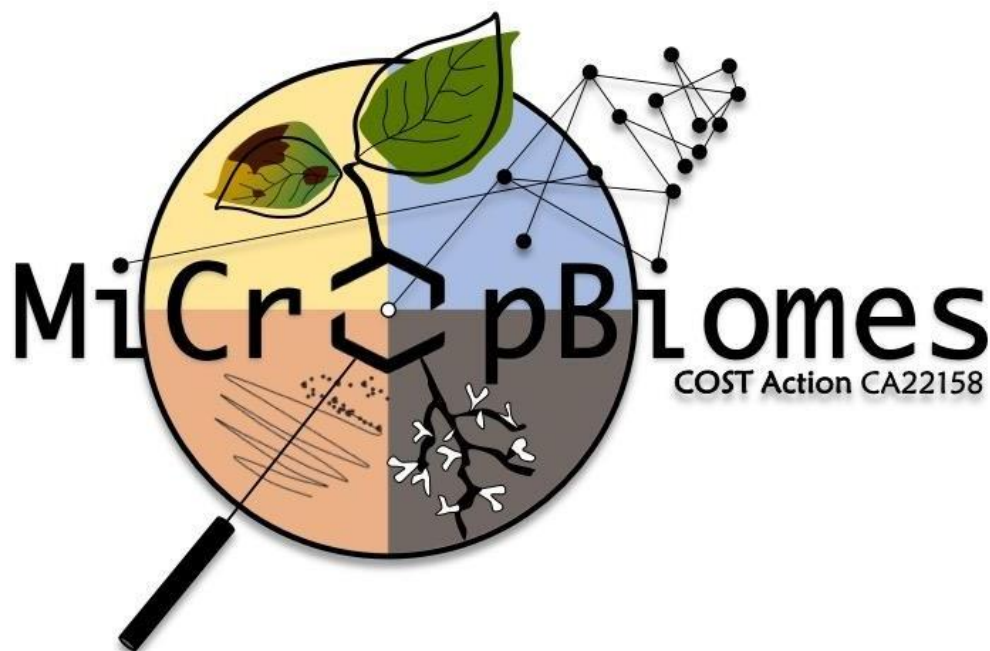
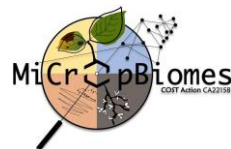


3RD ANNUAL CONFERENCE
OF THE

MiCropBiomes COST Action

Belgrade 3 – 5 June 2026



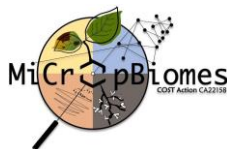


Conference Overview

Registration: Wednesday 8:15 – 9:00 am

Welcome: Friday 9:00am – 9:30 am

Wednesday 3 rd June	Thursday 4 th June	Friday 5 th June
9:30 – 10:30 Session 1 Exploiting Plant-Microbiome molecular crosstalks: diversity, distribution and eco-evolutionary perspectives	9:00 – 10:15 Session 4 From current microbial inoculants to synthetic communities	9:00 – 11:00 Working group meetings (WG1 - WG5)
Break	Break	Break
11:00 – 12:00 Session 1 Exploiting Plant-Microbiome molecular crosstalks: diversity, distribution and eco-evolutionary perspectives	11:00 – 12:00 Session 4 From current microbial inoculants to synthetic communities	11:30 – 12:00 Glossary/Terminology Session
		12:00 – 13:00 Education Task Force workshop
Lunch	Lunch	Lunch
13:30 – 14:45 Session 2 Crop microbiomes and plant diseases: from dysbiosis to increased defenses	13:30 – 15:00 Session 5 Crop-Microbiome assembly dynamics under specific environments	14:00 - 16:00 Management Committee Meeting
Break	Break	
15:15 – 16:00 Session 2 Crop microbiomes and plant diseases: from dysbiosis to increased defenses	15:30 – 16:30 Session 5 Crop-Microbiome assembly dynamics under specific environments	
16:00-17:30 Session 3 Communication, and engagement with society		
17:30 - 18:30 Poster session 1	16:30 - 18:00 Poster session 2	
20:00 Welcome cocktail Botanical Garden "Jevremovac"	19:30 Cruise on the Sava and Danube rivers	20:00 Dinner at Skadarlija



Local organizers

Ivan Nikolić	University of Belgrade - Faculty of Biology, Serbia
Tanja Berić	University of Belgrade - Faculty of Biology, Serbia
Slaviša Stanković	University of Belgrade - Faculty of Biology, Serbia
Jelena Lozo	University of Belgrade - Faculty of Biology, Serbia
Olja Medić	University of Belgrade - Faculty of Biology, Serbia
Iva Rosić	University of Belgrade - Institute of Physics, Serbia
Marina Sokić	University of Belgrade - Institute of Physics, Serbia
Ivana Marić	University of Belgrade - Institute of Physics, Serbia

Scientific committee

Conceição Santos	University of Porto, Portugal
Francesco Spinelli	University of Bologna, Italy
Ahmed Abdelfattah	ATB, Germany
Ellodie Vandelle	University of Verona, Italy
Joël Pothier	Zurich University of Applied Sciences, Switzerland
Anna Bonaterra	University of Girona, Spain
Caroline De Tender	Ghent University, Belgium
Gabriele Berg	TU Graz, Austria
Gordana Racić	Research and Development Institute Tamiš, Serbia
Renata Artimová	Institute of Forest Ecology, Slovakia
Claire Prigent-Combaret	University of Lyon, France
Ralf Koebnik	IRD, Montpellier, France
Tanja Berić	University of Belgrade, Serbia
Ivan Nikolić	University of Belgrade, Serbia

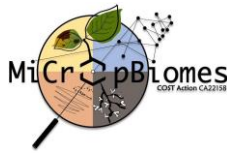


Table of Contents

Scientific Program

Session 1: Exploiting Plant-Microbiome molecular crosstalks: Diversity, distribution, and eco-evolutionary perspectives

Session 2: Crop microbiomes and plant diseases: From dysbiosis to increased defenses

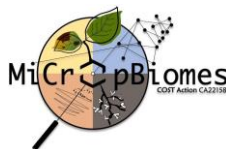
Session 3: Communication and engagement with society

Session 4: From current microbial inoculants to synthetic communities

Session 5: Crop-Microbiome assembly dynamics under specific environments

Posters

List of Participants



Scientific Program

Wednesday 3rd of June

08:15 – 09:00 Registration

09:00 – 09:30 Opening & Welcome by the organizers

Session 1 Exploiting Plant-Microbiome molecular crosstalks: Diversity, distribution, and eco-evolutionary perspectives

Chair: Ahmed ABDELFATTAH

Invited lectures

09:30 – 10:00 Jelena Lozo (University of Belgrade - Faculty of Biology, RS): The role of the type III secretion system in plant beneficial bacteria

10:00 – 10:30 Wisnu Wicaksono (Institute of Environmental Biotechnology, Graz University of Technology, AT): The Importance of Microbial Diversity Across Systems for Functional Stability and Resilience

10:30 – 11:00 Coffee Break

Oral Presentations

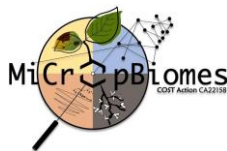
11:00 – 11:15 Daniel Hoefle (Leibniz Institute for Agricultural Engineering and Bioeconomy, DE): Fruit function beyond dispersal: effect of fruit decomposition on the plant microbiome assembly

11:15 – 11:30 Alexandra Pál (HUN-REN Biological Research Centre, HU): The *Medicago truncatula* nodGRP3C peptide is essential for proper bacteroid differentiation and symbiotic nitrogen fixation

11:30 – 11:45 Manikandan Ariyan (University of Tartu, EE): Plant phylogeny and mycorrhizal strategy shape multi-kingdom soil community assembly in a common garden experiment

11:45 – 12:00 Discussion

12:00 – 13:30 Lunch



Session 2 **Crop microbiomes and plant diseases: From dysbiosis to increased defenses**

Chairs: Joël F. POTHIER and Renata ARTIMOVÁ

Invited lecture

13:30 – 14:00 **Davide Bulgarelli (University of Dundee, UK):** Root immune receptors as drivers of the rhizosphere microbiota

Oral Presentations

14:00 – 14:15 **Elisenda Castellet Godall (IRTA Cabrils, ES):** Rootstock-Dependent Microbial Associations in the Root Microbiome in Response to *Armillaria mellea* soil-borne pathogen

14:15 – 14:30 **Dóra Krisztina Balázs (Institute of Biology, Faculty of Science and Informatics, University of Szeged, HU):** New peptides for the future biological plant protection - comprehensive investigation of peptaibiotics produced by *Trichoderma* species

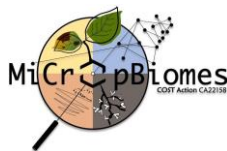
14:30 – 14:45 **Ivana Potočník (Institute of Pesticides and Environmental Protection, RS):** Microbial inoculants in cultivated mushrooms: interactions, disease control, and yield promotion

14:45 – 15:15 Coffee break

15:15 – 15:30 **Bojana Živanović (Institute for Multidisciplinary Research, University of Belgrade, RS):** Impact of *Bacillus velezensis* RD-FC 88 on the primary and secondary metabolism of cabbage cv. Futoški during infection with *Xanthomonas campestris* pv. *campestris*

15:30 – 15:45 **Maria-Dimitra Tsolakidou (Cyprus University of Technology, CY):** Linking soil management to microbiome-mediated suppressiveness against *Fusarium* wilt in tomato systems

15:45 – 16:00 **Anže Vozelj (National Institute of Biology, SL):** A novel potato endophytic *Fusarium oxysporum* isolate with disease-suppressive activity: genomic and biological characterization



Session 3

Communication and engagement with society

Chair: Ivan Nikolić

Invited lecture

16:00 – 16:30 **Bogdan Žigić (Biofor Systems Ltd, RS):** Microbiological soil analysis in the function of leading and understanding sustainable soil fertility

Oral Presentations

16:30 – 16:45 **Marina Arnaut Stefanović (Foodscale Hub, RS):** Dissemination, Exploitation and Communication in Horizon Europe Projects - Examples of Good Practice

16:45 – 17:00 **Marija Nedeljković (University of Belgrade - Faculty of Biology, RS):**
MICROPOLIS: A strategic board game for communicating microbiology

STSM shared experience

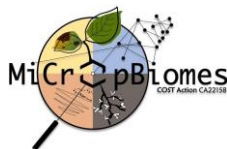
17:00 – 17:10 **Aleksandra Mesaroš (University of Belgrade - Faculty of Biology, RS):** The role of HCN-producing endophytes in improving the stress resistance of potatoes (STSM3)

17:10 – 17:20 **Lama Ramadan (Gebze Technical University, TR):** Exploring the power of seed microbiome to improve crops tolerance against drought (STSM6)

17:20 – 17:30 **Monika Faruga (Intermag z o.o., PL):** Transfer of Academic Knowledge on Bioreactor Methods for the Optimization of bacterial cultivation for bioproducts that support the plant microbiome (STSM4)

17:30 – 18:30 **Poster session 1**

20:00 **Welcome cocktail Botanical Garden “Jevremovac”**



Thursday 4th of June

Session 4 From current microbial inoculants to synthetic communities

Chairs: Anna BONATERA and Claire PRIGENT-COMBARET

Invited lecture

09:00 – 09:30 Marie Simonin (Institute Agro, INRAE, IRHS, SFR QUASAV, Université d'Angers, FR): Towards Plant Microbiome Engineering: Exploring Seed Microbial Diversity and its Impact on Plant Fitness using Synthetic Communities

Oral Presentations

09:30 – 09:45 Zisis Vryzas (Aristotle University of Thessaloniki, GR): European and international approaches to the approval of microbial inoculants and synthetic communities as biopesticides, biofertilizers and biostimulants

09:45 – 10:00 Luis Alejandro Moll Dos Santos (Institute for Sustainable Agriculture, ES): Rational assembly of Bacterial Synthetic Communities (SynCom) for the management of olive vascular diseases

10:00 – 10:15 Discussion

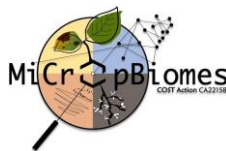
10:15 – 11:00 Coffee Break

11:00 – 11:15 Izzah Shahid (Universidad Pública de Navarra, ES): Metabolomic and genomic characterization of antifungal *Pseudomonas chlororaphis* strains for designing plant beneficial SynComs

11:15 – 11:30 Martin Stražar (National Institute of Biology, SL): Characterisation of potato microbiota for design of successful potatobiome communities

11:30 – 11:45 Daniele Nicotra (University of Catania, IT): Synthetic communities of core native bacteria induce rhizosphere microbiome restructuring in tomato

11:45 – 12:00 Discussion



12:00 – 13:30 Lunch

Session 5 **Crop-Microbiome assembly dynamics under specific environments**

Chairs: Elodie Vandelle and Gordana Racić

Invited lecture

13:30 – 14:00 **Jacob Malone (John Innes Center, UK):** How Pseudomonas interact with plant roots, and why it matters

Oral Presentations

14:00 – 14:15 **Elodie Vandelle (University of Verona, IT):** Exploring Rhizosphere Microbiomes in Mediterranean Vineyards through Metabarcoding analysis: insights from Italy, Portugal, Morocco, and Turkey

14:15 – 14:30 **Olja Medić (University of Belgrade - Faculty of Biology, RS):** Grapevine bacterial communities are shaped by compartment, phenology, and herbicide management

14:30 – 14:45 **Pablo Vargas (IRTA, ES):** Age-Driven Assembly of Root-Associated Bacterial, Fungal, and Arbuscular Mycorrhizal Communities in Almond Rootstocks

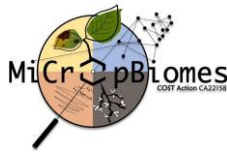
14:45 – 15:00 Discussion

15:00 – 15:30 Coffee break

15:30 – 15:45 **Iva Rosić (Institute of Physics Belgrade, RS):** Bacillus velezensis SS-38.4 as a preventive biocontrol agent in sugar beet phyllosphere

15:45 – 16:00 **Kamila Bokszczanin (Warsaw University of Life Sciences, PL):** Organic and inorganic mulching drive distinct and persistent rhizosphere microbiomes in Malus × domestica orchards

16:00 – 16:15 **Ghita Ammechante (Mohammed VI Polytechnic University, MA):** Extreme salinity overrides host specificity in plant-associated microbiomes in Moroccan Sabkhas



16:15 – 16:30 Discussion

16:30 – 18:00 **Poster session 2**

19:30 **Cruise on the Sava and Danube rivers**

Friday 5th of June

09:00 – 11:00 **Working group meetings (WG1 - WG5)**

11:00 – 11:30 Coffee break

11:30 – 12:00 **Glossary/Terminology Session**

Chairs: Juraj MEDO, Joël F. POTHIER and Renata ARTIMOVÁ

12:00 – 13:00 **Education Task Force Session**

Chair: Lara Amorim

13:00 – 14:00 Lunch

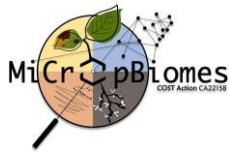
14:00 – 16:00 **Management Committee Meeting**

Chair: Conceição Santos

20:00 **Dinner at Skadarlija**

Poster session 1, Wednesday 3 June, 17:30 - 18:30h (A0 Portrait, 84.1 cm × 118.9 cm)		
P1.1	Melike Bakır, Erciyes University, TR	Exploring Indigenous Mesorhizobium ciceri Diversity in Semi-Arid Soils: Implications for Chickpea–Microbiome Interactions
P1.2	Irena Budić-Leto, Institute for Adriatic Crops and Karst Reclamation, HR	Indigenous Mycobiota of Maraština Grapes: Effects of Vineyard Location and Environmental Factors on Community Composition
P1.3	Igor Vukelić, Institute of Field and Vegetable Crops, RS	Early transcriptional responses of tomato cultivars to <i>Trichoderma harzianum</i> under short-term water deficit
P1.4	Iglė Vepškaitė-Monstavičė, State Scientific Research Institute Nature Research Center, LT	Characterization of pears' carposphere-associated fungal microorganisms
P1.5	Denis Gunia, Leibniz-Institut für Agrartechnik und Bioökonomie, DE	Regional and Management-driven Variation in Apple Microbiome and Resistome
P1.6	Juliana Lukša-Žebelović, State Scientific Research Institute Nature Research Center, LT	Where resistance hides and emerges: linking cultivable bacteria and environmental resistomes across pasture microbiomes
P1.7	Aleksandra Mesaroš, University of Belgrade - Faculty of Biology, RS	Hydrogen cyanide-mediated modulation of drought stress responses in pepper by <i>Pseudomonas urmiensis</i> A32
P1.8	Marija Nedeljković, University of Belgrade - Faculty of Biology, RS	Sugar-mediated modulation of Type III secretion system gene expression in <i>Pseudomonas marginalis</i> OL141
P1.9	Marija Anđelković, University of Belgrade - Faculty of Biology, RS	Comparative genomic characterization and functional potential of five plant-associated <i>Pseudomonas</i> strains from pepper and sugar beet
P1.10	Tamara Ranković, University of Belgrade - Faculty of Biology, RS	Comparative analysis of the type VI secretion system gene repertoires in <i>Pseudomonas putida</i>
P1.11	Gergő Terna, University of Szeged, Institute of Biology, HU	Sequence homology of peptaibiotics produced by <i>Trichoderma</i> species in the phylogenetically distant <i>Polysporum</i> and <i>Longibrachiatum</i> clades
P1.12	Hira Ikram, University of Modena and Reggio Emilia, IT	Bioremediation and restoration of a beneficial microbiota in a walnut grove through the input of different biofertilizers
P1.13	Duska Delić, University of Banja Luka, Faculty of Agriculture, BA	Seed microbiome signatures and their influence on early plant growth: A comparative study of <i>Lathyrus sativus</i> and <i>Phaseolus vulgaris</i> from the Western Balkans
P1.14	David Gramaje, Institute of Grapevine and Wine Sciences, ES	From dysbiosis to defense collapse: a pathobiome view of grapevine esca under abiotic stress
P1.15	Marina Sokić, University of Belgrade - Institute of Physics, RS	<i>Pseudomonas syringae</i> phylogroup 2 strains from irrigation waters highlight links to epidemic lineages and potential for crop infection
P1.16	Ivana Marić, University of Belgrade - Institute of Physics, RS	Bacteriogenic Fe-nanoparticles as selective antifungal agents
P1.17	Juliana Oliveira-Fernandes, Université de Rennes, FR	Grapevine Microbiome Dynamics Under Black Rot: Insights from the Anna Karenina Principle
P1.18	Tamara Krstić Tomić, Fruit Research Institute, RS	Biocontrol Strategy Shapes Plant Defense: Priming and Direct Antagonism in Sugar Beet—Microbe Interactions
P1.19	Isidora Knezević, Tamiš Research and Development Institute, RS	In Vitro Antagonistic Activity of <i>Trichoderma</i> Species against <i>Fusarium graminearum</i>
P1.20	Walczak Weronika, Intermag sp. z o.o., PL	Multifunctional Microbial Seed Treatments: Integrating Biostimulation, Biocontrol and Microbiome Interactions
P1.21	Stefan Stošić, Institute for Plant Protection and Environment, RS	What is the landscape of plant microbiome research in Serbia? A preliminary bibliometric analysis and the comparison with AI tool

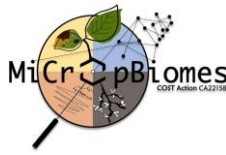
Poster session 2, Thursday 4 June, 16:30 - 18:00h (A0 Portrait, 84.1 cm × 118.9 cm)		
P2.1	Katalin Tajti , University of Szeged, Hungary and Biological Research Centre, Institute of Plant Biology, HU	Synergistic Biostimulatory Effects of <i>Chlorella</i> sp. MACC-360 and <i>Kocuria rhizophila</i> FSP120 Co-cultures on <i>Solanum lycopersicum</i>
P2.2	Inga Tamošiūnė , Institute of Horticulture, Lithuanian Research Centre for Agriculture and Forestry, LT	Microbial diversity and phosphorus solubilization potential in the rhizosphere of <i>Sedum acre</i> L.
P2.3	Hesam Mousavi , University of Inland Norway, NO	Mitigating salinity and cadmium stress in rice (<i>Oryza sativa</i> L.) using PGPR and salicylic acid: rhizosphere, health risk, and physiological insights
P2.4	Jovana Todorović , Fruit Research Institute, RS	Effects of an autochthonous PGPR consortium on fruit quality and health-promoting traits of European plum cv. 'Čačanska leptica'
P2.5	Núria Daranas , University of Girona, ES	Efficacy of two bacterial SynCom prototypes in promoting plant growth and stimulating plant response to stress under controlled-environment greenhouse conditions
P2.6	Louise Mathier , Zurich University of Applied Sciences, CH	FoodN'Feed: Locally adapted beneficial microbiomes and synthetic communities for enhanced grain legume performance and sustainable protein production
P2.7	Tina Arnšek , National Institute of Biology, SL	Assembly of microbial collection, isolated from potato field samples
P2.8	Jurgita Vinskienė , LRCAF Institute of Horticulture, LT	Effect of endophytic bacterial isolates on the regrowth of shoot tips of apple cv. Gala after cryopreservation
P2.9	Marian Malek , Austrian institute of Technology, AT	MICROBES-4-CLIMATE Project: Understanding microbiome-plant-soil-environment interactions for climate-resilient ecosystems
P2.10	Fanni Kovács , Faculty of Science and Informatics, University of Szeged, HU	Effect of Direct Plant–Fungus Interaction on Peptaibol Production of <i>Trichoderma longibrachiatum</i> f. <i>bisettii</i>
P2.11	Bulbul Ahmed , Mohammed VI Polytechnic University, MR	Hierarchical Microbiome Assembly from Desert Soils to Crops Drives Stress Resilience Under Salinity and Drought
P2.12	Refik Bozbuga , Faculty of Agriculture, Eskişehir Osmangazi University, TR	Microbiome and Nematode Interactions in Soil Ecosystems
P2.13	Maria Celeste Pereira Dias , University of Coimbra, PT	Boosting olive drought resilience using <i>Pseudomonas reactans</i>
P2.14	Denise Khouri Chalouhi , ICGEB, IT	Generational root endophytic enrichment through salinity: Bacterial consortia boost rice growth and resilience
P2.15	Jean Legeay , Université Mohamed 6 Polytechnique, MR	The rhizosheath microbiome of wild Poaceae across Morocco and its application to drought resistance of wheat
P2.16	Marijana Pešaković , Fruit Research Institute, RS	Microbial soil amendments shape the raspberry rhizosphere microbiome and enhance bioactive compounds in fruits
P2.17	Danka Kiperović , Institute of General and Physical Chemistry, RS	Microbial Bioremediation and Chemical Sensors: A Modern Solution for Heavy Metal Pollution in Agriculture



Session 1

Exploiting Plant-Microbiome molecular crosstalks: Diversity, distribution, and eco-evolutionary perspectives

Chair: Ahmed ABDELFAH



The role of the type III secretion system in plant beneficial bacteria

Jelena Lozo^{1,2*}

¹University of Belgrade – Faculty of Biology, Belgrade, Serbia

²Center for Pathogen Biocontrol and Plant Growth Promotion, Faculty of Biology, University of Belgrade, Belgrade, Serbia

*jlozo@bio.bg.ac.rs

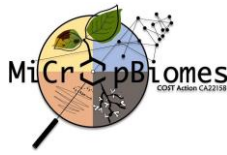
Keywords: *Pseudomonas*; Plant microbiome; Induced systemic resistance

Understanding the molecular mechanisms underlying plant–microbe interactions offers significant potential for sustainable agriculture. Proteins play a central role in these interactions, and their secretion by bacteria involves several distinct secretion systems. Among these, the type III secretion system (T3SS) is the most extensively studied, as it is present in many Gram-negative pathogenic bacteria. However, many commensal and beneficial bacteria also use T3SS to translocate proteins into host cells, promoting symbiosis or modulating the host immune system. Its function and role in these microorganisms remain unclear and insufficiently investigated. Due to the highly conserved structure of the apparatus and the secretory mechanism, we searched for T3SS in bacteria isolated from the sugar beet microbiome and identified *Pseudomonas* strains that possess it. The development of T3SS-deficient mutants enabled us to determine its specific role. The results suggest that T3SS-mediated interactions contribute to plant growth promotion and resistance to *P. syringae* pv. *aptata*. Additionally, we confirmed that in some strains, T3SS expression was induced by sugar beet extract (1). For *P. marginalis* ORh26, we confirmed that it induces systemic resistance in sugar beet through root colonisation, enhancing its defence against *P. syringae* pv. *aptata* (2). Genome sequencing of our three *Pseudomonas* spp. T3SS-positive strains confirmed that they are non-pathogenic, lacking virulence and antibiotic resistance genes. Interestingly, all strains lack the conventional needle subunit that forms the needle filament and needle tip, while they contain the *SctI* gene, which forms the inner rod of the needle. One characteristic of T3SS is the lack of conservation of its effectors (T3SEs), which may explain its prevalence even in non-pathogenic bacteria. Our research, using a customised bioinformatics pipeline based on the machine learning tool Effectidor, identified Ankyrin repeat-containing proteins and MaoC dehydratases as potential candidates for T3SEs in environmental *Pseudomonas* strains (unpublished data). By adopting this multidisciplinary approach, we aim to elucidate the role of T3SS in non-pathogenic bacteria for their efficient application in biofertilisers and biocontrol products.

References

1. Nedeljković, M., Mesaroš, A., Rašić, V., Nikolić I., Stanković S., Lozo J., Atanasković I. Effects of T3SS-positive *Pseudomonas* isolates on sugar beet growth stimulation and pathogen resistance. *Plant Soil* 512, 1101–1116 (2025). <https://doi.org/10.1007/s11104-024-07137-0>.
2. Nedeljković M, Mesaroš A, Radosavljević M, Đorđević N, Stanković S, Lozo J, Atanasković I. Type III Secretion system-mediated induction of systemic resistance by *Pseudomonas marginalis* ORh26 enhances sugar beet defence against *Pseudomonas syringae* pv. *aptata*. *Plants* (Basel). 2025 May 26;14(11):1621. <https://doi.org/10.3390/plants14111621>.

Funding: This study was funded by the Ministry of Science, Technological Development, and Innovation of the Republic of Serbia, Contract No 451-03-34/2026-03/200178 and 451-03-33/2026-03/200178. This presentation is based upon work from COST Action CA22158 MiCropBiomes.



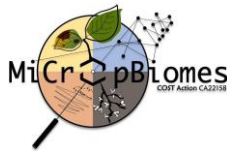
The Importance of Microbial Diversity Across Systems for Functional Stability and Resilience

Wisnu Adi Wicaksono

Institute of Environmental Biotechnology, Graz University of Technology, Graz, Austria

*wisnu.wicaksono@tugraz.at

Microbial diversity is a key determinant of stability, adaptability, and functionality across interconnected systems, including soils, plant-associated environments, extreme habitats, and food ecosystems. Growing evidence suggests that ecosystem resilience depends not only on dominant microbial groups but also on low-abundance and phylogenetically diverse taxa, which can act as keystone species and support critical functions under stressful conditions. Functional redundancy across diverse communities further helps maintain essential processes under changing environmental conditions. Here, I will discuss (i) how microbial diversity shapes community assembly and functional resilience across environmental gradients, (ii) the role of rare and low-abundant taxa as keystone components in maintaining stability under stress, and (iii) how diversity–function relationships are observed across different systems, from soil and plant-associated microbiomes to food-related microbial communities. I will also discuss how changes in microbial composition may be accompanied by relatively stable functional potential, suggesting a role for redundancy and adaptability. Overall, microbial diversity, encompassing taxonomic, functional, and ecological dimensions, emerges as a unifying principle underlying resilience across biological systems. Understanding and leveraging this diversity provides opportunities to enhance ecosystem stability, support sustainable practices, and promote health in dynamic environmental conditions.



Fruit function beyond dispersal: effect of fruit decomposition on the plant microbiome assembly

Daniel Hoefle^{1,2*}, Dinesh Kumar Ramakrishnan^{1,2}, Marie-Antoinette Holländer¹, Denis Kiplimo^{1,2}, William Konzag¹, Leonardo Schena³, Antonino Malacrinò⁴, Ayco J. M. Tack⁵ and Ahmed Abdelfattah¹

¹ Leibniz Institute for Agricultural Engineering and Bioeconomy (ATB), Potsdam, Germany

² Institute for Biochemistry and Biology, University of Potsdam, Potsdam, Germany

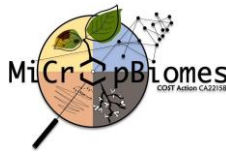
³ Department of Agriculture, Università degli Studi Mediterranea di Reggio Calabria, Reggio Calabria, Italy

⁴ Department of Biological Sciences, Clemson University, Clemson, USA

⁵ Department of Ecology, Environment and Plant Sciences, Stockholm University, Stockholm, Sweden

*dhoeffe@atb-potsdam.de

The ecological role of fruits has traditionally been viewed through the lens of seed dispersal. Yet, their effects on soil and plant microbiomes after decomposition remain unexplored. We proposed that decomposing fruits modify the soil microbiome and subsequently influence the plant microbiome and performance. Using amplicon sequencing, we characterized bacterial communities in soil, seed, fruit, rhizosphere, and phyllosphere of tomato and chili plants cultivated with or without their fruits. Fruit decomposition altered soil chemistry, increased bacterial diversity, and reshaped community composition. Further, fruit decomposition also reduced germination rates and affected shoot growth, while root length remained unchanged. In the phyllosphere, diversity decreased, and both rhizosphere and phyllosphere communities shifted markedly. Overall, our results demonstrate that fruits exert post-dispersal effects on the surrounding seedling environment and early plant microbiome assembly, challenging the classical view of fruit function and highlighting opportunities to harness fruit-derived microbiomes.



The *Medicago truncatula* nodGRP3C peptide is essential for proper bacteroid differentiation and symbiotic nitrogen fixation

Alexandra Pál¹, Edit Tímár¹, Lóric Pongor², Tamás Polgár³, Krisztián Laczi⁴, Sándor Jenei¹, Hilda Tiricz¹, Gabriella Endre¹, Rui M. Lima¹ and Éva Kondorosi^{1*}

¹ Institute of Plant Biology, HUN-REN Biological Research Centre, Szeged

² Hungarian Centre of Excellence for Molecular Medicine, Szeged

³ Institute of Plant Biophysics, HUN-REN Biological Research Centre, Szeged

⁴ Department of Biotechnology, Faculty of Science and Informatics, University of Szeged

*eva.kondorosi@gmail.com

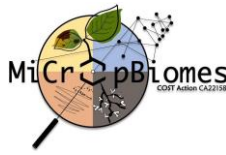
Keywords: Biological nitrogen fixation; *Medicago truncatula*; Endosymbiont differentiation; Nodule-specific glycine-rich proteins; Plant-microbe interaction

Biological nitrogen fixation is primarily driven by the root nodule symbiosis between leguminous plants and rhizobia. In the Inverted Repeat-Lacking Clade (IRLC), such as *Medicago truncatula*, the host produces symbiotic peptides to govern the terminal differentiation of bacterial endosymbionts into nitrogen-fixing bacteroids (1,2). While nodule-specific cysteine-rich (NCR) peptides are well-characterized effectors, the role of nodule-specific glycine-rich proteins (nodGRPs) remains poorly understood(3).

Here, we investigated *nodGRP3C*, one of 32 *nodGRP* genes in *M. truncatula*. Using RNA interference, we showed that NodGRP3C is essential for nodule development. In its absence, nodule growth arrests, bacteroid differentiation halts, and nitrogen fixation fails. Conversely, *nodGRP3C* overexpression induces early nodule senescence, host mitochondrial degradation, and decreased nitrogen fixation. Thus, tightly coordinated *nodGRP3C* expression is required for symbiotic homeostasis. To understand the underlying mechanisms, we performed biochemical, ultrastructural, and transcriptomic analyses. Altered *nodGRP3C* expression disrupted bacterial and host cellular integrity. Both silenced and overexpressing lines exhibited reduced ATP levels, elevated reactive oxygen species (ROS) accumulation, and altered defense-related gene expression. Transcriptome analysis revealed general *NCR* downregulation in RNAi nodules and upregulation in overexpression lines. Additionally, we mapped the minimal promoter region required for *nodGRP3C* expression. Taken together, NodGRP3C is a critical host-derived peptide targeting bacterial membranes to enforce endosymbiont differentiation. By modulating membrane properties, redox balance, and the symbiotic peptide repertoire, NodGRP3C plays an essential role in maintaining an effective nitrogen-fixing symbiosis.

References

1. Van de Velde W, Zehirov G, Szatmari A, Debreczeny M, Ishihara H, Kevei Z, Farkas A, Mikulass K, Nagy A, Tiricz H, Satiat-Jeunemaître B, Alunni B, Bourge M, Kucho K, Abe M, Kereszt A, Maroti G, Uchiumi T, Kondorosi E, Mergaert P (2010). Plant peptides govern terminal differentiation of bacteria in symbiosis. *Science* 327: 1122-1126.
2. Kevei Z, Vinardell JM, Kiss GB, Kondorosi A, Kondorosi E (2002). Glycine-rich proteins encoded by a nodule-specific gene family are implicated in different stages of symbiotic nodule development in *Medicago* spp. *Mol. Plant-Microbe Interact.* 15: 922-931.
3. Alunni B, Kevei Z, Redondo-Nieto M, Kondorosi A, Mergaert P, Kondorosi E (2007). Genomic organization and evolutionary insights on GRP and NCR genes, two large nodule-specific gene families in *Medicago truncatula*. *Mol. Plant-Microbe Interact.* 20: 1138-1148.



Plant phylogeny and mycorrhizal strategy shape multi-kingdom soil community assembly in a common garden experiment

Manikandan Ariyan^{1*} and Leho Tedersoo^{1,2}

¹ Institute of Ecology and Earth Sciences, University of Tartu, Liivi 2, 50409, Tartu, Estonia

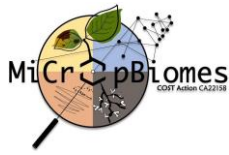
² Mycology and Microbiology Center, Institute of Technology, University of Tartu, Liivi 2, Tartu, 50409, Estonia

*manikandanariyan@gmail.com

Keywords: Plant phylogeny; Plant mycorrhizal type; Multikingdom; Community Composition

Understanding how plant evolutionary history shapes microbiome assembly is central to disentangling plant–microbiome crosstalk across ecological and evolutionary scales. Here, we investigate how plant phylogeny and mycorrhizal symbiosis jointly structure multi-kingdom soil communities using the MycoPhylo experimental field, comprising 218 monoculture plots of 105 phylogenetically diverse woody species with arbuscular (AM), ectomycorrhizal (EcM), and ericoid (ErM) associations. Using metabarcoding (16S rRNA, ITS, COI), we characterized soil bacteria, fungi, and metazoa and assessed both taxonomic and functional composition. While alpha diversity responses were kingdom-specific—fungal diversity varying strongly with mycorrhizal type and bacterial diversity responding weakly—beta diversity patterns revealed consistent structuring across all kingdoms. Mycorrhizal strategy emerged as a key axis of host-driven selection, with strong divergence between EcM- and AM-associated soils, indicating distinct belowground ecological niches shaped by plant–microbiome interactions. Plant growth form and leaf habit further influenced community assembly, while phylogenetic clustering across taxa suggested partial evolutionary conservatism in microbiome recruitment. Functional analyses highlighted coordinated shifts in trophic structure, including enrichment of ectomycorrhizal fungi and changes in saprotrophic and pathogenic guilds, alongside corresponding responses in bacterial functional groups and soil metazoa. These findings point to tightly linked, multi-trophic plant–soil feedbacks mediated by host traits. Overall, our results demonstrate that plant phylogeny and mycorrhizal strategy act as fundamental eco-evolutionary filters shaping multi-kingdom soil microbiomes, advancing our understanding of plant–microbiome crosstalk in terrestrial ecosystems.

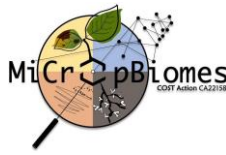
Funding: This work was funded by the Estonian Research Infrastructure programme through the EU Regional Development Fund (AnaEE Estonia 4.01.20-0285), Estonian Research Council grant (PRG1615), and the Novo Nordisk Foundation (Silva Nova, NNF20OC0059948).



Session 2

Crop microbiomes and plant diseases: From dysbiosis to increased defenses

Chairs: Joël F. POTHIER and Renata ARTIMOVA



Root immune receptors as drivers of the rhizosphere microbiota

Katie Arnton¹, Aman Jilani¹, Pete Thorpe², James Abbott² and Davide Bulgarelli^{1*}

¹Plant Sciences, Faculty of Life Sciences, University of Dundee, United Kingdom

²Computational Biology, Faculty of Life Sciences, University of Dundee, United Kingdom

*d.bulgarelli@dundee.ac.uk

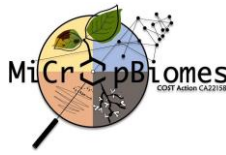
Keywords: Rhizosphere, microbiota, *NLRs*, domestication

My research group uses the global crop barley, the World's fourth most cultivated cereal, as a model to gain novel insights into the genetics of host-microbiota interactions in cultivated plants. Pioneering the use of microbiota composition as an “external” quantitative phenotype in genetic investigations, we previously identified a root immune receptor among primary candidates shaping microbial compositions at the root-soil interface in wild and domesticated genotypes. This candidate, designated *3H-NLR*, is predicted to code for a Nucleotide-Binding-Leucine-Rich-Repeat (NLR) receptor and maps to a region of structural variation of the barley genome. This suggests a selective pressure acting on this gene during domestication and breeding selection, comparable to one faced by other agronomic traits.

To gain insights into the functional significance of this receptor for microbiota recruitment, we developed a reduced-complexity synthetic community [SynCom] to probe barley genotypes harbouring contrasting alleles at *3H-NLR*. This approach allowed us to determine that inoculation with a “live” SynCom, but not the heat-inactivated one, produced a reproducible root growth phenotype fine-tuned by host genetics. Motivated by these observations, we performed a RNA-seq investigation of the roots of barley seedlings which revealed how genes underpinning immune responses were differentially regulated in a genotype-dependent fashion.

In a parallel line of investigation, we used genome editing to generate a novel allele of *3H-NLR* harbouring a premature stop codon. Gene-edited lines could be reproduced, suggesting that the induced mutation is not associated with deleterious pleiotropic effects. This allowed us to grow homozygous mutants in soil and determine that edited alleles of *3H-NLR* led to a reconfiguration of the microbiota in the rhizosphere.

Taken together, our results support a scenario in which *NLRs* play a wider, and not fully elucidated, role at the nexus of pathogen protection and microbiota establishment at the root-soil interface.



Rootstock-Dependent Microbial Associations in the Root Microbiome in Response to *Armillaria mellea* soil-borne pathogen

Elisenda Castellet^{1*}, Pablo Vargas¹, Javier Parladé¹, Carmen Biel¹, Marc Viñas², Amaia Nogales¹

¹ Sustainable Plant Protection, IRTA, Cabrils, Barcelona, Spain

² Sustainability in Biosystems, IRTA, Caldes de Montbui, Barcelona, Spain

*Elisenda.castellet@irta.cat

Keywords: Metabarcoding; arbuscular mycorrhiza; *Prunus*; white root rot disease; microbial recruitment

Soil-borne pathogens are a major problem in almond production, especially in Mediterranean areas where they coexist with water scarcity. *Armillaria mellea* (Arm) is the causal agent of *Armillaria* root rot, a particularly challenging fungal disease due to its persistence in orchard soils and its wide range of hosts. In this context, root-associated microbial communities are increasingly recognized as key drivers of plant health. Particularly, arbuscular mycorrhizal fungi (AMF) improve plant performance and its ability to recruit beneficial organisms, although their effects may vary depending on environmental conditions. Understanding how rootstock genotypes, mycorrhizal inoculations and abiotic stressors shape plant-pathogen interactions is essential for developing sustainable management strategies in almond orchards.

In this study, we evaluated the single and combined effects of the inoculation of the root pathogen *A. mellea* and the AMF *Rhizophagus irregularis* (Ri) in two *Prunus* rootstocks (Intensia and Pilowred®) under optimal (R100) and deficit (R50) drip irrigation in a potted assay with soil collected from a commercial almond orchard. Root associated fungal and bacterial communities were characterized at the end of the experiment, one year after inoculation, using a metabarcoding approach.

In Pilowred®, visually scored symptom severity was lower in plants co-inoculated with Ri and Arm under both irrigation regimes. In Intensia, under R100, the proportion of symptomatic plants decreased with Ri inoculation, whereas the opposite pattern occurred under R50. Furthermore, distinct microbial recruitment patterns driven by rootstock identity and inoculation treatments were found: Ri inoculation enhanced the abundance of potentially beneficial genera – such as *Talaromyces* in Intensia and *Trichoderma* and *Rhizobium* in Pilowred® – while reducing the relative prevalence of pathogenic taxa in Intensia. In contrast, Arm inoculation promoted an increase in *Thelonectria* and *Phaeoacremonium* abundance as pathogenic taxa, but also in beneficial genera including *Talaromyces*, *Trichoderma*, *Purpureocillium*, and *Rhizobium* in Intensia, and *Talaromyces* and *Brevundimonas* in Pilowred®.

Overall, our results showed that each rootstock had preferential associations with specific native soil microorganisms, and these associations shifted in response to Ri or Arm inoculation, as well as to water availability. This microbiome plasticity may represent an adaptive strategy to the edaphic environment, helping plants to modulate their responses under biotic and abiotic stress. These findings underscore the importance of considering altogether rootstock genotype, microbiome management, and irrigation practices in the development of resilient and sustainable almond production systems.

Funding: This research was supported by the Rootbome project (TED2021-130185B-I00), funded by MICIU/AEI/<https://doi.org/10.13039/501100011033> and European Union NextGeneration EU/PRTR.

New peptides for the future biological plant protection - comprehensive investigation of peptaibiotics produced by *Trichoderma* species

D. Balázs^{1*}, Á. Rozsnyói^{1,2}, G. Terna^{1,2}, F. Kovács^{1,2}, H. Hunkár^{1,2}, A. Szekeres¹, M. Varga¹, C. Vágvolgyi¹, T. Papp¹, C. Tyagi¹, T. Marik¹ and L. Kredics¹

¹ Department of Biotechnology and Microbiology, Institute of Biology, Faculty of Science and Informatics, University of Szeged, Szeged, Hungary

² Doctoral School of Biology, Institute of Biology, Faculty of Science and Informatics, University of Szeged, Szeged, Hungary

*balazs.dora.krisztina@szte.hu

Keywords: *Trichoderma*, peptaibiotics, biocontrol, plant protection

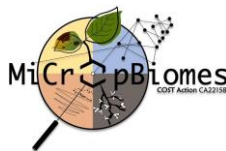
Increasingly extreme environmental impacts and widespread pathogens affecting agriculture and crop production are driving the search for new solutions. Filamentous fungal species of the genus *Trichoderma* have already been proven effective in biological plant protection, but their produced secondary metabolites may open new avenues for practical methods. Peptaibiotics, such as peptaibols are extremely stable compounds with a high content of non-proteinogenic amino acids, with the abilities to form ion channels in the membrane and exerting their bioactivity against bacterial and fungal species. The knowledge about *Trichoderma*-derived peptaibiotics is constantly expanding in the literature, thereby enhanced attention is being paid to their practical applicability¹.

During our studies we investigate the peptaibiotic production of *Trichoderma* species belonging to different clades using comprehensive methods such as analytical investigations, bioactivity tests and computational molecular modeling techniques to understand the underlying mechanisms of action. Based on our results, peptaibol extracts have proven to be effective against numerous bacterial and fungal pathogens that cause significant damage in agriculture. We are investigating the effects of selected extracts on plants under laboratory, plant growth chamber and field conditions and are developing new methods (e.g. spray method) that can effectively and safely apply the extracts and provide solutions against various infections. During ecotoxicological tests, effects of extracts are studied on model organisms to establish a safe application. By comparing their expressed activity and the structural properties of the peptides, we can establish the targeted and rapid selection of strains producing active peptaibiotics and the assembly of designed extracts. Our studies will reveal a comprehensive picture of the effects of peptaibiotics and lay the foundation for their future practical application.

References

1. Pereira-Dias L, Oliveira-Pinto PR, Fernandes JO, Regalado L, Mendes R et al. (2023). Peptaibiotics: Harnessing the potential of microbial secondary metabolites for mitigation of plant pathogens. *Biotechnol. Adv.*, 68, 108223.

Funding: This study was supported by the MMTA-Dynea Research-Education Grant (25/2026), the National Research, Development and Innovation Office (2022-1.2.6-TÉT-IPARI-TR-2022-00009) and the Scholarship Program of the Ministry of Culture and Innovation, Financed from the National Research, Development and Innovation Fund (EKÖP-570-SZTE and EKÖP-578-SZTE).



Microbial inoculants in cultivated mushrooms: interactions, disease control, and yield promotion

Ivana Potočnik*, Jelena Luković, Biljana Todorović, Ljiljana Šantrić and Svetlana Milijašević-Marčić

Institute of Pesticides and Environmental Protection, Belgrade, Serbia

*ivana.potocnik@pestring.org.rs

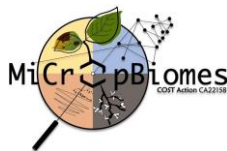
Keywords: Biocontrol agents; Disease control; *Agaricus*; *Bacillus*; *Streptomyces*

The white button mushroom is the most cultivated mushroom species in Europe and the fourth edible mushroom worldwide. A major problem in mushroom production is the green mould disease, caused by the fungal pathogen *Trichoderma aggressivum*. Disease control is difficult due to the development of pathogen resistance to available chemical pesticides. Additional problems represent chemical residues and their harmful impact on the environment. Biofungicide based on *Bacillus velezensis* QST 713 is the only one registered against *Trichoderma* spp. in mushrooms, but its variable efficacy against *T. aggressivum* was recently reported. Two indigenous beneficial microorganisms, bacterium *Bacillus amyloliquefaciens* B-241 and actinobacterium *Streptomyces flavovirens* A06, were obtained from the mushroom compost, and their respective fungicidal and stimulatory effects were previously confirmed. Simultaneous application of the two biocontrol agents was tested for their mutual relationship in both disease control and influence on yield. Both effects were evaluated in an experimental growing room of white button mushrooms (*Agaricus bisporus*), artificially infested with green mould disease agent *Trichoderma aggressivum* f. *europaeum* (10^4 conidia m^{-2}). Biocontrol agents *B. amyloliquefaciens* B-241 and *S. flavovirens* A06 were applied at standard application rates; decreased rates of 80%, 40%, or 20%; and combined at supplemented rates of 80:20% or 40:40%. The impact on mushroom productivity was estimated as the biological efficiency (BE) of the substrate, calculated as the ratio of the fresh weight of the total yield to the weight of the dry spawned substrate. Efficacy (E) in disease control was estimated based on disease incidence between the control and treatments. The synergy factor (SF) was calculated as a ratio between the observed and expected effects, either in efficacy against the pathogen or biological efficiency of the substrate in mushroom production. Each treatment was conducted in six replications, and all experiments were conducted twice. Combined microorganisms in respective proportions of 80:20% or 40:40% similarly affected disease control ($E_{80:20} = 66\%$; $E_{40:40} = 69\%$) or enhanced mushroom production ($BE_{80:20} = 142\%$; $BE_{40:40} = 138\%$). Bacterium B-241 and actinobacterium A06 achieved an additive interaction in disease control ($SE_{80:20} = 1$; $SE_{40:40} = 1$) and a synergistic relationship in relation to yield promotion ($SE_{80:20} = 1.6$; $SE_{40:40} = 1.3$). Based on these results, three to six split doses of microbial inoculants on a weekly basis were recommended (*B. amyloliquefaciens* $4-8 \times 10^8$ CFU $ml^{-1} m^{-2}$ and *S. flavovirens* $2-4 \times 10^7$ CFU $ml^{-1} m^{-2}$). The introduction of an optimal microbial combination improved the production and quality of the white button mushrooms, representing a possibility for biorational disease control without environmental pollution.

References

1. Milijašević-Marčić S, Šantrić Lj, Luković J, Potočnik I, Grujić N, Drobnjaković T, Marčić D (2024). Altering microbial communities in substrate to stimulate the growth of healthy button mushrooms. *Agriculture* 14: 1152.
2. Luković J, Milijašević-Marčić S, Šantrić Lj, Drobnjaković T, Anđelković N, Grujić N, Potočnik I (2025). Interactions among biocontrol agents in management of major pest and disease of button mushroom. *Pesticides & Phytomedicine* 40: 51-62.

Funding: Support was provided by the Ministry of Science of the Republic of Serbia: Contract Number 451-03-33/2026-03/200214.



Impact of *Bacillus velezensis* RD-FC 88 on the primary and secondary metabolism of cabbage cv. Futoški during infection with *Xanthomonas campestris* pv. *campestris*

Bojana Živanović^{1*}, Sonja Milić Komić¹, Nataša Stanojević¹, Ana Sedlarević Zorić¹, Sanja Marković¹, Dragana Bartolić¹, Danijel Milinčić², Mirjana Pešić², Sonja Veljović Jovanović¹ and Aleksandra Jelušić¹

¹Department of Life Sciences Institute for Multidisciplinary Research, University of Belgrade, National Institute of the Republic of Serbia, Kneza Višeslava 1, 11000 Belgrade, Serbia

²Department for Chemistry and Biochemistry, Faculty of Agriculture, University of Belgrade, Nemanjina 6, 11080 Belgrade, Serbia

*bojana.zivanovic@imsi.bg.ac.rs

Keywords: *Xanthomonas campestris* pv. *campestris*; Cabbage cv. Futoški; Biocontrol; Free amino acids; Secondary metabolism

Black rot, a disease caused by the bacterium *Xanthomonas campestris* pv. *campestris* (*Xcc*), has a significant effect on cabbage production worldwide, resulting in substantial economic losses. The aim of this study was to assess the effect of preventive foliar application of the biocontrol strain *Bacillus velezensis* RD-FC 88 on the primary and secondary metabolism of cabbage cv. Futoški plants infected with the *Xcc* strain XcFC 231. The activation of both, the antioxidative system and the immune response of the plants was analyzed in depth to ascertain the extent of host resistance modulation in the presence of the biocontrol strain. Special emphasis was placed on examining the interaction among the host plant, the biocontrol strain, and the pathogen, providing a new perspective on black rot control (1).

Pathogen inoculation caused a significant decrease in most of the measured metabolites (free amino acids, phenolic compounds, and glucosinolates). The content of free amino acids was significantly reduced, especially Gln, Ala, and branched-chain amino acids (BCAAs). However, preventive application of the RD-FC 88 strain in *Xcc*-infected plants restored the levels of aromatic amino acids, Asp, Glu, Leu, Val, and Ala to control values. The elevated biosynthesis of the aforementioned free amino acids in biocontrol-treated, *Xcc*-infected cabbage plants suggests that these compounds serve as precursors for the biosynthesis of defense-related metabolites involved in the plant's immune response to pathogen attack.

A similar trend was observed in glucosinolate content, where the application of the RD-FC 88 strain led to an increase in the levels of the aliphatic glucosinolates sinigrin and glucoiberin, as well as the indolic glucosinolate 4-methoxyglucobrassicin, in *Xcc*-infected plants compared with plants treated with *Xcc* alone. Biocontrol treatment in *Xcc*-infected plants led to increased accumulation of certain hydroxybenzoic acids, hydroxycinnamic acids, and kaempferol derivatives, which was accompanied by increased accumulation of epidermal flavonoids and reduced chlorophyll accumulation.

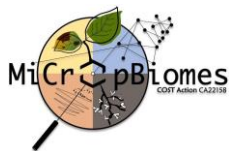
In order to examine the influence of the biocontrol candidate and the pathogen on the fluorescent profiles of phenolic compounds, fluorescence characterization of cabbage samples was performed. Based on principal component analysis (PCA), it was shown that biocontrol-treated, *Xcc*-infected cabbage plants were clearly separated from control samples, indicating activation of phenylpropanoid metabolism during pathogen attack.

The analysis of antioxidant defence enzymes revealed that *Xcc* infection significantly reduced peroxidase activity, while the activities of catalase and superoxide dismutase remained unchanged. Moreover, pathogen attack affected the plant's ascorbate–glutathione cycle, implying its involvement in the modulation of plant redox metabolism during infection.

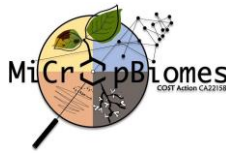
The plant's response to the application of the biocontrol strain during *Xcc* infection indicates that the biocontrol strain RD-FC 88 has the potential to mitigate the negative impact of *Xcc* by stimulating plant defence responses.

References

1. Stanojević N, Živanović B, Jelušić A, Milinčić D, Bartolić D, Sedlarević Zorić A, Pešić M, Veljović Jovanović S, Milić Komić S (2026). Host–pathogen–biocontrol Interactions: Effects of *Bacillus velezensis* on the suppression of black rot disease in cabbage cv. Futoški. *Agriculture*. 16(5): 544.



Funding: Support was provided by the Science Fund of the Republic of Serbia, #GRANT No. 10837, A "vaccine" for black rot — biocontrol of *Xanthomonas campestris* pv. *campestris* on autochthonous cabbage cultivar Futoški using plant-associated beneficial bacteria —XanthoSTOP; Ministry of Science, Technological Development and Innovation of the Republic of Serbia (Contract Nos. 451-03-33/2026-03/200053, 451-03-33/2026-03/200116) and the Centre for Green Technologies of the University of Belgrade—Institute for Multidisciplinary Research, Contract No. 451-03-33/2026-03/200053.



A novel potato endophytic *Fusarium oxysporum* isolate with disease-suppressive activity: genomic and biological characterization

Anže Vozelj^{1,2*}, Tim Godec^{1,2}, Paula Iriondo Ocampo³, Marko Petek¹, Tjaša Lukan¹, José María Díaz-Mínguez³, Kristina Gruden¹

¹ National Institute of Biology, Department of Biotechnology and Systems Biology, Večna pot 121, SI-1000 Ljubljana, Slovenia

² Jožef Stefan International Postgraduate School, Jamova cesta 39, 1000 Ljubljana, Slovenia

³ Institute for Agrobiotechnology Research (CIALE), C/ Del Duero, 12; Campus Villamayor-Parque Científico; 37185 Villamayor (Salamanca); Spain

*anze.vozelj@nib.si

Keywords: *F. oxysporum*; tissue cultures; endophytes; potato; bean; tomato; sustainable agriculture

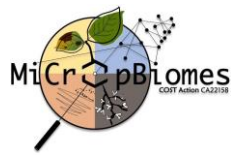
Endophytic microorganisms represent an innovative approach to enhance plant resistance to pathogens and are recognized as an important in sustainable crop protection strategies. Understanding the molecular and ecological determinants that distinguish beneficial from pathogenic plant–fungal interactions is therefore essential for the development of effective agricultural practices and ecosystem management.

We isolated a strain of *Fusarium oxysporum* (*F. oxysporum*) from our potato plants grown in sterile conditions of tissue culture. After sequencing and assembly of the genome, comparative genomic analyses were used to compare our isolate with other pathogenic and non-pathogenic (endophytic) *F. oxysporum* strains.

Since our isolate originates from potato, we first evaluated its abundance in potato tissue cultures. Furthermore, we also assessed its natural abundance in potato fields across different potato cultivars under organic and conventional management. Its occurrence varied depending on both cultivation system and plant tissue, highlighting the influence of agricultural practices on its distribution and ecological relevance. To further characterize our isolate, protocol for efficient plant inoculation using defined concentrations of *F. oxysporum* microconidia was established. Inoculation assays demonstrated disease-suppressive activity of our *F. oxysporum* endophytic isolate in tomato and bean.

Together, our findings provide an integrative genomic, experimental, and ecological perspective on endophytic *F. oxysporum*–plant interactions and highlight the potential of beneficial endophytic strains as tools for sustainable disease management.

Funding: Financial support was provided by Slovenian research agency (ARIS) project J4_3089 and STSM grant obtained in the frame of COST MiCropBiomes action (CA22158).



Session 3

Communication and engagement with society

Chair: Ivan NIKOLIĆ

Dissemination, Exploitation and Communication in Horizon Europe Projects - Examples of Good Practice

Marina Arnaut Stefanović¹, Mladen Radišić^{1,2}, Maja Radišić¹, Gordana Racić^{1,3}

¹ Foodscale Hub, Novi Sad

² Faculty of Technical Sciences, University of Novi Sad

³ Research and Development Institute Tamiš, Novoseljski put 33, Pančevo

*marina@foodscalehub.com

Keywords: dissemination, communication, stakeholder engagement, Horizon Europe

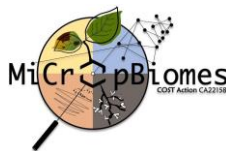
The European Union's research and innovation (R&I) agenda increasingly emphasises the importance of effective dissemination, communication, and exploitation (DCE) to maximise the impact of funded projects. Despite their central role in translating research into societal and economic value, DCE activities remain unevenly implemented and relatively underexplored in the literature. This article addresses this gap by examining how DCE practices are designed and applied within Horizon Europe projects, and how they align with broader EU R&I priorities.

In Foodscale Hub, dissemination and communication activities are strategically developed to enhance the visibility, accessibility, and uptake of project results through comprehensive strategies, tailored materials, and targeted campaigns across both traditional and digital channels. In parallel, exploitation activities focus on ensuring the long-term sustainability and scalability of outcomes by supporting stakeholders in translating innovations into practical applications. Through business modelling, capacity-building initiatives, and targeted training, these approaches facilitate the uptake and continued development of project results beyond the project lifecycle. FSH is partner in more than 20 Horizon Europe projects leading work packages dedicated to enlarging the impact of project results and research through strategic dissemination, communication, exploitation, and sustainability strategies.

This work presents good practices in dissemination and communication of European projects, with the aim of analysing how three Horizon Europe initiatives, RefreSCAR, CrackSense and INCiTIS-FOOD, apply these practices in real-world settings. RefreSCAR provides a strong example of how continuous and targeted communication enables outreach to a wide range of stakeholders, including ministry representatives, national Cluster 6 delegates, researchers, farmers, and entrepreneurs. CrackSense demonstrates how early and timely communication can increase farmers' interest in digital solutions in agriculture while simultaneously raising public awareness of the challenges faced by fruit producers. INCiTIS-FOOD highlights the value of interactive approaches, such as webinars, workshops, and roadshow events, in fostering direct engagement between researchers and small-scale farmers, while also promoting the benefits of cascade funding mechanisms.

The findings offer practical guidance for future Horizon Europe projects seeking to enhance visibility, strengthen stakeholder engagement, and improve knowledge exchange.

Funding: The research leading to this publication has received funding from the European Union's Horizon Europe research and innovation program under grant agreement No. 101083790 (project INCiTIS-FOOD); No. 101060553 (project RefreSCAR); No. 101086300 (project CrackSense).



MICROPOLIS: A strategic board game for communicating microbiology

Marija Nedeljković^{1,2*}, Aleksandra Mesaroš^{1,2}, Marija Anđelković^{1,2}, Mina Milošević³, Dušan Đorđević⁴, Dejan Dobričić⁵, Olivera Kostić¹, Anđela Golubović¹, Đorđe Milanović⁶, Slaviša Stanković^{1,2}, Jelena Lozo^{1,2}

¹ University of Belgrade - Faculty of Biology, Belgrade, Serbia

² Center for Pathogen Biocontrol and Plant Growth Promotion, Faculty of Biology, University of Belgrade, Belgrade, Serbia

³ University of Novi Sad – Academy of Arts, Novi Sad, Serbia

⁴ University of Niš – Faculty of Science and Mathematics, Niš, Serbia

⁵ First Grammar School of Kragujevac, Kragujevac, Serbia

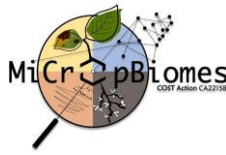
⁶ University of Belgrade, Institute of Physics, Belgrade, Serbia

*marija.nedeljkovic@bio.bg.ac.rs

Keywords: science communication; serious games; microbial ecology; environmental awareness;

Communicating the complexity and diversity of the microbial world to the general public remains a significant challenge, often limited by the dominant perception of bacteria as pathogenic organisms. To address this gap, we developed MICROPOLIS, a serious card-based strategy game aimed at fostering interest in microbiology and reshaping public understanding of bacteria as essential and adaptable form of life on Earth. The game is designed for players aged 8 and above and is set in a post-apocalyptic scenario in which only seven bacterial species have survived. Players assume control of individual bacterium and compete to become the ancestor of future life by adapting to diverse environments. Gameplay is based on collecting traits that enable survival in neutral and extreme conditions (thermal, saline, and pH-related), allowing players to earn tokens and claim habitats. Each player is assigned a hidden objective, ensuring strategic variability and uncertainty until the end of the game. The game concludes when a player claim a predefined number of environments (4–6, depending on player number), followed by a scoring phase triggered by global catastrophic events such as climate change, acid rain, and resource depletion. The game was evaluated through 78 playtesting sessions involving varying numbers of participants. Feedback indicated high engagement and improved conceptual understanding of microbial adaptability, environmental pressures, and ecosystem dynamics. MICROPOLIS demonstrates the potential of serious games as effective tools for science communication, promoting microbiological literacy and awareness of human impact on environmental conditions.

Funding: This research was funded by the Ministry of Science, Technological Development, and Innovation of the Republic of Serbia, grant numbers 451-03-34/2026-03/200178 and 451-03-33/2026-03/200178 and by the Center for the Promotion of Science through the Public Call 2025 (Project No.2525). This presentation is based on work from COST Action CA22158 MiCropBiomes.



Exploring the power of seed microbiome to improve crops tolerance against drought

Lama Ramadan^{1,2*} and Paolina Garbeva^{1*}

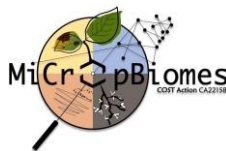
¹ Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, The Netherlands.

² Gebze Technical University, Kocaeli, Türkiye.

*l.ramadan2021@gtu.edu.tr; lama.maisoun@gmail.com

Keywords: Seed microbiome; Drought stress; Endophytes; Synthetic microbial communities

Seed microbiomes are increasingly recognized as key contributors to early plant development and stress resilience. However, the functional roles and mechanisms underlying these interactions remain insufficiently understood. This study investigates the role of seed-associated endophytic microorganisms in enhancing plant performance under drought stress, with a focus on tomato (*Solanum lycopersicum*). In this work, we aimed to identify seed endophytes with beneficial effects on germination under drought conditions and to evaluate their potential interactions in synthetic microbial communities (SynComs). Seed endophytes were isolated using a culture-dependent approach following surface sterilization. A total of 73 isolates were obtained, of which 31 were identified by 16S rRNA gene sequencing. The microbial community was dominated by Firmicutes (48%), followed by Proteobacteria (27%), Actinobacteria (22%), and Bacteroidetes (3%). To assess drought tolerance, isolates were screened in polyethylene glycol (PEG)-amended media at different osmotic potentials. We found that 68% of the isolates were sensitive to drought, whereas 13% were tolerant and 19% were highly tolerant. Selected drought-tolerant isolates were further evaluated for their effects on seed germination under control and drought conditions. Four strains, namely *Acinetobacter indicus*, *Staphylococcus pasteurii*, *Streptomyces* sp., and *Microbispora* sp., significantly increased germination under drought stress by 10–18% compared to non-inoculated controls. In addition, SynComs constructed from these isolates showed enhanced effects by around 25%, indicating synergistic or additive interactions among community members. To explore potential mechanisms, microbial volatile organic compounds (VOCs) were collected from isolates grown under control and drought stress conditions, allowing comparison of VOCs profiles and assessment of stress-induced metabolic shifts. These analyses are ongoing and are expected to provide further insight into indirect mechanisms of plant-microbe interaction. This study demonstrates that seed-associated microorganisms can enhance plant tolerance to drought stress and that combining selected isolates into SynComs can further improve this effect. These findings contribute to understanding the role of keystone microorganisms in plant microbiomes and support the development of microbiome-based strategies to improve crop resilience under abiotic stress conditions.



Transfer of Academic Knowledge on Bioreactor Methods for the Optimization of -bacterial cultivation for bioproducts that support the plant microbiome

Monika Faruga¹, Magdalena Jopek¹, Anna Gierut-Kot¹, Weronika Walczak¹, Jakub Drewniak¹, Krzysztof Ambroziak¹, William Casey¹, Kevin O'Connor¹

¹ *Intermag sp. z o. o., Al. 1000-lecia 15G 32-300 Olkusz*

*monika.faruga@intermag.pl

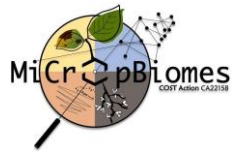
Keywords: bioreactor cultivation; fed-batch; plant microbiome; bioproducts; HPLC analysis

The development of microbial bioproducts for sustainable agriculture requires efficient and scalable cultivation strategies. This study summarizes the outcomes of a Short-Term Scientific Mission (STSM) focused on transferring academic knowledge on bioreactor-based optimization of bacterial cultivation. The training, conducted at University College Dublin, aimed to enhance competencies in microbial process optimization and analytical techniques.

The work began with shake-flask experiments to optimize carbon and nitrogen sources, monitored by optical density measurements. These studies were followed by batch bioreactor cultivations, where key process parameters and sterile sampling techniques were implemented. Analytical methods included nitrogen determination using the indophenol method and substrate consumption analysis (sugars and fatty acids) using HPLC. Biomass production was assessed through centrifugation, lyophilization, and dry weight measurement. A key element of the training was fed-batch cultivation using different feeding strategies. The results demonstrated a strong influence of feeding regime on biomass yield, highlighting the importance of feed timing, concentration, and dosing strategy for process efficiency. Additional skills included optimization of sterilization procedures and participation in downstream processing such as biomass extraction. The acquired knowledge has already been implemented at the home institution, including the introduction of HPLC-based analyses and improved experimental design.

Overall, this work demonstrates the importance of integrating bioreactor control, analytical monitoring, and feeding strategies to optimize bacterial cultivation for industrial biotechnology and plant microbiome applications.

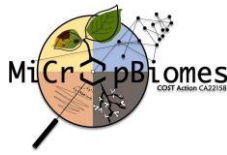
Funding Acknowledgement: this work was supported by COST (European Cooperation in Science and Technology) under COST Action MiCropBiomes (CA22158).



Session 4

From current microbial inoculants to synthetic communities

Chairs: Anna BONATERA and Claire PRIGENT-COMBARET



Towards Plant Microbiome Engineering: Exploring Seed Microbial Diversity and its Impact on Plant Fitness using Synthetic Communities

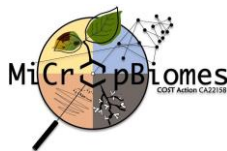
Marie Simonin¹

¹ Institut Agro, INRAE, IRHS, SFR QUASAV, Université d'Angers, F-49000 Angers, France

*marie.simonin@inrae.fr

Keywords: seed microbiota, microbiota assembly, microbial transmission, synthetic ecology

Seed microbiota serve as critical drivers of plant microbiome assembly and establishment, yet the relative contributions of different microbial taxa and the mechanisms underlying seed-to-plant transmission remain poorly understood. Using synthetic communities (SynComs) as experimental tools, we have dissected the transmission dynamics of seed-derived microorganisms and their functional impacts on early plant development and growth. Our work demonstrates that SynCom inoculation on seeds effectively manipulates and tracks microbial colonization across distinct plant compartments and developmental stages. During this talk, I will present different strategies to design, monitor and assess the effects of synthetic communities, providing examples from seeds but that are transferable to other ecosystems.



European and international approaches to the approval of microbial inoculants and synthetic communities as biopesticides, biofertilizers and biostimulants

Zisis Vryzas*, Paula Barciela

¹ Pesticide Science Lab, School of Agriculture Aristotle University of Thessaloniki, Greece

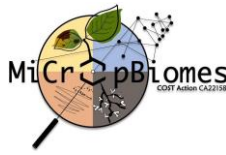
² Universidade de Vigo, Nutrition and Food Group (NuFoG), Department of Analytical Chemistry and Food Science, Instituto de Agroecoloxía e Alimentación (IAA) – CITEXVI, 36310 Vigo, Spain

*zvryzas@agro.auth.gr

Keywords: SynComs; Biopesticides; Biofertilizers; Biostimulants; Regulation

Microbial inoculants and synthetic communities (SynComs) are increasingly developed for agricultural use as biopesticides, biostimulants, and biofertilizers, but their regulatory assessment remains fragmented across product categories and jurisdictions. In the European Union, the regulatory framework for microorganisms used in plant protection products has recently been revised toward a more fit-for-purpose approach. Since 21 November 2022, microbial active substances intended for use as pesticides have been assessed under Part B of Regulation 283/2013, as amended by Regulation (EU) 2022/1439. This amendment establishes a distinct data-requirement framework for microorganisms, separate from the conventional Part A regime that applies primarily to chemical pesticides and certain microbial metabolites. In contrast, microbial products intended for use as biostimulants are regulated mainly under Regulation (EU) 2019/1009 on EU fertilising products, which provides the harmonised framework for CE-marked plant biostimulants. No specific structured regulatory provision currently exists for SynComs, particularly where products contain multiple interacting inter-kingdom communities with potentially emergent properties. This presentation analyses the current regulatory differences between microbial products intended as biopesticides, biostimulants, and biofertilizers, with particular focus on the challenges associated with SynComs. It further examines relevant approaches developed in other jurisdictions and evaluates the potential contribution of New Approach Methodologies (NAMs), weight-of-evidence strategies, problem formulation, and pathways-to-harm approaches to regulatory decision-making. These tools may support the development of more proportionate, scientifically robust, and operational approval pathways for complex microbial products. Overall, the case of SynComs highlights the need for regulatory frameworks that better reflect the biological complexity, functional diversity, and intended uses of next-generation microbial technologies.

Funding: Support was provided by the EU-FORA Fellowship Programme (EUBA-EFSA-2024-ENREL-01), which supports the LowRiskPesticides project.



Rational assembly of Bacterial Synthetic Communities (SynCom) for the management of olive vascular diseases

Luis Moll^{1*}, Lucía Alonso-Villar¹, Concepción Olivares-García¹, Juan Carlos Rivas¹, Guillermo León-Ropero¹, José Luis Trapero-Casas¹, Juan Antonio Navas-Cortés¹, Blanca B. Landa¹.

¹ Department of Crop Protection, Institute for Sustainable Agriculture, Spanish National Research Council (IAS-CSIC), Córdoba, Spain

*ljmoll@ias.csic.es

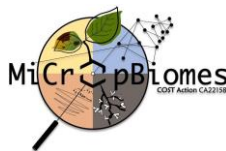
Keywords: *SynCom*, *Xylella fastidiosa*, *Verticillium dahliae*, biological control

Infections caused by the fungus *Verticillium dahliae* (Vd) and the EU quarantine bacterium *Xylella fastidiosa* (Xf) represent major threats to olive production and other economically important crops such as almond and grapevine. These vascular pathogens are particularly difficult to manage due to their systemic colonization and the current lack of effective curative control measures, with existing strategies relying mainly on preventive practices that provide limited efficacy. In the context of the European Green Deal which promotes the transition toward more sustainable agricultural practices, biological control based on endophytic microorganisms is emerging as a promising alternative. Specifically, Synthetic Bacterial Communities (SynComs) composed of xylem-inhabiting bacteria from olive trees offer a novel and environmentally friendly approach for the management of diseases caused by Xf and Vd.

In this study, two SynCom each composed of three compatible strains, were designed based on: i) phenotypic characterization of 18 traits related to biocontrol potential and/or plant growth promoting ability, ii) carbon source utilization profiles and tolerance to abiotic stresses, iii) *in vitro* inhibition of Xf and Vd, and iv) compatibility and complementarity of traits among promising selected strains. These SynComs were further tested against Xf and Vd under microfluidic chamber conditions simulating xylem vessels.

The *in planta* efficacy of both SynComs against Xf and Vd was subsequently assessed in *Nicotiana benthamiana* as a model host and *Olea europaea* as the target host. Specifically, disease severity, Xf and Vd population levels by qPCR and plant fitness-related parameters (plant growth and leaf-associated physiological traits using proximal sensors) were determined. In *N. benthamiana*, both SynComs significantly reduced disease severity (~75%) and Xf populations (1–2.5 log reduction across different stem sections). They also improved plant fitness, as reflected by increases in plant height (10–15%), fresh weight (25–30%), and chlorophyll content (40–60%) compared to non-treated controls. Similar trends were observed for both SynComs against Vd in the same host, with reductions in disease severity (~35%) and pathogen populations (1–1.5 log reduction), together with improved plant fitness, including increases in plant height (10–25%), fresh weight (50%), and chlorophyll content (~50%). Ongoing experiments in *O. europaea* are showing similar trends. In addition, field trials are currently underway in Italy and Mallorca to evaluate the effectiveness of these SynComs in reducing Xf symptom severity and limiting infection success in olive following trunk application by endotherapy.

Funding: This work was funded by BeXyl (Grant ID 101060593, EU-Horizon Europe), MCIN/AEI/10.13039/501100011033 (PID2020-114917RB-100), MICIU/AEI/10.13039/501100011033 “European Union Next Generation EU/PRTR” (TED2021-130110BC41), JDC2024-053655-I funded by MICIU/AEI/10.13039/501100011033 and ESF+.



Characterisation of potato microbiota for design of successful potatobiome communities

Martin Stražar^{1,*}, Karmen Pogačar¹, Anže Vozelj¹, Tina Arnšek¹, Klara Šuštar¹, Marko Petek¹, Peter Dolničar², Polonca Štefanič³, Ines Mandić Mulec³, Kristina Gruden^{1,*}

¹ Department of Systems biology and Biotechnology, National Institute of Biology, Ljubljana, Slovenia

² Crop Science Department, Agricultural Institute of Slovenia, Ljubljana, Slovenia

³ Chair of Microbial Ecology and Physiology, Department of Microbiology, Biotechnical Faculty, University of Ljubljana, Ljubljana, Slovenia

[*martin.strazar@nib.si](mailto:martin.strazar@nib.si), kristina.gruden@nib.si

Keywords: *Solanum tuberosum*, plant microbiome, culturomics, syncoms, untargeted metabolomics, machine learning

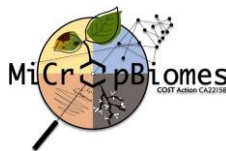
The plant microbiota offers key ecosystem services to the plant host, including nutrient exchange, community regulation, production of phytohormones and protection against biotic and abiotic stresses^{1,2}. To investigate the effects of potato microbiota under field conditions, we sampled eight tetraploid cultivars, grown under conventional and organic agricultural management between 2022 and 2023. Sampling of roots and leaves was performed at the time of tuber initiation and at the end of tuber filling. We split each sample, ferociously sterilising half of it to select for endophytic microbes, while the remaining samples predominantly included epiphytes. A total of 1016 samples were analysed using V3V4 sequencing and clustered according to alpha and beta diversity. Of these, 24 samples were selected for isolation of bacterial microbes as representatives of identified clusters to maximize the captured diversity. Cultivation was performed on three different media and isolated bacteria were classified using the MALDI Biotyper mass spectrometer. A total of 550 unique strains were stored as NIB potato microbiota collection, representing an unprecedented resource for mechanistic studies and community design. Here, we perform deep characterization of the collection on the level of genome, metabolome, plant growth-promoting and protecting properties.

The mechanistic basis of interaction between plant and bacteria was investigated through untargeted metabolomics of exometabolites — compounds bacteria secrete into media. To this end, we profiled eleven of the endophyte strains and three known growth-promoting strains, detecting at least twofold changes in 31 identified metabolites, including purines and aromatic amino acids, potentially important in natural product synthesis. To shed light on the more than 36,000 increased, unannotated features, we adapt and retrain MS1-Tools³ — a machine-learning based method for molecular fingerprint prediction — to plant and plant-bacterial molecular repertoires. Using experimental and computational techniques, we aim towards comprehensive identification of microbially-derived phytohormones.

References

1. Lukan, T., Kraigher, B., Pogačar, K., Stare, K., Kovačič, T. G., Zagorščak, M., ... & Gruden, K. (2025). An ERF transcription factor StPTI5, a novel regulator of endophyte community maintenance in potato. *bioRxiv*, 2025-04.
2. Gruden, K., Lidoy, J., Petek, M., Podpečan, V., Flors, V., Papadopoulou, K. K., ... & Pozo, M. J. (2020). Ménage à trois: unraveling the mechanisms regulating plant–microbe–arthropod interactions. *Trends in Plant Science*, 25(12), 1215-1226.
3. Martin Stražar, Ahmed Mohamed, Eivgeni Mashin, Rachele Invernizzi, Sarah Jeanfavre, & ... & Clary B. Clish, Ramnik J. Xavier. Probabilistic inference of metabolites across inflammation states and microbiomes (in revision, 2026). <https://broad.io/ms1-tools>

Funding: Support was provided by Slovenian Research and Innovation Agency grant J1-60024 to M.S. and program P4-0463 to K.G. This presentation is based upon work from COST Action CA16107 EuroXanth, supported by COST (European Cooperation in Science and Technology).



Synthetic communities of core native bacteria induce rhizosphere microbiome restructuring in tomato

Daniele Nicotra^{1*}, Alexandros Mosca¹, Giulio Dimaria¹, Matilde Tessitori¹, Ramesh Vetukuri² and Vittoria Catara¹

¹ Department of Agriculture, Food and Environment, University of Catania, Via Santa Sofia, 100, 95123 Catania, Italy.

² Department of Plant Breeding, Swedish University of Agricultural Sciences, Sundsvägen, 14, 230 53 Alnarp, Sweden.

*daniele.nicotra@unict.it

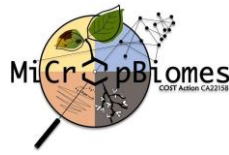
Keywords: SynCom; microbiome dynamics; rare biosphere; rhizosphere; PGPR

Modern intensive agriculture has significantly eroded soil microbial diversity, thus necessitating a shift toward sustainable, microbially-mediated solutions. While single-strain inoculants have paved the way, the development of Synthetic Communities (SynComs) represents the next frontier in achieving functional resilience under fluctuating field conditions. Building upon previous research that identified and characterized the tomato core microbiome across the cultivation chain (1), this study explores the transition from individual core members inoculants to functional consortia. We designed three taxonomically diverse SynComs (MIX1, MIX2, and MIX3) of increasing complexity, comprising four, six, and ten native bacterial strains, respectively. These strains—belonging to key genera including *Bacillus*, *Pseudomonas*, *Glutamicibacter*, *Paenarthrobacter*, *Chryseobacterium*, and *Leclercia*—were selected based on their prevalence in healthy tomato rhizospheres and their documented plant growth-promoting traits (1). A previous study already assessed the beneficial effect of some of the single strains and a consortium on the growth and production of soilless-grown tomato plants under water stress, also investigating the impact on resident bacterial communities (2). In this study, the experimental trials focused on the longitudinal monitoring of the rhizosphere microbiome following a soil drench application of the bacterial consortia on three-week-old ‘Proxy’ tomato plants. Rhizosphere microbial dynamics were monitored via 16S rRNA and ITS amplicon-based metagenomics at four time points: few hours post inoculation (T0) and one (T1), two (T2) and four (T4) weeks post inoculation. Our findings indicate that while temporal factors are the primary drivers of community assembly, the application of SynComs triggers a sophisticated, time-dependent restructuring of the “rare biosphere”, mainly by altering the composition of less abundant bacterial taxa. Rather than maintaining high-density colonization, the SynCom strains appeared to act as ecological catalysts, inducing early-stage indirect modulations that favored rare bacterial taxa primarily involved in nitrogen and sulfur cycling. Furthermore, the consortia demonstrated a cross-kingdom influence by stabilizing fungal succession patterns, favoring Basidiomycota and Mucoromycota over Ascomycota. This work highlights the importance of temporal dynamics in microbiome engineering, suggesting that small, host-derived SynComs can effectively unlock the latent functional potential of the soil-root continuum microbiome. Overall, these findings support the transition to sustainable agriculture by showing how targeted microbial interventions can drive meaningful ecological shifts in the rhizosphere.

References

1. Nicotra D, Ghadamgahi F, Ghosh S, Anzalone A, Dimaria G, Mosca A, Massimino ME, Vetukuri RR, Catara V (2024). Genomic insights and biocontrol potential of ten bacterial strains from the tomato core microbiome. *Front. Plant Sci.* 15:1437947.
2. Nicotra D, Mosca A, Dimaria G, Massimino ME, Di Stabile M, La Bella E, Ghadamgahi F, Puglisi I, Vetukuri RR, Catara V (2025). Mitigating Water Stress in Plants with Beneficial Bacteria: Effects on Growth and Rhizosphere Bacterial Communities. *Int. J. Mol. Sci.* 26:1467.

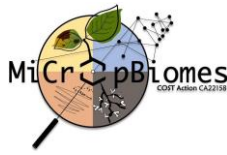
Funding: Support was provided by PON “RICERCA E INNOVAZIONE” 2014–2020, Azione II—Obiettivo Specifico 1b—“WATER4AGRI FOOD”, n. ARS01_00825, Cod. CUP: B64I20000160005; the European Union Next-Generation EU (Piano Nazionale di Ripresa e Resilienza (PNRR)—missione 4, componente 2, investimento 1.4—D.D. 1032 17/06/2022, CN00000022): CUP E63C22000960006, within the Agritech National Research Center; FORMAS (2019–01316), Carl Tryggers Stiftelse för Vetenskaplig Forskning (CTS 20:464), The Swedish Research Council (2019–04270), NOVO Nordisk Foundation (0074727), SLU Centre for Biological Control and Partnerskap Alnarp.). This presentation is based upon work from COST Action MiCropBiomes CA22158, supported by COST (European Cooperation in Science and Technology).



Session 5

Crop-Microbiome assembly dynamics under specific environments

Chairs: Elodie VANDELLE and Gordana RACIĆ



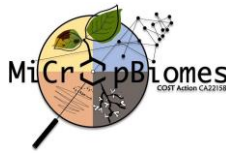
How *Pseudomonas* interact with plant roots, and why it matters

Jacob Malone

The John Innes Centre, Norwich Research Park, Norwich, NR4 7UH, UK

* Jacob.Malone@jic.ac.uk

Harnessing the ability of soil microbes to support healthy plant growth is a critical component of the move to sustainable, high-productivity agriculture. Many plant-associated microbes form beneficial relationships with plants, positively affecting health and nutrition and effectively suppressing pests and pathogens. Given their importance for plant health, plants secrete a range of different metabolites into the rhizosphere to attract beneficial microbes. Exudate composition defines the nature of microbial recruitment, with different plant species, and varieties, attracting distinct microbiota to enable optimal adaptation to the soil environment. The central aim of my lab is to understand how members of the growth-promoting rhizobacterial genus *Pseudomonas* interact with plants, in the context of the natural environment. We study how plants interact with *Pseudomonas* spp. at the molecular level, how the plant/soil environment influences *Pseudomonas* genetics, and how microbial ecosystems are shaped by evolution and horizontal gene transfer. A major focus of our work is to exploit this knowledge to support fundamental and applied progress towards sustainable agricultural solutions. In this talk I will outline some of our recent progress towards these goals.



Exploring Rhizosphere Microbiomes in Mediterranean Vineyards through Metabarcoding analysis: insights from Italy, Portugal, Morocco, and Turkey

E. Soriato¹, M. Calgaro¹, N. Vitulo¹, R. Shmulevitz¹, G.B. Tornielli², F. Spinelli³, C. El Modafar⁴, M. E. Duru⁵, Y. Uysal⁶, M. Yıldız⁷, L.-T. Dinis⁸, J. Prada⁹, M.C. Santos⁹, E. Vandelle^{1,*}

¹ Dipartimento di Biotecnologie, Università degli Studi di Verona, Strada Le Grazie, 15, 37 134 Verona, Italy

² Dipartimento di Agronomia, Animali, Alimenti, Risorse naturali e Ambiente, Università di Padova, Via dell'Università 16, 35020 Legnaro (PD)

³ Dipartimento di Scienze e Tecnologie Agro-Alimentari, Università di Bologna, viale G. Fanin 44, 40127 Bologna, Italy

⁴ Laboratory of Biotechnology and Molecular Bioengineering, Department of Biology, Faculty of Sciences and Techniques Guéliz, Cadi Ayyad University, Marrakech, Morocco

⁵ Department of Chemistry, Faculty of Science, Muğla Sıtkı Koçman University, 48000 Muğla, Turkey

⁶ Environmental Engineering Department, Mersin University, 33343, Mersin, Turkey

⁷ Apricot Research Institute, Malatya, Turkey

⁸ Centre for the Research and Technology of Agro-Environmental and Biological Sciences (CITAB), University of Trás-os-Montes and Alto Douro, P.O. Box 1013, 5001-801 Vila Real, Portugal

⁹ Department of Biology, LAQV-REQUIMTE, Faculty of Sciences, University of Porto, Porto, Portugal.

* elodigenevieve.vandelle@univr.it

The Mediterranean basin represents a historically and ecologically complex viticultural region, where grapevine cultivation has long been shaped by environmental, soil, and management factors. Together, these components define the concept of *terroir*, which increasingly includes the structure and function of soil microbial communities.

In this study, we investigated the rhizosphere microbiome of vineyards across four Mediterranean countries—Italy, Morocco, Portugal, and Turkey—using a metabarcoding approach targeting both bacterial (16S) and fungal (ITS) communities. Our aim was to assess how microbial diversity and organization vary across geographically distinct terroirs.

We observed a strong biogeographic signature in microbial communities, with clear country-specific patterns despite the relatively confined geographic scale. Bacterial and fungal communities, however, showed contrasting ecological organization. Bacterial communities were more structured and interconnected, displaying consistent responses to key environmental variables such as soil pH and nutrient availability. In contrast, fungal communities were more modular and heterogeneous, with weaker and more context-dependent environmental associations.

Notably, Portuguese vineyards exhibited a distinct fungal community, with soil pH emerging as a dominant selective factor and driving an isolated network configuration. This highlights the role of local environmental filtering in shaping fungal community assembly. Despite clear differences in taxonomic composition and network structure, functional predictions suggested a degree of redundancy across communities, particularly for fungi.

Overall, our results support the concept of a *microbial terroir*, demonstrating that vineyard microbiomes are shaped by both biogeographic processes and environmental filtering, with distinct assembly patterns for bacteria and fungi.

Funding: The research funded by the VineProtect Prima/0011/2021.

Grapevine bacterial communities are shaped by compartment, phenology, and herbicide management

Olja Medic^{1,2*}, Ivan Nikolić^{1,2}, Tamara Ranković^{1,2}, Jelena Lozo^{1,2}, Tanja Berić^{1,2,3} and Slaviša Stanković^{1,2}

¹ University of Belgrade – Faculty of Biology, Belgrade, Serbia

² Center for Pathogen Biocontrol and Plant Growth Promotion, Faculty of Biology, University of Belgrade, Belgrade, Serbia

³ University of Belgrade, Institute of Physics Belgrade, Belgrade, Serbia

*olja.medic@bio.bg.ac.rs

Keywords: *Vitis vinifera*; metabarcoding; co-occurrence network; functional prediction

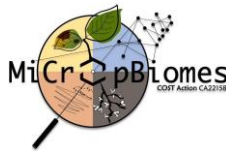
Grapevine-associated microbial communities contribute to plant productivity and, consequently, grape and wine quality, by influencing stress tolerance, nutrient acquisition, and pathogen suppression. A deeper understanding of grapevine microbial ecology can support improved vineyard management strategies and enable the identification of microorganisms with potential biotechnological applications. This study investigated the effects of phenology and herbicide management on bacterial community structure, interaction networks, and functional potential in the phyllosphere and rhizosphere of grapevine (cv. Prokupac).

Phyllosphere and rhizosphere samples from herbicide-treated and untreated grapevines were collected in June, July, and September, corresponding to the flowering, early berry development, and ripening stages of grapevine phenology. Short-read metabarcoding of the V3–V4 region of the 16S rRNA gene was performed using the Illumina NovaSeq PE250 platform. Differential bacterial taxa were identified using linear discriminant analysis effect size (LEfSe). High-confidence co-occurrence networks were constructed based on Spearman correlation coefficients ($|p| > 0.6$, $p < 0.05$). Functional profiles were predicted using PICRUSt2 and compared between treatments across phenological stages.

In the untreated phyllosphere, *Sphingomonas* and Acidobacteriales were identified as the most significant biomarker taxa at flowering and early berry development, respectively. The untreated rhizosphere was enriched in Solirubrobacteraceae and Bacteroidales, while the herbicide-treated rhizosphere showed enrichment in Nitrosphaeraceae and Gammaproteobacteria at the corresponding stages. Network analysis of bacterial communities from herbicide-treated and untreated phyllosphere and rhizosphere revealed differences in topological structure across compartments and management practices. Node numbers ranged from 290 to 357, and filtered edges ranged from 20 to 54. Rhizosphere networks exhibited higher graph density, clustering coefficient, and modularity than phyllosphere networks, suggesting more complex and structured microbial interaction patterns. Spearman correlation analysis at the genus level revealed the predominance of positive associations across all networks, accounting for 76.9–81.6% of total correlations, while negative associations ranged from 18.4% to 23.1%. PICRUSt2 analysis revealed functional differences between phyllosphere and rhizosphere communities across phenological stages and treatments, primarily in carbohydrate metabolism, aromatic compound degradation, and nutrient cycling pathways. Herbicide treatment was associated with reduced predicted biosynthetic activity. Functional profiles also varied with grapevine phenology, indicating a shift in substrate utilization from simple sugars to more complex plant-derived compounds.

Grapevine bacterial communities are shaped by compartment, phenology, and herbicide management, affecting both their structure and predicted functional potential. These findings contribute to elucidating plant-microbiome interactions and support the development of microbiome-based strategies for sustainable viticulture and reduced chemical inputs.

Funding: The research was supported by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia (grant no. 451-03-33/2026-03/200178 and 451-03-34/2026-03/200178). This presentation is based on work from COST Action CA22158 MiCropBiomes.



Age-Driven Assembly of Root-Associated Bacterial, Fungal, and Arbuscular Mycorrhizal Communities in Almond Rootstocks

Pablo Vargas, Elisenda Castellet, Jordi Luque, Carmen Biel, Javier Parladé, Amaia Nogales *

IRTA, Sustainable Plant Protection, Centre de Cabrils, Cabrils Catalonia, Spain.

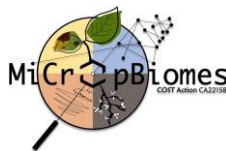
*amaia.nogales@irta.cat

Keywords: metabarcoding; batch effect; holobiont; microbiome drivers

Rootstock selection is a critical determinant of almond production success, influencing disease resistance, stress tolerance, and overall plant performance. While rootstock genotype shapes some important plant physiological traits, the microbial communities colonizing root tissues may play equally important roles in mediating these outcomes. However, the temporal dynamics of root microbiome assembly and the relative contributions of host genotype versus plant age remain poorly understood in woody fruit crops. This study investigated the root-associated bacterial, fungal, and arbuscular mycorrhizal fungal (AMF) communities of two commercially important almond rootstocks —Rootpac 40 (R40) and Rootpac R (RR)— across contrasting developmental stages: young plants (2 years old) and mature trees (15 years old). Using amplicon sequencing targeting 16S rRNA, ITS1, and 28S rRNA regions, we characterized bacteria, fungi and AMF community structure, diversity, and composition across 20 root tissue samples. Roots from young plants were obtained from plants grown in pots under semi-controlled conditions, while those from mature plants were obtained from plants grown in an experimental orchard. All samples shared the same soil. Samples from different age classes were processed at separate sequencing facilities, introducing a potential batch effect; however, addition of a third public dataset (fungal ITS1 sequences from young Nemaguard roots) confirmed that biological signals dominated technical variation, enabling a more robust interpretation of age-related patterns.

Across all three microbial communities, plant age emerged as the primary driver of microbiome differentiation, while rootstock genotype (R40 vs. RR) exerted no detectable influence on community assembly. While no significant differences were observed between age groups in alpha diversity, beta diversity analyses revealed clear age-based clustering, with young and mature root microbiomes occupying distinct compositional space regardless of rootstock identity. Differential abundance analyses, using young plants as the reference baseline, identified multiple taxa significantly enriched in mature root systems. In the bacterial community, roots of mature trees were enriched in amplicon sequence variants (ASVs) identified as *Cryptosporangium*, *Rhodomicrobium*, *Microtrichales*, and *Kineosporaceae* —taxa often associated with nutrient cycling and stress adaptation in established rhizosphere environments. Within the fungal community, four distinct ASVs identified as *Rhizophagus* were enriched in mature trees, alongside *Fusarium* and *Verticillium*, suggesting age-dependent shifts in both mutualistic and potentially pathogenic fungal colonization. The AMF-specific analysis revealed enriched genera including *Sclerocystis*, *Nanoglomus*, and *Entrophospora* in mature trees, indicating progressive diversification of arbuscular mycorrhizal partnerships over time in contrast to *Rhizoglosum*-enriched young roots.

These findings demonstrate that root microbiome assembly in almond trees is a temporally dynamic process, with microbial community composition undergoing substantial taxonomical and functional restructuring as trees transition from juvenile to mature life stages.



***Bacillus velezensis* SS-38.4 as a preventive biocontrol agent in sugar beet phyllosphere**

Iva Rosić^{1,2*}, Ivan Nikolić^{2,3}, Marina Sokić^{1,2}, Tanja Berić^{1,2,3}, Slaviša Stanković^{2,3}, Olja Medić^{2,3}

¹ University of Belgrade, Institute of Physics, Belgrade, Serbia

² Center for Pathogen Biocontrol and Plant Growth Promotion, Faculty of Biology, University of Belgrade, Belgrade, Serbia

³ University of Belgrade - Faculty of Biology, Belgrade, Serbia

*riva@ipb.ac.rs

Keywords: *Bacillus*; *Pseudomonas syringae*; plant colonization; plant protection; biocontrol

The genus *Bacillus* has dominated the field of biological control since its early development, largely due to its environmental safety, resistance to diverse physical and chemical stresses, ability to form endospores, and multiple synergistic modes of action in plant protection. In phytopathogen control, both purified metabolites and living cells of *Bacillus* species have been widely used as biopesticides or microbial-based products in classical biocontrol and plant growth promotion strategies.

However, despite decades of research and numerous commercial products, *Bacillus*-based biocontrol agents often still fall short in effectiveness and consistency compared to chemical pesticides and fertilizers (1). A commonly proposed explanation is their limited ability to rapidly adapt to the environment in which they are applied, whereas phytopathogens are typically highly adapted to plant-associated niches due to long-term coevolution with their hosts (2).

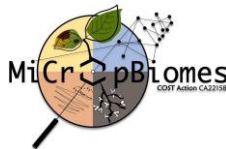
Our research shows that preventive application of *B. velezensis* SS-38.4 on sugar beet leaves prior to the arrival of the phytopathogen *Pseudomonas syringae* pv. *aptata* P21, a highly virulent strain causing bacterial leaf spot and severe crop losses, may provide an effective control strategy. We demonstrate that the primary mechanism of action of SS-38.4 is rapid niche colonization. The strain quickly expands its population on the leaf surface, effectively preventing establishment of the pathogen population and subsequent disease development. Preventive application therefore provides sufficient time for SS-38.4 to establish a stable population before pathogen arrival. This mechanism is further supported by competition for essential nutrients. SS-38.4 produces high levels of siderophores, limiting iron availability to *P. syringae* pv. *aptata* P21. In addition, a diverse array of antimicrobial metabolites further supports its antagonistic activity. Genome analysis identified eleven biosynthetic gene clusters involved in secondary metabolite production, two of which may encode previously undescribed antimicrobial compounds.

Although the impact of preventive application of SS-38.4 on the native plant microbiota has not yet been fully explored, the observed reduction in disease severity and inhibition of pathogen growth suggest no major negative effects on the leaf microbial community. Nevertheless, long-term effects under diverse environmental conditions in sugar beet fields require further investigation.

Overall, our findings demonstrate that successful biocontrol in the phyllosphere may depend less on antimicrobial activity alone and more on the ability of beneficial bacteria to rapidly colonize and occupy the ecological niche before pathogen arrival.

References

1. Bonaterra A, Badosa E, Daranas N, Francés J, Roselló G, Montesinos E (2022). Bacteria as biological control agents of plant diseases. *Microorganisms* 10: 1759.
2. Saberi Riseh R, Fathi F, Gholizadeh Vazvani M, Tarkka MT (2025). Plant colonization by biocontrol bacteria and improved plant health: A review. *Front. Biosci. (Landmark Ed.)* 30: 23223.



Organic and inorganic mulching drive distinct and persistent rhizosphere microbiomes in *Malus × domestica* orchards

Kamila Łucja Bokszczanin^{1*}, Aleksandra Chojnacka², Marzena Suchocka³, Hazem M. Kalaji⁴, Ryszard Malinowski⁵ & Marcin Kubus⁶

¹Department of Pomology and Horticulture Economics, Institute of Horticultural Sciences, Warsaw University of Life Sciences-SGGW, Nowoursynowska 159 Str., 02-787 Warsaw, Poland

²Department of Biochemistry and Microbiology, Institute of Biology, Warsaw University of Life Sciences-SGGW, Nowoursynowska 159 Str., 02-787 Warsaw, Poland

³Department of Landscape Architecture, Institute of Environmental Engineering, Warsaw University of Life Sciences-SGGW, Warsaw, Poland

⁴Department of Plant Physiology, Institute of Biology, Warsaw University of Life Sciences - SGGW, Nowoursynowska St. 159, 02-776 Warsaw, Poland.

⁵Department of Environmental Management, West Pomeranian University of Technology in Szczecin, Słowackiego 17 Street, 71-434 Szczecin, Poland

⁶Department of Landscape Architecture, West Pomeranian University of Technology in Szczecin, Słowackiego 17 Street, 71-434 Szczecin, Poland

*kamila_bokszczanin@sggw.edu.pl

Keywords: rhizosphere microbiome; orchard management; mulching systems; microbial diversity; apple production

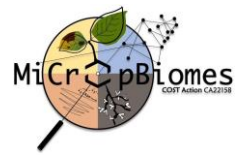
Soil management practices are a key determinant of rhizosphere microbiome structure and stability in orchard systems. In this study, we examined bacterial and eukaryotic communities associated with apple (*Malus × domestica*) roots under seven mulching treatments representing organic and inorganic management across two growing seasons (2020 and 2023). To reduce potential biases linked to separate sequencing runs, datasets from each year were analyzed comparatively to identify consistent microbial patterns.

Amplicon sequencing targeting 16S rRNA and ITS regions revealed that management-specific microbial signatures were reproducible over time despite inter-run variability. Bacterial alpha diversity differed significantly among treatments, while beta diversity consistently separated management regimes in both seasons. In contrast, fungal alpha diversity remained relatively stable, whereas beta diversity indicated clear compositional differences between organic and inorganic systems.

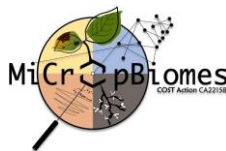
Organic mulches, including shredded *Miscanthus* straw and spent mushroom compost, promoted the abundance of bacterial taxa associated with organic matter turnover, such as Sphingomonadaceae, Flavobacteriaceae, and Moraxellaceae. Inorganic treatments favored taxa including Comamonadaceae and Nitrosomonadaceae. Organic systems were also enriched in saprotrophic fungi (e.g., Lasiosphaeriaceae) and diverse eukaryotic groups such as Ciliophora, while Mortierellaceae were more characteristic of inorganic conditions.

Network analysis revealed a relatively stable bacterial core microbiome, whereas fungal and broader eukaryotic communities showed greater modularity and responsiveness to management practices. These results suggest that long-term organic mulching supports consistent and functionally relevant microbial assemblages, highlighting the role of soil management in shaping resilient orchard ecosystems.

Funding: This research was funded by the National Science Center, Poland, MINIATURA.



Posters



Indigenous Mycobiota of Maraština Grapes: Effects of Vineyard Location and Environmental Factors on Community Composition

Irena Budić-Leto^{1*}, Federica Cardinali², Ilario Ferrocino³, Ana Boban¹, Lucia Aquilanti² and Vesna Milanović²

¹ Institute for Adriatic Crops and Karst Reclamation, Put Duilova 11, 21000 Split, Croatia

² Dipartimento di Scienze Agrarie, Alimentari ed Ambientali, Università Politecnica delle Marche, via Brecce Bianche, 60131 Ancona, Italy

³ Department of Agricultural, Forest, and Food Science, University of Turin, Largo Paolo Braccini 2, 10095 Grugliasco, Turin, Italy

*irena@krs.hr

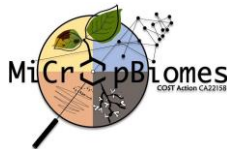
Keywords: Grapevine; Metataxonomic approach; Non-*Saccharomyces* yeasts

Indigenous grapevine microbial communities, together with environmental conditions and physicochemical parameters during fermentation, play a key role in shaping the organoleptic properties of wine (1). The surface of grape berries represents a complex habitat for diverse microorganisms, including non-*Saccharomyces* yeasts, fungi and bacteria, whose composition and abundance are primarily influenced by grape variety, vineyard location, micro- and regional climate, soil characteristics, berry developmental stage, and viticultural practices.

To evaluate the total grapevine microbial communities associated with the Croatian white cultivar Maraština, Illumina MiSeq sequencing technology was employed. A manually curated database of indigenous mycobiota was used for taxonomic classification via the QIIME feature-classifier plugin against the SILVA database. At the same time, the BLAST suite was used to confirm taxonomic assignments (2). This metataxonomic approach enabled the identification of 25 fungal genera present on grape berries collected from 11 vineyards across the Croatian coastal winegrowing region of Dalmatia, including Northern Dalmatia, the Dalmatian hinterland, and Central and Southern Dalmatia. The results revealed fungal taxa with beneficial effects on wine production and potential applications in biocontrol, as well as taxa with possible negative impacts on grapevine health, thereby contributing to improved vineyard management strategies. The surface of Maraština grapes was predominantly colonized by highly abundant, weakly fermentative yeast-like *Aureobasidium* species and filamentous fungi such as *Cladosporium*, as well as the non-*Saccharomyces* yeast *Metschnikowia*, followed by basidiomycetous, oxidative non-*Saccharomyces* yeasts including *Filobasidium*, *Cryptococcus*, and *Rhodotorula*. In addition, the mycobiota of Maraština grape samples included low-abundance genera of obligate plant pathogen *Erysiphe*, moulds such as *Botrytis cinerea*, and filamentous fungi including *Aspergillus*, *Cladosporium*, and *Penicillium*, some of which are associated with grape diseases and mycotoxin production (3).

Pronounced differences in community composition were observed at both regional and local scales, indicating strong spatial structuring of the grape-associated mycobiota. Climate conditions and soil characteristics contributed significantly to the observed spatial variability. Regional patterns indicated that *Pichia* was more prevalent in Northern Dalmatia. The Dalmatian hinterland subregion exhibited the highest relative abundance of *Buckleyzyma*, *Cladosporium*, *Eremothecium*, *Fusarium*, *Papiliotrema*, and *Rhodotorula*, while *Hanseniaspora* and *Metschnikowia* were least abundant in Central and Southern Dalmatia.

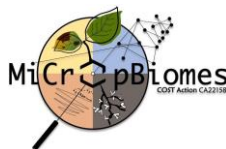
Differences were also observed in most physicochemical properties, which correlated with specific fungal taxa. Higher malic acid content was positively associated with *Metschnikowia* and negatively with *Fusarium*. A positive correlation between *Erysiphe* and pH was detected, while *Sporobolomyces* and *Cystobasidium* were negatively associated with elevated glucose levels.



References

1. Capozzi V, Garofalo C, Chiriatti M A, Grieco F, Spano G (2015). Microbial terroir and food innovation: The case of yeast biodiversity in wine. *Microbiol. Res.* 181: 75–83.
2. Milanović V, Cardinali F, Ferrocino I, Boban A, Franciosa I, Gajdoš Kljusurić J, Mucalo A, Osimani A, Aquilanti L, Garofalo C, Budić-Leto I (2022). Croatian white grape variety Maraština: First taste of its indigenous mycobiota. *Food Res. Int.* 162: Article 111917.
3. Franciosa I, Coton M, Ferrocino I, Corvaglia MR, Poirier E, Jany JL, Rantsiou K, Cocolin L, Mounier J (2021). Mycobiota dynamics and mycotoxin detection in PGI Salame Piemonte. *J. Appl. Microbiol.* 131: 2336–2350.

Funding: Support was provided by the Croatian Science Foundation under the Research project: IP-2020-02-1872 Impact of native non-Saccharomyces wine yeast on wine aromas (WINE AROMAS). This presentation is enabled by CA22158 - Exploiting Plant-Microbiomes Networks and Synthetic Communities to improve Crops Fitness (MiCropBiomes) supported by COST (European Cooperation in Science and Technology).



Early transcriptional responses of tomato cultivars to *Trichoderma harzianum* under short-term water deficit

Igor Vukelić^{1*}, Marija Đikandić¹, Gordana Racić², Svetlana Glogovac¹, Dragana Trkulja¹ and Ankica Kondić Špika¹

¹ Institute of Field and Vegetable Crops, Maksima Gorkog 30, 21000 Novi Sad, Serbia

² Research and Development Institute Tamiš, Novoseljski put 33, Pančevo

*igor.vukelic@ifvcns.ns.ac.rs

Keywords: Gene expression; Symbiotic endophyte; Signalling pathways; *Solanum lycopersicum*

Fungi of the genus *Trichoderma* are beneficial plant symbionts known to stimulate plant growth and increase tolerance to various types of biotic and abiotic stress. However, their early transcriptional effects under short-term water deficit remain insufficiently understood. This study investigated the early effects of *T. harzianum* on the transcriptional activation of genes related to jasmonate signaling (JA), the phenylpropanoid pathway and abscisic acid (ABA) metabolism in tomato leaves during a 48 h drought cycle.

Two tomato cultivars, Gružanski zlatni and Narvik, were grown in pots under controlled conditions in a growth chamber. Plants were exposed to cessation of watering, with or without inoculation of *T. harzianum* (8×10^6 CFU) applied to the root zone at the four-leaf stage. Genes related to JA (PIN II) and ABA (NCED2) signalling, as well as genes involved in the biosynthesis of secondary metabolites (FLS, C3H, SJJAF13 and TPX1) were analyzed. Measurements were performed at 6 and 48 h after inoculation.

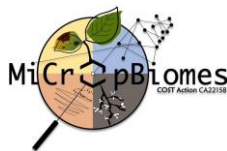
The results showed cultivar-specific transcriptional responses and a significant effect of sampling time. In the cultivar Gružanski zlatni, an early and uniform activation of all examined genes was observed after 6 h. In the cultivar Narvik, a delayed but more sustained transcriptional response was observed, with most genes remaining upregulated after 48 h.

These findings indicate that *T. harzianum* differentially modulates early stress-induced transcriptional responses in tomato cultivars under conditions of short-term water deficit, highlighting the potential of the fungus as a biological agent to improve early stress responses of plants.

References

1. Natsiopoulou D, Topalidou E, Mantzoukas S, Eliopoulos PA (2024) Endophytic *Trichoderma*: Potential and Prospects for Plant Health Management. *Pathogens* 2024, 13, 548

Funding: This research was supported by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, grant number: 451-03-33/2026-03/ 200032. This presentation is based upon work from COST Action CA16107 EuroXanth, supported by COST (European Cooperation in Science and Technology).



Characterization of pears' carposphere-associated fungal microorganisms

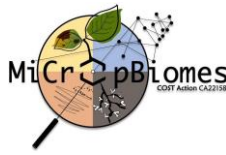
Iglė Vepškaitė-Monstavičė*, Juliana Lukša, Ramunė Stanevičienė, Živilė Strazdaitė-Žielienė and Elena Servienė

State Scientific Research Institute Nature Research Center, Vilnius, Lithuania

*igle.vepstaitė-monstavice@gamtc.lt

Keywords: Pear; Fungal community; Biocontrol yeast; Coexistence; Natural antimicrobials

Pear (*Pyrus communis*) fruits, due to their benefits in taste and nutrition, are widely used in the daily diet. The various microorganisms that inhabit them can influence fruit quality, postharvest behavior, susceptibility to spoilage, and affect human health. In this study, by applying culture-dependent methods and ITS2-based Next Generation Sequencing, we determined the composition of fungal microorganisms associated with naturally fallen pears' carposphere. Metagenomic analysis revealed that dominant genera were *Hanseniaspora*, *Aureobasidium*, and *Microcyclospora*, representing more than 90% of the total mycobiota. *Hanseniaspora uvarum* was confirmed as the dominating species among cultivable yeasts, followed by *Metschnikowia* sp. and *Pichia* sp. The growth rates of isolated yeast strains were evaluated and detected that *H. uvarum* and *P. terricola* demonstrated the lowest generation times, while *M. fructicola* and *P. fermentans* – the highest. The yeast interactions were tested using a pairwise co-culture assay, and the complete inhibition of *P. terricola* by *H. uvarum* was observed. *H. uvarum* exhibited moderate suppressive effects toward *P. fermentans* and *M. fructicola*. Other pairwise interactions of yeasts were weak. Antagonistic activity revealed that *M. fructicola* exhibited inhibitory effects against *Saccharomyces cerevisiae* yeasts and *Staphylococcus aureus*, *Listeria innocua*, and *Salmonella typhimurium* bacteria. The spectrum of research on *M. fructicola* has been expanded, and these studies have demonstrated its biocontrol properties against potentially pathogenic bacteria in a real food system. This investigation can contribute to a broader understanding of the complex relationships between fruit host and their resident mycobiota, including both pathogenic and beneficial species. A comprehensive analysis of the modes of action of antagonistic yeasts, along with their interactions, is important for improving fruit quality and ensuring food biosafety as well as developing sustainable agriculture.



Regional and management-driven variation in apple microbiome and resistome

Denis Kiplimo^{1,2*}, Sebastian Sperber^{1,2}, Muhammad Kabiru Nata'ala¹, Michael Wisniewski³, Samir Droby⁴, Marina M.-C. Höhne^{1,7}, Romano Mwirichia⁵, Gabriele Berg^{1,6} and Ahmed Abdelfattah¹

¹ Leibniz Institute for Agricultural Engineering and Bioeconomy (ATB), 14469 Potsdam, Germany.

² Institute of Biochemistry and Biology, University of Potsdam, 14476 Potsdam, Germany.

³ Department of Biological Sciences, Virginia Polytechnic Institute, and State University, Blacksburg, Virginia, USA

⁴ Department of Postharvest Science, Agricultural Research Organization, The Volcani Institute, Rishon LeZion, Israel

⁵ Department of Biological Sciences, University of Embu, P.O. Box 6-60100 Embu, Kenya.

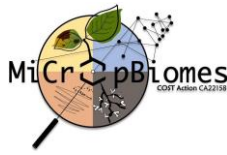
⁶ Institute of Environmental Biotechnology, Graz University of Technology, Graz, Austria.

⁷ Department of Computational Science, University of Potsdam, 14476 Potsdam, Germany

*dgunia@atb-potsdam.de

Keywords: Antimicrobial resistance; Apple Microbiome; Resistome; Shotgun Metagenomic

Antimicrobial resistance (AMR) in plant-associated microbiomes is increasingly recognized as One-Health concern. Apples are widely consumed, yet little is known about how agricultural practices and geography shape its microbiome and resistome. Using shotgun metagenomics, we compared the bacterial, plasmid, and phage communities, and antibiotic resistance genes (ARGs) in apples from organic and conventional orchards in Israel and the USA. Microbiome composition analysis revealed that geographical regions explained the largest proportion of variation in microbial composition, whereas management had a smaller effect but statistically significant across the domains ($p \leq 0.003$). Pairwise PERMANOVA analyses further showed that most regional contrasts explained substantial variation, however, when USA orchards were pooled, the contrasts were statistically significant ($p = 0.003 - 0.006$). In contrast, within-region management showed a sizable effect ($R^2 = 0.34 - 0.56$), however the differences were not statistically significant. Bacterial diversity was significantly higher in organic orchards compared to conventional ones. Phage diversity showed no significant differences, while plasmid diversity was consistently higher in conventional compared to organic orchards, with multiple significant differences. Five genera were identified as the main carriers of ARGs, with *Pseudomonas* being the predominant contributor to ARG transmission, accounting for 14 - 32% of the microbes. ARG diversity varied across the management, the majority of ARGs encoded for multidrug resistance. Smaller but consistent resistance were observed in Macrolide-Lincosamide-Streptogramin (MLS), aminoglycoside, β -lactam and glycopeptide. Efflux pumps, antibiotic inactivation and target alteration were the most dominant resistance mechanisms. Additionally, conventional presented a higher burden of mobile ARGs compared to organic orchards. Our findings reveal that apples carry unique regional microbial signatures and management practices contribute to the context-dependent variation in the resistome composition. Overall, our study highlights an integrated ecological framework linking microbiome, resistome, and horizontal gene transfer events, providing critical insights into AMR management in plant associated microbes.



Where resistance hides and emerges: linking cultivable bacteria and environmental resistomes across pasture microbiomes

Juliana Lukša-Žebelovič^{1,2*}, Alper Melih Ucar^{1,2}, Živilė Strazdaitė-Žiėlienė¹ and Elena Servienė^{1,2}

¹ State Scientific Research Institute Nature Research Centre, Laboratory of Genetics, Vilnius, Lithuania ² Vilnius Gediminas Technical University, Vilnius, Lithuania

*juliana.luksa@gamtc.lt

Keywords: Antibiotic resistance; Metagenomics; Resistome; Agricultural ecosystems

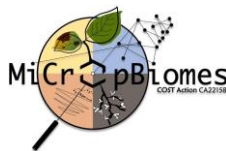
Pasture-based agricultural environments host interconnected microbiomes that link soil, water, and plant-associated compartments. These systems support diverse antibiotic-resistant bacteria (ARB) and resistance genes (ARGs) and represent dynamic microbial networks with potential implications for plant-associated microbiota and crop fitness. In this study, we combined culture-based approaches with shotgun metagenomic analysis to characterize both phenotypic resistance and resistome composition across soil, feed (grass), and freshwater samples collected from Lithuanian pasture-based farms.

A total of 44 bacterial isolates obtained under antibiotic-selective conditions were assigned to 14 genera based on 16S rRNA gene sequencing. Phenotypic resistance profiling using minimum inhibitory concentration (MIC) assays revealed a high prevalence of resistance to ampicillin (59%) and streptomycin (48%), while tetracycline resistance was rare (9%). Multidrug resistance was observed in 41% of isolates, with substantial variability both between and within genera.

Shotgun metagenomic analysis demonstrated clear habitat-specific resistome differences. ARG abundance was highest in feed (~242 RPM), followed by soil (~72 RPM) and freshwater (~34 RPM). Across all environments, multidrug resistance genes associated with efflux mechanisms dominated, especially in feed (74.8%). Additional ARG classes included β -lactam, glycopeptide, tetracycline, and streptogramin resistance genes, whereas freshwater samples were enriched in glycopeptide-associated regulatory elements (e.g., VanR/VanS), indicating resistance potential.

These results reveal a mismatch between cultivable resistance phenotypes and the broader environmental resistome. Plant-associated substrates emerge as potential hotspots of antimicrobial resistance. The observed distribution of ARGs suggests that plant microbiomes may act as interfaces for resistance transmission, potentially reshaping microbial interactions, community stability, and functional outcomes relevant to plant health and productivity.

Funding: This work was supported by the Research Council of Lithuania (LMTLT), grant number SMIP-23-7.



Hydrogen cyanide-mediated modulation of drought stress responses in pepper by *Pseudomonas urmiensis* A32

Aleksandra Mesaroš^{1,2*}, Marija Nedeljković^{1,2}, Marija Anđelković^{1,2}, Slaviša Stanković^{1,2} and Jelena Lozo^{1,2}

¹ University of Belgrade - Faculty of Biology, Belgrade, Serbia

² Center for Pathogen Biocontrol and Plant Growth Promotion, Faculty of Biology, University of Belgrade, Belgrade, Serbia

*aleksandra.mesaros@bio.bg.ac.rs

Keywords: Endophyte; Abiotic stress; Antioxidant enzymes; Hydrogen cyanide (HCN)

Plant-beneficial bacteria can enhance plant tolerance to abiotic stresses, including drought, offering sustainable strategies to mitigate the impact of climate change on crop productivity. This study investigated the role of the pepper endophyte *Pseudomonas urmiensis* A32 in improving plant responses to water deficit, with particular focus on hydrogen cyanide (HCN) production and its involvement in physiological and biochemical adaptations to drought stress. To determine the role of HCN in drought tolerance, an HCN-deficient mutant of *P. urmiensis* A32 was constructed. Pepper seeds were treated with either the wild-type (wt) or the mutant strain. After six weeks, pepper plants were exposed to controlled drought conditions. Plant performance was assessed by measuring growth parameters and stress markers, including hydrogen peroxide (H₂O₂), lipid peroxidation, and proline accumulation. In addition, the activity of key antioxidant enzymes (peroxidase, superoxide dismutase, ascorbate peroxidase) and phenylalanine ammonia lyase was evaluated in treated and control plants. Plants treated with the wt strain exhibited improved drought tolerance, as reflected in reduced oxidative damage compared to control and mutant-treated plants. H₂O₂ levels and lipid peroxidation were significantly lower in plants inoculated with the wt strain. In contrast, proline accumulation was lowest in wt-treated plants, while control and mutant-treated plants showed similarly elevated levels, indicating reduced stress perception in the presence of the HCN-producing strain. Notably, the activity of antioxidant enzymes was significantly modulated in wt-treated plants, whereas mutant-treated plants showed responses comparable to controls, suggesting a role for HCN in regulating antioxidant defence under drought stress. These findings highlight the contribution of HCN production by *P. urmiensis* A32 to enhanced drought tolerance through mitigation of oxidative stress and reduced activation of osmotic stress responses. Further investigation of HCN-mediated signalling pathways and gene expression will provide deeper insight into plant–endophyte interactions under abiotic stress conditions.

Funding: This research was funded by the Ministry of Science, Technological Development, and Innovation of the Republic of Serbia, grant numbers 451-03-34/2026-03/200178 and 451-03-33/2026-03/200178. This presentation is based on work from COST Action CA22158 MiCropBiomes.

Sugar-mediated modulation of Type III secretion system gene expression in *Pseudomonas marginalis* OL141

Marija Nedeljković^{1,2*}, Aleksandra Mesaroš^{1,2}, Marija Anđelković^{1,2}, Elodie Vandelle³, Slaviša Stanković^{1,2} and Jelena Lozo^{1,2}

¹ University of Belgrade - Faculty of Biology, Belgrade, Serbia

² Center for Pathogen Biocontrol and Plant Growth Promotion, Faculty of Biology, University of Belgrade, Belgrade, Serbia

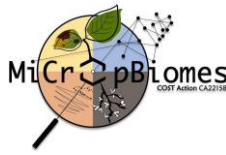
³ Department of Biotechnology, University of Verona, Verona, Italy

*marija.nedeljkovic@bio.bg.ac.rs

Keywords: Type III secretion system; *Pseudomonas*; Plant signals; Interactions

The Type III secretion system (T3SS) is a specialised protein delivery apparatus commonly associated with pathogenicity in Gram-negative bacteria. However, this system is also present in certain non-pathogenic strains such as *Pseudomonas marginalis* OL141, where its regulatory mechanisms remain insufficiently understood. In plant-associated bacteria, T3SS expression is typically triggered by host-derived signals. The role of specific plant metabolites, particularly soluble sugars, in this process is not fully characterised. We investigated the expression of three T3SS-associated genes (*sctR*, *sctS*, and *sctI*) in response to sugar beet (*Beta vulgaris*) leaf extracts collected in May, July and October. Bacterial cultures were grown in HIM medium supplemented with seasonal extracts to induce gene expression. Gene expression levels were quantified by RT-qPCR, with ΔC_t values normalised to 16S rRNA and $\Delta\Delta C_t$ values relative to HIM medium without fructose. The highest expression levels of all three genes were observed in HIM medium without fructose supplemented with the October extract, while increased expression was also detected in fructose-containing medium supplemented with the May extract. Chemical profiling of the extracts using HPLC-MS revealed glucose, fructose and trehalose as the predominant sugars, with the highest total sugar concentration detected in the October extract. Furthermore, assays with individual sugars and their combinations, reflecting concentrations found in the October extract, confirmed their role in modulating T3SS gene expression. These findings indicate that plant-derived sugars act as key environmental signals regulating T3SS expression in *P. marginalis* OL141, providing new insights into bacteria-plant interactions and a foundation for future mechanistic and applied studies.

Funding: This research was funded by the Ministry of Science, Technological Development, and Innovation of the Republic of Serbia, grant numbers 451-03-34/2026-03/200178 and 451-03-33/2026-03/200178. This presentation is based on work from COST Action CA22158 MiCropBiomes.



Comparative genomic characterization and functional potential of five plant-associated *Pseudomonas* strains from pepper and sugar beet

Marija Anđelković^{1,2*}, Bojana Lovrov¹, Aleksandra Mesaroš^{1,2}, Marija Nedeljković^{1,2}, Nikola Đorđević³, Slaviša Stanković^{1,2} and Jelena Lozo^{1,2}

¹ University of Belgrade - Faculty of Biology, Belgrade, Serbia

² Center for Pathogen Biocontrol and Plant Growth Promotion, Faculty of Biology, University of Belgrade, Belgrade, Serbia

³ Agrounik Ltd., Belgrade, Serbia

*marija.andjelkovic@bio.bg.ac.rs

Keywords: *Pseudomonas*; Pangenome analysis; Plant growth-promoting bacteria; Plant-microbe interactions

The genus *Pseudomonas* comprises metabolically versatile bacteria widely recognized for their roles in plant growth promotion, biocontrol, and plant-microbe interactions. Accurate genomic characterization of newly isolated strains is essential for evaluating their ecological roles and biosafety potential. In this study, whole-genome sequencing was performed for five plant-associated strains from two economically important crops, pepper (*P. urmiensis* A32 and *P. atacamensis* A238) and sugar beet (*P. marginalis* OL141, *P. thivervalensis* OR228, and *P. marginalis* ORh26). The main aim was to establish the taxonomic identity, phylogenetic relationships, and functional genomic potential of the five strains, with particular emphasis on plant growth-promoting traits and biosafety-related features. Genome screening revealed no significant virulence-associated determinants or antibiotic resistance genes, indicating a favourable biosafety profile. Secondary metabolite prediction using AntiSMASH identified several biosynthetic clusters in all analyzed strains. Furthermore, analysis using PlaBbase identified a wide array of genes associated with plant growth promotion in all five strains. Comparative genomic analysis using the EDGAR platform highlighted both core and accessory genomic features. Notably, all five strains possess a flagellar gene cluster, while a Type III Secretion System (T3SS) was found only in OL141, ORh26, and OR228. The strains lacking T3SS correspond to endophytic isolates, raising eco-evolutionary questions about its role in plant-microbe communication and niche adaptation. Future work will focus on experimental validation of genomic predictions through wet-lab assays investigating the regulation of flagellar genes in response to different plant extracts. In addition, targeted mutagenesis of selected flagellar genes and their T3SS homologues will be performed. Induction of these systems using selected plant extracts will allow assessment of their effects on bacterial physiology and host plant responses, contributing to a deeper understanding of plant-microbe interaction mechanisms.

Funding: This research was funded by the Ministry of Science, Technological Development, and Innovation of the Republic of Serbia, grant numbers 451-03-34/2026-03/200178 and 451-03-33/2026-03/200178. This presentation is based on work from COST Action CA22158 MiCropBiomes.

Comparative analysis of the type VI secretion system gene repertoires in *Pseudomonas putida*

Tamara Ranković^{1,2*}, Iva Rosić³, Ivan Nikolić^{1,2}, Olja Medić^{1,2}, Tanja Berić^{1,2,3} and Slaviša Stanković^{1,2}

¹ Center for Pathogen Biocontrol and Plant Growth Promotion, Faculty of Biology, University of Belgrade, Belgrade, Serbia

² University of Belgrade – Faculty of Biology, Belgrade, Serbia

³ University of Belgrade, Institute of Physics Belgrade, Belgrade, Serbia

*tamara.rankovic@bio.bg.ac.rs

Keywords: *Pseudomonas putida*; T6SS; Comparative genomics; Pangenome analysis

Pseudomonas putida is a ubiquitous saprophytic bacterium, commonly isolated from rhizosphere and phyllosphere, and frequently considered to be included in microbial consortia due to its plant growth promoting and biocontrol traits. Recently, type VI secretion system effectors have been recognized as *P. putida* crucial weapon for eradicating phytopathogens. Genes encoding effectors and cognate immunity proteins can be found within main or orphan clusters. In *P. putida*, research has focused almost exclusively on the KT2440 strain, while the diversity of T6SS weaponry across other strains remains poorly investigated. This study aimed to provide preliminary overview of the diversity of T6SS-related gene repertoires among *P. putida* strains based on genome annotations.

We performed CheckM2 analysis to select genomes from NCBI with completeness >98% and contamination <2%. Genome comparisons were made between all pairwise combinations of strains using FastANI. Genomes were annotated with Prokka v.1.15.6 and pangenome analysis was performed with Roary v.3.13.0. The T6SS gene presence/absence matrix was visualized in R software v.4.3.0 based on PGAP annotation.

Among 613 genomes of *P. putida* deposited in NCBI, 95 genomes showed high quality. Based on FastANI, 11 different clades with a similarity level >95% were observed among 83 strains, while 12 strains were <95% similar to any of the analysed genomes, and potentially misidentified as *P. putida*. For the pangenome analysis, we selected 53 strains that showed >95% similarity with KT2440. Among 23,948 total genes, 3,496 are core and soft-core, while 20,452 are accessory genes. The extensive accessory genome reveals a high degree of genetic variability among different strains. Focusing on T6SS-related genes, we observed that 52.8% of strains have three complete clusters, 26.4% have two and 3.8% have only one T6SS cluster, while 17% of strains lack T6SS structural genes. We identified the presence of potential orphan clusters, ranging from one to eight, reflecting the effectors diversity across *P. putida* strains. Among potential effectors, we detected genes for BTH_I2691 family protein, ADP-ribosylarginine hydrolase, proteins containing Ntox46, DUF6861, and DUF6531 domains, along with Rhs repeat-containing proteins. Additionally, genes for immunity proteins from the Tsi6 family and DUF6708 domain-containing proteins were detected.

These results provide insight into the diversity of the T6SS gene repertoire based on genome annotations. However, the diversity of effectors and immunity genes may be greater, as they are often annotated as hypothetical proteins. Nevertheless, detected T6SS genes across the strains revealed localization of T6SS clusters within the genomes. This enables targeted searches for putative effector and immunity genes in their vicinities, which require further validation using BLAST-based methods. This variability in T6SS effectors may influence *P. putida* competitive behavior, highlighting its potential relevance in selecting strains for design of microbial consortia to be applied in sustainable agricultural practices.

Funding: The research was supported by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia (grant no. 451-03-33/2026-03/200178 and 451-03-34/2026-03/200178). This presentation is based on work from COST Action CA22158 MiCropBiomes.

Sequence homology of peptaibiotics produced by *Trichoderma* species in the phylogenetically distant *Polysporum* and *Longibrachiatum* clades

Gergő Terna^{1,2*}, Fanni Kovács^{1,2}, Henriett Hunkár^{1,2}, Dóra Krisztina Balázs¹, Ákos Rozsnyói^{1,2}, Chetna Tyagi¹, András Szekeres¹, Mónika Varga¹, Tamás Papp¹, László Kredics¹ and Tamás Marik¹

¹ University of Szeged, Institute of Biology, Department of Biotechnology and Microbiology, Szeged

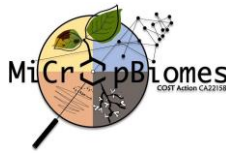
² University of Szeged, Institute of Biology, Doctoral School of Biology, Szeged

*ternag1@gmail.com

Keywords: *Trichoderma*; Peptaibiotics; HPLC-HRMS

Peptaibols are diverse antimicrobial peptides produced by members of the filamentous fungal genus *Trichoderma*. These peptides are assembled by non-ribosomal peptide synthetases (NRPSs) which build in non-proteinogenic amino acids, such as α -aminoisobutyric acid (Aib) and D-isovaline. The C-terminus is modified with an amino-alcohol group, and the N-terminus contains an acetyl group. Due to these properties, peptaibols can form voltage-dependent ion channels in the phospholipid bilayers of living cells which can lead to cell death. On the other hand, peptaibols can activate induced systemic resistance in plants. Several *Trichoderma* species produce not only peptaibols, but lipopeptaibols as well, which are similar to peptaibols containing a fatty-acid modification on the N-terminus instead of the acetyl group. Peptaibiotics comprise both peptaibols and lipopeptaibols, and collectively, the suite of these compounds synthesized by a specific *Trichoderma* strain is known as its peptaibiome. The aim of our work is to characterize the peptaibiome of the phylogenetically distant *Polysporum* and *Longibrachiatum* clades. The *Longibrachiatum* clade is generally described as a phylogenetically derived, highly distinct, and monophyletic group. Phylogenetically the *Longibrachiatum* and *Polysporum* clades emerge as distinct terminal groups, separated by several other species complexes. We selected *T. longibrachiatum* f. *bissettii* from the *Longibrachiatum* clade, which produces one of the strongest antimicrobial peptaibols to our recent knowledge, and two species from the *Polysporum* clade to study their peptaibiomes. The strains were cultivated on malt extract media for 7 days and the peptaibols were extracted by the solvent mix chloroform:methanol 2:1. In order to achieve our goals, we utilize High Performance Liquid Chromatography-High Resolution Mass Spectrometry (HPLC-HRMS). Surprisingly, the genetically distant fungal species were found to produce numerous similar peptaibols. The long peptaibols (20 amino acids) belong to the same peptaibol group, Longibrachins, which were produced by all examined species. Interestingly, *T. longibrachiatum* f. *bissettii* produces only peptaibols, while *Polysporum* clade members produce 7-11-residue lipopeptaibols, namely Lipostrigocins, as well as 13-residue Trichogin GB IX lipopeptaibols. Apart from the known peptaibols and lipopeptaibols, new sequences belonging to these known groups of peptaibiotics were also discovered. This divergence highlights how closely related biosynthetic frameworks can be differentially elaborated, potentially reflecting adaptation to distinct ecological niches. Further research is needed to gain a deeper insight into the synergistic effects of lipopeptaibols and peptaibols.

Funding: This research was supported by the National Research, Development and Innovation Office (projects 2025-1.2.4.-TÉT-2025-00035, EKÖP-570-SZTE, and EKÖP-578-SZTE).



Bioremediation and restoration of a beneficial microbiota in a walnut grove through the input of different biofertilizers

Hira Ikram^{1*}, Fares Bellameche¹, Davide Giovanardi¹, Maurizio Quartieri², Moreno Toselli², Emilio Stefani¹

¹ Department of Life Sciences, University of Modena and Reggio Emilia, Reggio Emilia, Italy

² Department of Agricultural and Food Sciences, University of Bologna, Bologna, Italy

*hira.ikram@unimore.it

Keywords: Soil microbiota; Soil metagenomics; Bioremediation; Organic fertilizers; *Juglans regia*

Walnut (*Juglans regia*) is a high-value crop of growing importance for Europe; this tree species is valued not only for its nutritious fruits, but also to produce premium timber. Walnut, although adaptable to several agroforestry systems, is conveniently grown in loose, well-aerated soil, which promotes deep root growth, optimal aeration, and proper drainage, thus preventing root rot by fungal pathogens and tree physiological decay. In the eastern part of Emilia-Romagna, several hundreds of hectares have been planted in the last two decades, in some cases in areas repeatedly subjected to flooding: in such areas, young orchards are showing symptoms of reduced growth, premature phylloptosis, scarce fruit set, root decay and increased susceptibility to heat and water stress.

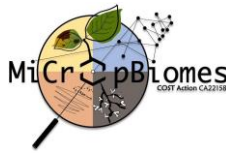
In a walnut grove (approx. 160 ha), soil samples were taken for metagenomic analyses from areas where the trees are suffering from progressive decline (DW), together with soil samples from fields with healthy and productive trees (HW). Metagenomic analyses of healthy and diseased walnut soils revealed that, although both shared a conserved core microbiota at the genus level, their relative abundances differed markedly. Focusing on the top 20 most abundant genera, DW soils were enriched in *Pelobacter*, *Burkholderia*, *Rhodospirillum*, *Azoracus*, and *Desulfuromonas*, whereas HW soils favored *Geobacter*, *Sorangium*, *Phycoccus*, *Friedmanniella*, and *Pirellula*, reflecting higher alpha-diversity and microbial evenness. Species-level biomarker analysis highlighted *Geobacter metallireducens* and *Sorangium cellulosum* as potential contributors to nutrient cycling and pathogen suppression. Bray–Curtis PCoA confirmed a clear structural separation between the communities. Additionally, healthy soil contained a remarkable amount of *Klebsiella* spp., notoriously bacteria with diazotrophic metabolism: *Klebsiella* spp. were absent in diseased soil, which, conversely, contained a significant higher number of myxobacteria. These findings reveal soil dysbiosis associated with walnut decline and define candidate microbial indicators for soil health, providing a scientific foundation for targeted interventions, biofertilizer applications, and sustainable orchard management in European agroecosystems.

To restore the soil physical and chemical structure and support the development of a beneficial soil microbial community, the following commercial biofertilizers were used: 1) municipal organic waste compost and 2) compost from agri-food chain scraps. First results confirmed the increase of microbial activity after both treatments, compared to untreated soil, with a better performance in soil amended with the agri-food waste, supporting the hypothesis of an increase of the microbial biomass (Baldi et al., 2026). Additionally, metagenomic analyses are done to assess the virome in the compost to quantify phages that may affect the structure of soil microbiota. A three-year monitoring of soil structure, chemistry and microbiota will lead to a better understanding of the possibility to restore a beneficial soil microbiota, together with crop productivity, and the role of biofertilizer inputs on the microbial population structure.

References

1. Baldi E, Quartieri M, Messini M, Tassinari A, Büyükfiliz F, Toselli M (2026). Effect of different organic amendment supply on young bearing walnut trees nutritional status and soil fertility. *Agronomy*, 16(2), 262. <https://doi.org/10.3390/agronomy16020262>

Funding: Support was provided by the European Commission through the European Marie Skłodowska-Curie Actions (MSCA) COFUND project: FutureData4EU; Grant agreement ID: 101126733. This presentation is based upon work from COST Action CA22158 MiCropBiomes, supported by COST (European Cooperation in Science and Technology)



Seed microbiome signatures and their influence on early plant growth: A comparative study of *Lathyrus sativus* and *Phaseolus vulgaris* from the Western Balkans

Mihajlo Voruna¹, Jelena Zindović², Duška Delić¹

¹ University of Banja Luka, Faculty of Agriculture, Bulevar vojvode Petra Bojovića 1A, 78000 Banja Luka, Bosnia and Herzegovina

² University of Montenegro, Biotechnical faculty, Mihajla Lalića 15, 81000 Podgorica, Montenegro

Keywords: plant–microbe interactions; rhizosphere microbiome; 16S rRNA sequencing; ITS2; next- generation sequencing (NGS); sustainable agriculture; Balkan crop varieties

The seed microbiome plays a vital role in early plant development, stress resilience, and ecological adaptation. Understanding the composition of seed-associated bacterial communities is critical for improving crop resilience, nutrient uptake, and advancing sustainable agriculture. This study explores and compares the bacterial microbiomes associated with seeds of *Lathyrus sativus* L., commonly grown for consumption in the Trebinje locality of the Herzegovina region (Bosnia and Herzegovina), and a local *Phaseolus vulgaris* L. variety from the Berane municipality in Montenegro, widely used in traditional cuisine.

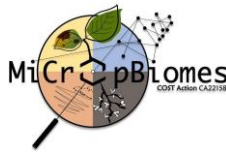
To further investigate the functional implications of these microbiomes, a controlled growth experiment was conducted using lettuce (*Lactuca sativa* L.) as a model plant. Lettuce was cultivated in three treatments: (i) inoculated with *L. sativus* seed, (ii) inoculated with *P. vulgaris* seed-, and (iii) a non-seed control.

Plant growth parameters, including biomass and yield, were measured to assess the influence of different microbiomes from *L. sativus* and *P. vulgaris*. Root samples were collected for DNA extraction and subsequent next-generation sequencing (NGS), targeting bacterial 16S rRNA (V3–V4 region) and fungal ITS2 regions to characterize rhizosphere microbial communities.

Preliminary findings suggest that seed-derived microbiomes differentially influence plant growth and root-associated microbial assembly. This research highlights the importance of seed-associated microbes in shaping plant–microbe interactions and underscores the value of preserving local crop varieties and their native microbiomes as a resource for sustainable agricultural practices in the Balkans.

References

1. Trivedi P, Leach JE, Tringe SG, Sa T, Singh BK (2020) Plant-microbiome interactions: from community assembly to plant health. *Nat Rev Microbiol.* 18(11):607-621. doi: 10.1038/s41579-020-0412-1. Epub 2020



From dysbiosis to defense collapse: a pathobiome view of grapevine esca under abiotic stress

David Gramaje^{1*} and Ales Eichmeier²

¹ Instituto de Ciencias de la Vid y del Vino (ICVV), Consejo Superior de Investigaciones Científicas - Universidad de la Rioja - Gobierno de La Rioja, Ctra. LO-20 Salida 13, Finca La Grajera, 26071 Logroño, Spain;

² Mendeleum - Institute of Genetics, Mendel University in Brno, Valticka 334, 691 44 Lednice, Czech Republic

*david.gramaje@icvv.es

Keywords: abiotic stress; dysbiosis; esca; holobiont; multi-omics

Esca is among the most devastating diseases of grapevine, but it continues to resist explanation within a classical pathogen-centered framework. The fungi most consistently associated with trunk necroses, including *Phaeomoniella chlamydospora*, *Phaeoacremonium minimum* and wood-decay basidiomycetes, are also frequently detected in asymptomatic vines, while inoculation experiments rarely reproduce the hallmark foliar symptoms. This persistent mismatch suggests that esca is not the deterministic outcome of infection by one or a few pathogens, but rather an emergent disease state driven by disruption of the grapevine holobiont.

Here, we synthesize recent evidence and propose that esca should be understood as a stress-mediated pathobiome disorder in which disease results from interactions among trunk-associated microbiomes, host physiology and environmental conditions. Multi-omics studies consistently show that symptom expression is more closely associated with functional shifts in the microbiome than with pathogen presence alone. In symptomatic vines, fungal communities exhibit transcriptional activation of virulence, wood-decay and detoxification pathways, together with metabolic reprogramming of host tissues and systemic regulatory changes, including persistent epigenetic signatures. These findings point to dysbiosis as a transition from a relatively buffered microbial network toward a simplified and unstable community dominated by functionally active disease-associated taxa.

Abiotic stress, particularly drought, emerges as a major trigger of this transition. Drought reshapes trunk microbial communities, alters host vascular function and modifies defense-related metabolism, yet does not translate into symptom expression in a simple linear way. Instead, current evidence supports an integrated feedback model in which microbial dysbiosis, hydraulic dysfunction, defense responses and environmental stress interact over time to determine whether vines remain asymptomatic, develop chronic leaf symptoms or undergo sudden collapse. Within this framework, esca becomes a model for understanding how latent microbiomes shift from coexistence to pathogenicity under stress.

This perspective is highly relevant to current efforts aimed at decoding crop microbiomes in relation to disease and host defense. It opens new avenues for microbiome-informed disease management based on early dysbiosis detection, identification of keystone microorganisms, support of protective microbial networks and vineyard practices that enhance holobiont resilience under climate stress. Beyond grapevine, esca provides a valuable conceptual system for investigating how crop microbiomes mediate the transition from dysbiosis to reduced defense capacity in perennial plants.

***Pseudomonas syringae* phylogroup 2 strains from irrigation waters highlight links to epidemic lineages and potential for crop infection**

Marina Sokić^{1,3*}, Iva Rosić^{1,3}, Olja Medić^{2,3}, Tamara Ranković^{2,3}, Tanja Berić^{1,2,3}, Slaviša Stanković^{2,3}, Ivan Nikolić^{2,3}

¹ University of Belgrade, Institute of Physics Belgrade, Serbia

² University of Belgrade - Faculty of Biology, Department of Microbiology, Belgrade, Serbia

³ Center for Pathogen Biocontrol and Plant Growth Promotion, Faculty of Biology, University of Belgrade

*amarina@ipb.ac.rs

Keywords: *Pseudomonas syringae*; phylogroup 2; irrigation; plant pathogenicity; host range

Pseudomonas syringae is a species complex of phyllosphere-associated bacterial plant pathogens causing diseases in herbaceous, woody, and ornamental plants (1). Although widely studied as a model of plant–pathogen interactions, it has also been isolated from diverse environmental sources, including freshwater, precipitation, and plant debris, suggesting a life cycle beyond the plant host (2). Among its phylogenetic lineages, phylogroup 2 (PG2) stands out due to its broad host range, abundance, and ubiquity across habitats (2). However, its ecological and epidemiological significance remains insufficiently characterized, limiting our understanding of its dissemination pathways and role in plant disease emergence.

In this study, we assessed the pathogenicity of PG2 isolates obtained from the Danube–Tisa–Danube (DTD) hydrosystem in Serbia, a major irrigation water source, by inoculating nine economically important vegetable species. Symptom severity was recorded as the percentage of leaf area affected at 3, 7, and 10 days post-inoculation.

The results show that these environmental isolates exhibit a consistently broad host range across the tested species, highlighting their potential to infect multiple hosts, with sugar beet, pea, and cabbage being the most susceptible. Isolates exhibiting the narrowest host range were still able to infect five different plant species. Statistically significant differences in symptom severity across plant hosts depending on the bacterial isolate were confirmed (Kruskal–Wallis test, $p < 0.001$), indicating differences in isolate aggressiveness. Average symptom severity 10 days post-inoculation revealed two distinct groups of strains differing in aggressiveness: a less aggressive group, originating from a single site with no recorded disease outbreaks and characterized by only occasional severe symptoms, and a more aggressive group, comprising isolates from multiple locations associated with frequent outbreaks and inducing high symptom severity across a greater number of hosts. Strain identification based on the citrate synthase housekeeping gene, combined with comparison to sequences in the NCBI GenBank database, revealed that some isolates from the DTD hydrosystem share haplotypes with previously reported causal strains of sugar beet epidemics in the DTD region, implying epidemiological links and local strain circulation.

PG2 strains with a broad host range detected in irrigation sources highlight the potential role of these populations in plant disease emergence following environmental exposure, as well as their capacity to influence plant-associated microbial communities and trigger plant defense responses. These strains can reach crops through irrigation water, while infected plants may, in turn, release them back into the surrounding environments. Such bidirectional movement underscores their potential for dissemination and persistence across agroecosystems.

References

1. Xin XF, Kvitko B, He SY (2018). *Pseudomonas syringae*: what it takes to be a pathogen. *Nat. Rev. Microbiol.* 16: 316–28.
2. Berge O, Monteil CL, Bartoli C, Chandeysson C, Guilbaud C, Sands DC, Morris CE (2014). A user's guide to a database of the diversity of *Pseudomonas syringae* and its application to classifying strains in this phylogenetic complex. *PLoS One.* 9: e105547.

Bacteriogenic Fe-nanoparticles as selective antifungal agents

Ivana Marić^{1,2*}, Iva Rosić^{1,2}, Ana Ćirić³, Jasmina Glamočlija³, Marina Sokić^{1,2}, Tanja Berić^{1,2,4}

¹ University of Belgrade, Institute of Physics, Belgrade, Serbia

² University of Belgrade, Faculty of Biology, Center for biological control and plant-growth promotion, Belgrade, Serbia

³ University of Belgrade, Institute for Biological Research “Siniša Stanković” - National Institute of Serbia, Belgrade, Serbia

⁴ University of Belgrade - Faculty of Biology, Department of Microbiology, Belgrade, Serbia

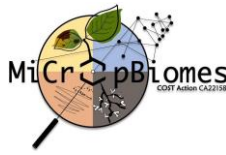
*mivana@ipb.ac.rs

Keywords: Fe-nanoparticles, fungal phytopathogens, antifungal agents, MIC, sustainable agriculture

Fungal phytopathogens significantly constrain global agricultural productivity. Their control mainly depends on synthetic fungicides, which pose considerable environmental risks. Because of their physicochemical properties, fungicides can spread into non-targeted habitats, causing unintended biological effects. Their broad-spectrum activity often harms beneficial plant-associated microbiota, reducing plant health and resilience. These issues raise concerns about sustainability and the integrity of agriculture. Therefore, developing alternative plant-protection strategies is crucial. Among these, biosynthesized Fe-nanoparticles by bacteria offer a promising option that provides effective antifungal activity while reducing ecological disturbance (1). In this study, we investigated bacteriogenic Fe-nanoparticles (FeNPs) produced by two bacterial strains, *Bacillus cereus* (RDJA_1) and *Lysinibacillus* sp. (CB_1.2), as targeted antifungal agents. Their antifungal activity was tested against a broad range of phytopathogenic and non-pathogenic fungi found in plant-associated microbiota, using minimum inhibitory concentration (MIC) and minimum fungicidal concentration (MFC) assays. The bacteriogenic Fe-nanoparticles were initially tested against phytopathogenic fungi isolated from two apple varieties (leaves and fruits): *Aspergillus niger*, *A. aflatoxiformans*, *Penicillium paneum*, *Fusarium hechiense*/*F. fujikuroi*, *Diplodia seriata* using the microdilution method in 96-well microtiter plates. Fe-nanoparticles biosynthesized by both strains inhibited *P. paneum* and *D. seriata*. Notably, Fe-nanoparticles from CB_1.2 exhibited broader activity showing both inhibitory and fungicidal effects (expressed in volumes of Fe-nanoparticles suspension applied) against *A. niger* (MIC 45 μ l; MFC 90 μ l), *A. aflatoxiformans* (MIC 90 μ l) and *F. hechiense*/*F. fujikuroi* (MIC 45 μ l; MFC 90 μ l). A second panel of true, opportunistic and postharvest pathogens (*Alternaria alternata*, *A. niger*, *Penicillium citrinum*, *P. venetum*, *P. funiculosum*) and nonpathogenic fungi (*P. chrysogenum*, *P. ochrochloron*, and *A. oryzae*) revealed selective antifungal activity of FeNPs by both strains using the microdilution method in 96-well microtiter plates. FeNPs by RDJA_1 inhibited several species, such as *A. alternata* (MIC 50-60 μ l, MFC 80-90 μ l), *A. niger* (MIC 30-40 μ l, MFC 70-80 μ l), *P. citrinum* (MIC 80-90 μ l), *P. venetum* (MIC 40-50 μ l, MFC 80-90 μ l) and *P. funiculosum* (MIC 80-90 μ l). FeNPs by CB_1.2 demonstrated persistently stronger and broader inhibition specifically against *A. niger* (MIC 30-40 μ l, MFC 70-80 μ l) and several *Penicillium* species, including *P. ochrochloron* (MFC 80-90 μ l). Notably, certain taxa (*A. oryzae* and *P. chrysogenum*) remained unaffected, suggesting a more selective rather than broad-spectrum antifungal activity. These findings demonstrated that bacteriogenic Fe-nanoparticles, especially those biosynthesized by CB_1.2, inhibit specific fungal phytopathogens while exerting minimal or no effects on non-pathogenic fungi associated with plants. In conclusion, biosynthesized Fe-nanoparticles offer a green, alternative, and sustainable approach for controlling plant pathogens, with targeted effects on non-pathogenic plant-associated fungi and the overall goal of reducing synthetic fungicide use.

References

1. Yassin MT, Al-Otibi FO, Al-Askar AA, Alharbi RI (2023). Green Synthesis, Characterization, and Antifungal Efficiency of Biogenic Iron Oxide Nanoparticles. *Applied Sciences*, 13(17), 9942. <https://doi.org/10.3390/app13179942>



Funding: This study was financially supported by SAIGE (Serbia Accelerating Innovation and Growth Entrepreneurship Project) as a Collaborative Proof of Concept Project “Bacteriogenic Fe-nanoparticles as agents for the control of pathogenic fungi”, between the Institute of Physics, Belgrade, and the Institute for Biological Research “Siniša Stanković”.

Grapevine Microbiome Dynamics Under Black Rot: Insights from the Anna Karenina Principle

Juliana Oliveira-Fernandes^{1,2*}, Conceição Santos² and Philippe Vandenkoornhuys²

¹ REQUIMTE Department of Biology, Faculty of Sciences, University of Porto, Porto, Portugal

² Université de Rennes, CNRS, UMR6553 ECOBIO, Campus Beaulieu, Rennes, France

*juliana.fernandes@univ-rennes.fr

Keywords: Anna Karenina Principle; Dysbiosis; Grapevine; Holobiont; Microbial Assembly

The holobiont concept defines the microorganism host and all of its symbiotic microbiota as an integrated ecological unit, inducing a deep conceptual shift, with the holobiont as an additional level of biological organization (1). This revolutionized the current perception of health and disease. Within this framework, elucidating the relative proportion of deterministic and stochastic processes governing microbial community assembly remains a key challenge in microbial ecology. This aligns with the Anna Karenina Principle (AKP), which takes a causation view of disease, describing it as a deviation from microbial composition homeostasis, in which dysbiosis manifests as increased stochasticity in community assembly (2). We addressed this question for the pathosystem involving the fungal pathogen *Phyllosticta ampellicida*, the causal agent of grapevine black rot (BR). Using 16S rRNA and ITS amplicon sequencing technologies, we characterized the bacterial and fungal microbial communities associated with leaf and root grapevine tissues from asymptomatic and symptomatic plants across three different timepoints. Our goal was to assess the grapevine microbiome diversity and shifts in homeostasis within the context of the AKP framework. Overall, our findings indicate that, despite the presence of visible BR symptoms, *P. ampellicida* infection did not strongly disrupt the overall structure of the grapevine microbiome but is associated with subtle shifts in diversity. The predominance of stochastic processes in both symptomatic and asymptomatic tissues challenges the expectation of disease-driven dysbiosis under the AKP, suggesting a no-AKP scenario. These results suggest a limited role of host-mediated control in microbiome assembly during infection and highlight the need to reconsider how plant disease is interpreted within a holobiont framework.

References

1. Vandenkoornhuys P, Quaiser A, Duhamel M, Le Van A, Dufresne A (2015). The importance of the microbiome of the plant holobiont. *New Phytol.* 206(4): 1196-1206.
2. Arnault G, Mony C, Vandenkoornhuys P (2023). Plant microbiota dysbiosis and the Anna Karenina Principle. *Trends Plant Sci.* 28(1): 18-30.

Funding: This work was funded by the France AgriMer within the 'GetUP' project and Fundação para a Ciência e a Tecnologia (FCT) within the 'SynBiomes' project (2023.17320.ICDT). Juliana Oliveira-Fernandes work is supported by a FCT doctoral grant (2023.03121.BD).

Biocontrol Strategy Shapes Plant Defense: Priming and Direct Antagonism in Sugar Beet—Microbe Interactions

Tamara Krstić Tomić^{1*}, Marija Nedeljković^{2,3}, Aleksandra Mesaroš^{2,3}, Marija Anđelković^{2,3}, Jovana Todorović¹, Marijana Pešaković¹, Slaviša Stanković^{2,3} and Jelena Lozo^{2,3}

¹ Fruit Research Institute, Čačak, Serbia

² University of Belgrade—Faculty of Biology, Belgrade, Serbia

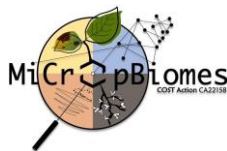
³ Center for Biological Control and Plant Growth Promotion, Faculty of Biology, University of Belgrade, Belgrade, Serbia

*tkrstictomic@institut-cacak.org

Keywords: Induced systemic resistance; *Bacillus* spp.; *Stenotrophomonas maltophilia*; Redox regulation; Salicylic acid/jasmonate signaling

Pseudomonas syringae pv. *aptata* causes significant disease in sugar beet, and sustainable management requires strategies that enhance plant innate defenses. This study compared the effectiveness and underlying mechanisms of indirect and direct biocontrol strategies using three bacterial strains (*Bacillus safensis* – MRh275, *Bacillus pseudomycoides* – JRh226, *Stenotrophomonas maltophilia* – JRh266). Indirect biocontrol involved pre-treating seeds with biocontrol strains before pathogen exposure, whereas direct biocontrol involved simultaneous application of biocontrol strains and the pathogen, allowing comparison between plant-mediated and direct antagonistic effects. Both approaches reduced lesion size, with strains JRh226 and JRh266 being the most effective. However, they differed markedly in their effects on plant physiology. Hydrogen peroxide (H₂O₂) accumulation under indirect biocontrol was elevated even in uninfected plants compared to the control, indicating controlled oxidative signaling associated with microbial colonization. Following infection, strains MRh275 and JRh266 maintained lower H₂O₂ levels, reflecting balanced redox regulation. In contrast, direct treatments showed more variable H₂O₂ dynamics, with strain MRh275 inducing elevated accumulation upon infection, while other treatments exhibited reduced levels. Antioxidant enzyme responses supported these patterns. Under indirect biocontrol, superoxide dismutase (SOD) increased in uninfected plants (strain JRh266) and after infection (strain MRh275), while peroxidase (POD) was enhanced post-infection (strain JRh266). In direct treatments, POD was consistently elevated, whereas SOD decreased in uninfected plants and remained largely unchanged after infection. Phenylalanine ammonia-lyase (PAL) activity further reflected these differences, with increased activity in uninfected plants under indirect treatments (strains MRh275 and JRh226) and strong induction after infection with strain JRh266, while in direct treatments, increased PAL activity was observed only with strain JRh226. Gene expression analyses revealed coordinated activation of *NPR1*, *MYC2*, and *LOX* under indirect biocontrol, supporting primed salicylic acid (SA) and jasmonate (JA)-dependent signaling and enabling a faster, integrated defense. In contrast, direct biocontrol induced strain-specific transcriptional responses, with *NPR1* and *MYC2* strongly upregulated in JRh226-treated plants, reflecting a reactive and less coordinated activation. Overall, the results indicate that indirect biocontrol promotes a primed physiological state characterized by coordinated biochemical and molecular responses, enabling more efficient defense activation upon pathogen challenge, while direct biocontrol provides rapid but less integrated protection, highlighting the importance of application strategy in sustainable sugar beet disease management.

Funding: This study was funded by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, Contract No 451-03-34/2026-03/200178, 451-03-33/2026-03/200178 and 451-03-33/2026-03/200215. This presentation is based upon work from COST Action CA22158 MiCropBiomes, supported by COST (European Cooperation in Science and Technology).



In Vitro* Antagonistic Activity of *Trichoderma* Species against *Fusarium graminearum

Isidora Knežević¹, Helena Todorović¹, Jovan Lazarević¹, Igor Vukelić², Jelena Damjanović¹, Tamás Marik³, László Kredics³, Svetlana Roljević-Nikolić¹, Gordana Racić^{*1}

¹ Tamiš Research and Development Institute, Novoseljanski put 33, Pančevo, Serbia

² Institute of Field and Vegetable Crops, Novi Sad, Serbia

³ Department of Microbiology, Faculty of Science and Informatics, University of Szeged, Szeged, Hungary

*racic@institut-tamis.rs

Keywords: *Trichoderma* sp., dual cultivation, *Fusarium graminearum*

Fungi of the genus *Trichoderma* inhabit various ecosystems, but are predominantly present in different types of soil. They are widely used in various branches of biotechnology and agriculture. Owing to their antagonistic abilities, they play a significant role in the biological control of plant pathogens [1]. *Fusarium graminearum*, one of the most important pathogens of cereals, can cause a serious problems in crop production; therefore, its timely control is of great importance.

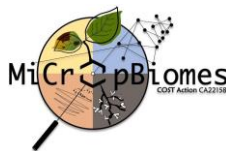
The aim of this study was to examine the antagonistic potential of five different strains of *Trichoderma* (SZMC 22660, 22661, 22664, 22666, and 22668), isolated from different soil types, against *F. graminearum*. The activity of *Trichoderma* isolates was evaluated in dual cultures on PDA medium by placing 5 mm mycelial plugs on opposite sides of Petri dishes (3 cm from the centre). Each *Trichoderma* sp./*F. graminearum* combination was set up in three replicates and incubated for 7 days at 25°C. After the incubation period, results were recorded by measuring the colony diameter of *F. graminearum* under treatment and control conditions. The inhibition values were transformed using the V_x formula, and the transformed data were analysed by one-way analysis of variance (ANOVA) using the software package Statistica (version 14.1.0.8). The significance of differences was tested using Duncan's test at the significance level of $p < 0.05$. In dual cultures, all isolates showed a high percentage of growth inhibition, ranging from 86.66% to 89.63%. The highest observed inhibition was for isolate SZMC 22666 (89.63%). Statistical analysis using Duncan's test showed significant differences among the tested isolates, with isolate SZMC 22666 differing significantly from isolates SZMC 22661 and SZMC 22668.

These results indicate that different *Trichoderma* species exhibit antagonistic activity against *F. graminearum*, highlighting their potential for further investigation under practical crop production conditions, i.e., under field (in vivo) conditions.

Acknowledgment: This research was supported by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, grant number 451-03-33/2026-03/200054 and by the Serbian–Hungarian Scientific and Technological Cooperation Programme (2026–2027) through the project 'Effect of *Trichoderma* spp. on the productive traits of common wheat (*Triticum aestivum* spp.) and the investigation of their peptabiotic profiles'

References

1. Kredics, L., Hatvani, L., Naeimi, S., Körmöczi, P., Manczinger, L., Vágvölgyi, C., Druzhinina I. (2014). Biodiversity of the genus *Hypocrea/Trichoderma* in different habitats, in: Gupta V.K., Schmoll M., Herrera-Estrella A., Upadhyay R.S., Druzhinina I. and Tuohy M. (Eds.), *Biotechnology and Biology of Trichoderma*, Elsevier Science B.V., Amsterdam, pp. 3–24.



Multifunctional Microbial Seed Treatments: Integrating Biostimulation, Biocontrol and Microbiome Interactions

Weronika Walczak^{1*}, Magdalena Jopek¹, Roksana Rakoczy-Lelek¹, Monika Faruga¹, Anna Gierut-Kot¹, Krzysztof Ambroziak¹

¹Intermag, Olkusz, Poland

*Weronika.walczak@intermag.pl

Keywords: plant microbiome; microbial inoculants; seed treatment; biostimulation; biocontrol

The urgent need to reduce chemical plant protection products has shifted attention toward microbiome-based solutions that enhance plant growth and resilience through beneficial plant–microbe interactions. Rhizospheric bacteria are key components of plant microbiomes and can significantly improve crop fitness.

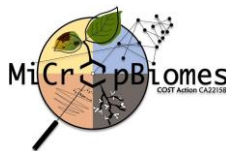
This study, conducted within the SPIN-FERT project, evaluates selected rhizospheric bacterial strains as seed-applied microbial inoculants with a dual mode of action: promotion of plant nutrition and protection against soil-borne pathogens. Particular emphasis was placed on microbiome-relevant traits, including nutrient mobilization, signaling, and antagonistic activity.

In the laboratory phase, strains were selected based on their capacity for atmospheric nitrogen fixation and solubilization of insoluble phosphorus. Biochemical assays confirmed their ability to produce phytohormones and siderophores, indicating involvement in plant–microbe molecular crosstalk. Their biocontrol potential against *Rhizoctonia* spp. was also assessed. In dual-culture assays, selected isolates inhibited mycelial growth by 40.0–55.4%, likely due to the production of extracellular enzymes and antimicrobial metabolites.

Field experiments validated these traits under complex soil microbiome conditions. Seed treatment with selected strains significantly improved early plant vigor and root system development, suggesting a positive impact on rhizosphere microbiome assembly. Under artificial pathogen pressure, treated plants showed increased biomass compared to the control, demonstrating the establishment of a protective microbiome-mediated “bio-shield”.

Chemical analyses confirmed enhanced nitrogen and phosphorus accumulation in plant tissues, indicating improved nutrient uptake efficiency mediated by microbial activity. These findings demonstrate that targeted microbial inoculants can function as both biostimulants and biocontrol agents, supporting the development of sustainable, microbiome-informed agricultural practices.

Funding: Research carried out as part of the SPIN-FERT project entitled “Innovative practices, tools, and products to increase soil fertility and peat substitution in horticultural crops,” funded under the European Union's Horizon 2020 research and innovation program, project no. 101157265.



What is the landscape of plant microbiome research in Serbia? A preliminary bibliometric analysis and the comparison with AI tool.

Stefan Stošić^{1*}, Jovana Blagojević¹, Svetlana Živković¹, Ivan Vučurović¹, and Danijela Ristić¹

¹ Department of Plant Diseases, Institute for Plant Protection and Environment, Belgrade, Serbia

*stefan.stosic@gmail.com

Keywords: microbial community, indexing databases, bibliometry, ChatGPT

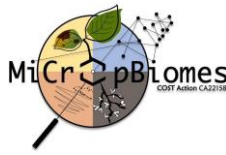
Plant microbiome is defined as „microbial community occupying a reasonably well-defined habitat which has distinct physio-chemical properties, and refers to the microorganisms involved but also encompasses their theatre of activity” (Berg et al. 2020). It represents a „hot topic” in the last decade in the plant sciences. In this work, we present a preliminary bibliometric analysis of plant microbiome research in Serbia, to get a quick overview of this emerging topic in our country. For that purpose, we explored 3 bibliographic/indexing databases – Google Scholar, PubMed and Scopus, with the search term „plant microbiome Serbia”. Furthermore, we used a Large Language Model (LLM), OpenAI ChatGPT (Plus version 5.3) to have a quick glance and assessment of the same search term. Depending on the search database, the resulted metrics provided the total number of publications, document types, distribution by country or by affiliation, etc. As part of an experiment, we asked ChatGPT to create an abstract for this Plant Microbiomes conference based on its results. At the moment of search, Google Scholar provided around 8,250 results, PubMed presented only 59 results and Scopus database found 1,578 documents. Google Scholar search only provides separation by article type, publication year or by relevance and no other deeper statistic. Therefore, we selected „Review Article” filter which revealed that 1600 articles were classified as this publication type. On PubMed, 15 articles belonged to the review articles while the rest included original full papers and conference abstracts. On Scopus, 895 results (56.7%) were classified as original articles, while the remaining results belonged to review articles, conference work, book chapters etc.

ChatGPT analysis encompassed the articles published from 2010 to 2025 and it only provided an estimate. The total number of found publications was in the range of 30 to 80, with a broader estimation of 60-150 articles, which includes plant growth promotion rhizobacteria (PGPR) and rhizosphere studies. In this analysis, the most prevalent article type were original papers (65-80%), while the rest included review articles and conference work. The most studied plant systems were maize, wheat, medicinal plants and horticultural crops. At the end, this LLM gave a suggestion for the specific query we can enter into the Web of Science or Scopus database.

It has to be noted that the search results does not necessarily present only plant microbiome studies, but the studies who contain the words used for bibliography search. Therefore, possible mismatches were expected. For a deeper analysis, more comprehensive and in-depth search needs to be performed. Relying on indexing database search or LLM models is not sufficient enough. However, these tools can be used in a preliminary phase of some research, to get a quick glance of the specific field or topic of interest.

References

1. Berg, G., Rybakova, D., Fischer, D. et al. (2020). Microbiome definition re-visited: old concepts and new challenges. *Microbiome* 8:103. <https://doi.org/10.1186/s40168-020-00875-0> **Funding:** Ministry of Science, Technological Development, and Innovation of the Republic of Serbia (contract number 451-03-33/2026-03/ 200010)



Synergistic Biostimulatory Effects of *Chlorella* sp. MACC-360 and *Kocuria rhizophila* FSP120 Co-cultures on *Solanum lycopersicum*

Katalin Tajti^{1,2,3*}, Attila Farkas¹, Milán Farkas⁴, Gergely Maróti^{1,3,5}

¹ Institute of Plant Biology, HUN-REN Biological Research Center, Szeged, Hungary

² Faculty of Science and Informatics, University of Szeged, Szeged, Hungary

³ Seqomics Biotechnology Ltd., Mórahalom, Hungary

⁴ Department of Molecular Ecology, Institute of Aquaculture and Environmental Safety, Hungarian University of Agriculture and Life Sciences, Gödöllő, Hungary;

⁵ Department of Aquatic Environmental Sciences, Faculty of Water Sciences, Ludovika University of Public Service, Baja, Hungary

*tajti.katalin@brc.hu

Keywords: plant biostimulation; green alga *Chlorella*; *Kocuria rhizophila*; PGPB; photosynthetic efficiency; EPS

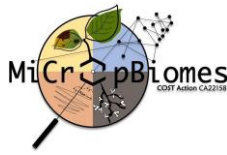
The transition toward sustainable agricultural intensification necessitates the development of innovative biostimulant strategies that can enhance crop resilience and productivity while simultaneously reducing the ecological footprint of synthetic fertilizers. This study investigates the plant growth-promoting (PGP) potential of a novel inter-kingdom microbial consortium, consisting of the eukaryotic green microalga *Chlorella* sp. MACC-360 and the actinobacterium *Kocuria rhizophila* FSP120. Using the cherry tomato cultivar *Solanum lycopersicum* var. Vilma as a model organism, we evaluated the efficacy of individual and combined microbial treatments under controlled greenhouse conditions (24–26 °C, 16h photoperiod) using a nutrient-poor sand-soil (2:1 v/v) growth medium to simulate resource-limited conditions, characterized by low nutrient availability and reduced water-holding capacity.

The experimental design included four groups: an untreated control, *Chlorella*-only, *Kocuria*-only, and the combined co-culture. Total microbial cultures were standardized to a cell density of 10^7 cells mL⁻¹ and applied via the soil drench method (100 mL per pot). Treatments were administered at three critical phenological stages—15, 22, and 29 days post-sowing—to target the transition from seedling emergence to early flowering.

Our findings demonstrate that the integrated algal–bacterial consortium significantly surpassed both the individual applications and the control in several key parameters associated with the plant host (1). Most notably, the co-inoculation resulted in a 43.7% increase in mean fruit yield, a result further validated by statistically significant improvements in individual fruit weight and diameter ($p < 0.05$). Beyond yield enhancement, the combined treatment induced profound phenotypic alterations. Inoculated plants exhibited significantly higher shoot biomass and increased axillary branching, creating a more robust canopy. A particularly striking observation was the alteration of the root architecture. Treated plants displayed a denser, more complex root system characterized by enhanced lateral branching. Although direct phytohormone quantification was not performed in this study, these morphological shifts are highly consistent with microbial auxin-mediated effects. This suggests a potential metabolic synergy where the microalgal partner may augment the bacterium's hormone synthesis pathways or provide precursors that stimulate the host plant's endogenous signaling.

The synergy was further elucidated through the analysis of extracellular polymeric substances (EPS). Using Confocal Laser Scanning Microscopy (CLSM) and Scanning Electron Microscopy (SEM), we observed that the co-cultivation of *Chlorella* and *Kocuria* led to a specifically restructured EPS matrix and biofilm architecture. This EPS layer was primarily observed surrounding the algal cells, suggesting it is predominantly generated by the microalgae. We hypothesize that the consortium's ability to generate these EPS structures even in the soil matrix, potentially improving soil characteristics, moisture retention, and overall soil health.

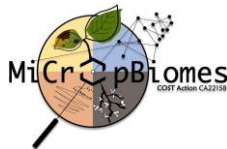
Finally, metagenomic analysis of the rhizosphere revealed that the treatments significantly restructured the native microbial community. Algal application led to a significant increase in the relative abundance of the *Pseudomonas* genus, widely recognized for its phosphate solubilization and IAA synthesis capabilities. Simultaneously, while the relative abundance of indigenous *Streptomyces* species shifted (decreased), their



essential protective functions remained stable across treatments, contributing to the suppressive nature of the soil. In conclusion, the strategic integration of microalgae and PGP bacteria offers a multifaceted approach to sustainable crop production by integrating hormonal stimulation, physical soil modification via EPS, and beneficial restructuring of the rhizosphere microbiome.

References:

1. Tajti, K.; Farkas, A.; Farkas, M.; Bíró, T.; Ördög, V.; Maróti, G. Synergistic Plant Biostimulatory Effects of an Inter-Kingdom Interaction: Chlorella Sp. and Kocuria Rhizophila Algal–Bacterial Co-Culture for Sustainable Crop Production. *Plants* **2026**, *15*, doi:10.3390/plants15020292.



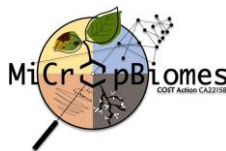
Microbial diversity and phosphorus solubilization potential in the rhizosphere of *Sedum acre* L.

Muhammad Fahad Hakim, Danas Baniulis, Elena Andriūnaitė, Inga Tamošiūnė

Institute of Horticulture, Lithuanian Research Centre for Agriculture and Forestry, Kaunas Str. 30, 54333 Babtai, Kaunas reg., Lithuania

*inga.tamosiune@lammc.lt

Phosphorus (P) is an essential macronutrient for plant growth, yet in most soils, the majority of it exists in insoluble mineral or organic forms that are largely unavailable for direct uptake. Plants depend on mutualistic interactions with rhizosphere microbiota to mobilize P, primarily through the activity of phosphorus-solubilizing microorganisms that release organic acids and other metabolites to convert insoluble phosphates into plant-available forms. Crassulaceae succulent species, such as *Sedum acre* L., which thrive in nutrient-poor and arid environments, represent valuable models for studying these plant-microbe associations in extreme oligotrophic systems. In this study, shotgun metagenomics was used to compare the microbial communities of bulk soil and *S. acre* rhizosphere across five populations inhabiting sandy pine forest habitats, and AlPO_4 -solubilizing bacterial strains were isolated from the rhizosphere. Alpha diversity metrics revealed similar microbial richness and evenness between bulk soil and rhizosphere samples. In contrast, beta diversity analysis indicated clear compositional differences, with the *S. acre* rhizosphere significantly enriched in Betaproteobacteria (including *Haliae*, *Pelomonas*, *Variovorax*, *Mitsuaria*, *Caenimonas*, and *Acidovorax* spp.) and Alphaproteobacteria (particularly *Caulobacter* spp.). Although functional profiles showed less pronounced divergence than taxonomic composition, suggesting a degree of functional redundancy, the rhizosphere microbiome exhibited enhanced genetic potential for nutrient acquisition, stress adaptation, and active interaction with the plant host. Culture-dependent screening yielded 44 AlPO_4 -solubilizing isolates belonging to 12 bacterial genera. *Pseudomonads* comprised approximately half of the collection, spanning five distinct subgroups. Members of the Enterobacteriaceae family formed another major group, including *Enterobacter*, *Pantoea*, *Rahnella*, *Rouxiiella*, *Serratia*, and *Cedecea* spp. Three Gram-positive isolates were assigned to *Staphylococcus* and *Microbacterium* spp. Phosphorus solubilization efficiency was highly strain-dependent, with the strongest activity observed among isolates from the *P. fluorescens* subgroup as well as *Pantoea* and *Enterobacter* sp. Overall, these findings demonstrate that succulents such as *S. acre* could serve as a valuable model to study plant-microbe symbioses in nutrient-poor environments and its rhizosphere could be used as a source of phosphorus-solubilizing bacteria with potential applications in sustainable agriculture.



Mitigating salinity and cadmium stress in rice (*Oryza sativa* L.) using PGPR and salicylic acid: rhizosphere, health risk, and physiological insights

Arwa Abdulkreem Al-Huqail¹, Muna Abdul-Rahman Al-Malki², Dalia Mohammad Melebari², Hanan El Sayed Osmanb^{2,3}, Dikhnah Alshehri⁴, Suliman Mohammed Suliman Alghanem⁵, Amany H.A. Abeed⁶, Hesam Mousavi^{7*}

¹ Department of Biology, College of Science, Princess Nourah bint Abdulrahman University, Riyadh, Saudi Arabia

² Biology Department, College of Science, Umm Al-Qura University, Makkah, Saudi Arabia

³ Botany and Microbiology Department, Faculty of Science, Al-Azhar University, Cairo, Egypt

⁴ Department of Biology, Faculty of Science, University of Tabuk, Tabuk, Saudi Arabia

⁵ Department of Biology, College of Science, Qassim University, Burydah, Saudi Arabia

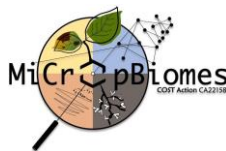
⁶ Botany and Microbiology Department, Faculty of Science, Assiut University, Assiut, Egypt

⁷ Faculty of Applied Ecology, Agricultural Science and Biotechnology, University of Inland Norway, Elverum, Norway

[*hesam.mousavi@inn.no](mailto:hesam.mousavi@inn.no)

Keywords: Salt stress; metal accumulation; acids; growth bacteria; gene expression

Soil contamination by salinity and heavy metals, such as cadmium (Cd), is becoming a serious global problem due to rapid socioeconomic development. Although plant growth-promoting rhizobacteria PGPR and organic agents such as salicylic acid (SA) are considered major protectants to alleviate abiotic stresses, the study of these bacteria and organic acids to ameliorate the toxic effects of salinity and Cd remains limited. Therefore, the present study was conducted to investigate the individual and combined effects of PGPR and SA on enhancing the phytoremediation of salinity (100 mM NaCl) and Cd (50 μ M CdCl₂) using rice (*Oryza sativa* L.) plants. The research results indicated that elevated salinity and Cd stress in soil significantly decreased plant growth and biomass, photosynthetic pigments, and gas-exchange attributes. However, salinity and Cd stress also induced oxidative stress in the plants by increasing malondialdehyde (MDA) and hydrogen peroxide (H₂O₂) by 44% and 38%, respectively, which also led to increased levels of various enzymatic and nonenzymatic antioxidants, as well as gene expression and sugar content. Furthermore, significant increases in cadmium accumulation, potential health risk indices, proline metabolism, the AsA–GSH cycle, and pigmentation of cellular components were observed. The application of PGPR and SA resulted in a significant increase in plant growth and biomass, gas-exchange characteristics, microbial diversity, functional gene abundance in the rhizosphere, enzymatic and nonenzymatic compounds and their gene expression, and a decrease in oxidative stress. In addition, the application of PGPR and SA enhanced cellular fractionation and decreased metal accumulation by 37% in shoots, as well as proline metabolism and the AsA–GSH cycle in *O. sativa* plants. These results provide new insights for sustainable agricultural practices and hold immense promise in addressing the pressing challenges of salinity and heavy metal contamination in agricultural soils.



Effects of an autochthonous PGPR consortium on fruit quality and health-promoting traits of European plum cv. 'Čačanska lepotica'

Jovana Todorović¹, Marijana Pešaković¹, Tamara Krstić Tomić¹, Ivan Nikolić^{2,3}, Tamara Ranković^{2,3}, Boris Rilak¹, Jelena Lozo^{2,3} and Slaviša Stanković^{2,3}

¹Fruit Research Institute, Čačak, Serbia

²University of Belgrade-Faculty of Biology, Belgrade, Serbia

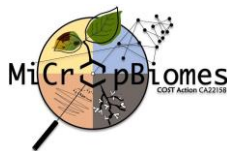
³Center for Biological Control and Plant Growth Promotion, Faculty of Biology, University of Belgrade, Belgrade, Serbia

*jtodorovic@institut-cacak.org

Keywords: bacterial consortium, *Pseudomonas* spp., *Bacillus* spp., plum, antioxidant activity

Plant growth-promoting rhizobacteria (PGPR) represent an effective strategy for enhancing fruit quality while reducing dependence on conventional fertilization practices. This study aimed to evaluate the effects of a selected bacterial consortium on the quality attributes of plum (*Prunus domestica* L.) cultivar 'Čačanska lepotica', with particular emphasis on bioactive compounds and morphometric traits. Following the evaluation of plant growth-promoting traits, five bacterial isolates were selected according to their complementary properties and assembled into a consortium. Molecular identification based on 16S rRNA gene sequencing revealed that the selected isolates belonged to the genera *Pseudomonas* and *Bacillus*. A field experiment was carried out with four treatment groups: an untreated control (C), a bacterial consortium (BC), the consortium combined with mineral fertilization (MIX), and mineral fertilizer alone (MIN). Treatments were applied four times throughout the 2025 growing season via foliar spraying and rhizosphere drenching. After harvest, fruit quality was assessed by evaluating morphometric traits (size and weight) and biochemical parameters, including total anthocyanins, total phenolic content, and antioxidant activity measured using the DPPH assay. The BC treatment significantly improved (Dunnett $p < 0,05$) morphometric traits, including fruit size and weight, indicating a stimulatory effect on fruit development. The same treatment also resulted in a significant increase (Dunnett $p < 0,05$) in the accumulation of anthocyanins and total phenolics, accompanied by enhanced antioxidant activity, as evidenced by increased DPPH radical scavenging capacity in the fruits. Overall, the findings confirm that the application of selected bacterial consortium can positively influence the compositional and morphometric parameters of plum fruits. The increased levels of bioactive compounds and antioxidant capacity indicate stimulation of secondary metabolism, particularly the phenylpropanoid pathway, leading to enhanced synthesis of phenolic compounds and anthocyanins. These changes contribute to improved nutritional value and health-promoting potential of the fruits, supporting the integration of PGPR-based strategies into sustainable fruit production.

Funding: Support was provided by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, Contract No 451-03-33/2026-03/200215, 451-03-137/2025-03/200178 and 451-03-136/2025-03/200178. This presentation is based upon work from COST Action CA22158 MiCropBiomes, supported by COST (European Cooperation in Science and Technology).



Efficacy of two bacterial SynCom prototypes in promoting plant growth and stimulating plant response to stress under controlled-environment greenhouse conditions

Núria Daranas*, Gemma Roselló, Núria Giralt, Esther Badosa, Emili Montesinos, Anna Bonaterra

CIDSAV, Institute of Food and Agricultural Technology, University of Girona, Girona, Spain.

*nuria.daranas@udg.edu

Keywords: synthetic microbial communities, plant growth promotion, plant defense stimulation

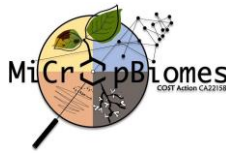
Currently, agriculture requires the development of new approaches to sustainably increase crop productivity and quality. Synthetic microbial communities (SynComs), which can act as biopesticides or biostimulants, are promising biological products that enhance water absorption, nutrient acquisition, tolerance to abiotic and biotic stresses, plant vigor, crop quality, and yield. After isolation from natural sources, characterization, and compatibility testing of the microbial components within SynCom prototypes, it is essential to evaluate their efficacy and performance under controlled environment greenhouse conditions.

The aim of this study was to evaluate the efficacy of two bacterial SynCom prototypes composed of *Azospirillum brasilense*, *Pseudomonas* sp. and *Bacillus subtilis* strains in promoting plant growth and stimulating plant defense responses. These bacteria were previously isolated from plant environments and were selected based on key functional traits, including nitrogen fixation, phosphate solubilization, phytohormone production, ACC deaminase activity, and siderophore production. In addition, the selected strains exhibited high levels of compatibility.

Two plant growth–promotion assays were performed in wheat. Specifically, the first assay was conducted under optimal growth conditions, while the second assay was carried out under hydric stress. In both trials, a significant growth-promoting effect was observed for the two SynCom prototypes, affecting in both conditions the aerial parts of the wheat plants and leaf parameters, such as chlorophyll content and nitrogen balance index (NBI).

Plant defense stimulation was determined in tomato plants by analyzing the transcription of 11 genes implicated in the plant response to stress. One of the prototypes overexpressed genes involved in the synthesis of pathogenesis-related proteins and transcription factors, which could indicate its ability to reduce the severity of bacterial and fungal infections in tomato plants, as well as to better tolerate abiotic stresses. This prototype would therefore have greater potential for the further development.

Funding: Support was provided by a student grant (2024-FI-1 00773). This presentation is based upon work from COST Action MiCropBiomes, CA22158, supported by COST (European Cooperation in Science and Technology).



FoodN'Feed: Locally adapted beneficial microbiomes and synthetic communities for enhanced grain legume performance and sustainable protein production

Louise Mathier^{1,2*}, Claire Prigent-Combaret³, Saskia Bindschedler² and Joël F. Pothier¹

¹ Environmental Genomics and Systems Biology Research Group, Institute of Natural Resource Sciences, Zurich University of Applied Sciences (ZHAW), Life Sciences and Facility Management, Wädenswil, Switzerland

² Laboratory of Microbiology, University of Neuchâtel, Neuchâtel, Switzerland

³ Ecologie Microbienne, Université Claude Bernard Lyon 1, Université de Lyon, CNRS UMR-5557, INRAe UMR-1418, VetAgroSup, Villeurbanne, France

*louise.mathier@zhaw.ch

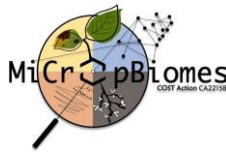
Keywords: Grain legumes; Plant-microbe interactions; Symbiotic nitrogen fixation; Synthetic communities; Metagenome-assembled genomes

Europe's increasing demand for sustainable, low-emission protein sources highlights the importance of grain legumes, such as soybeans, faba beans, and peas. These crops depend on root-associated beneficial microorganisms, particularly nitrogen-fixing rhizobia, to reduce the need for synthetic nitrogen fertilizers and support soil health. However, these interactions are underutilized in European agriculture, where commercial inoculants often perform inconsistently due to competition with already well-adapted native soil communities. The FoodN'Feed project aims to develop a locally adapted microbial resource base for major Swiss grain legumes, consisting of indigenous, functionally relevant microbial strains and communities. Through collaborations with the ROOT-BENEFIT and MiCropBiomes COST Actions, we will test their broader applicability across Central and Northern Europe. Our objectives are to:

1. Characterize the diversity and functional potential of rhizobial and non-rhizobial beneficial microbes in nodules, rhizosphere, and soils using 16S rRNA and ITS metabarcoding;
2. Identify true nodule-forming partners through targeted sequencing of the *nodD* regulatory gene;
3. Recover high-resolution genomic information from nodules via whole metagenomics to obtain metagenome-assembled genomes (MAGs);
4. Isolate, identify, and sequence the genome of promising bacterial and fungal strains to build a curated culture collection;
5. Design and assemble synthetic communities (SynComs) of native, complementary microbes tailored to Swiss edaphic and climatic conditions;
6. Co-evaluate the performance, stability, and transferability of these SynComs with partners in contrasting agro-climatic environments.

This project lays the foundation for robust, highly efficient microbial inoculants by integrating community profiling, genome-resolved analyses, and SynCom design. The anticipated impact includes reduced fertilizer dependency, improved legume performance, enhanced soil health, and greater regional protein self-sufficiency in the face of climate change.

Funding: Support was provided by the Swiss National Science Foundation (SNSF; grant 10006234). This presentation is based upon work from COST Actions CA22142 ROOT-BENEFIT and CA22158 MiCropBiomes, supported by COST (European Cooperation in Science and Technology).



Assembly of microbial collection, isolated from potato field samples

Tina Arnšek^{1*}, Anže Vozelj¹, Karmen Pogačar¹, Martin Stražar¹, Marko Petek¹, Ines Mandič Mulec², Kristina Gruden¹

¹ Department of Biotechnology and Systems Biology, National Institute of Biology, Ljubljana, Slovenia

² Biotechnical faculty, University of Ljubljana, Ljubljana, Slovenia

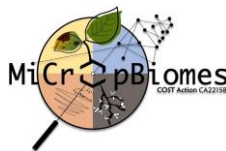
* tina.arnsek@nib.si

Keywords: potato microbiome, microbial collection, SynCom

Potato (*Solanum tuberosum* L.) is one of the world's most cultivated crops. The growth and yield of potato highly depend on the diversity and structure of the bacterial and fungal communities with which the potato plant coexists. Specific microbes can help the plant to adapt to particular environmental conditions and resist pathogens (1). To better understand these interactions between potato plant and microbes, we have prepared a microbial collection, with microbes isolated from potato field samples. In our poster we will present a protocol for preparation of such collection, from isolation of bacteria and fungi, to characterisation of these microbes. For our collection we used potato root and leaf samples, which were collected from different cultivars in the field and grown with two different agricultural managements. Isolated microbes were identified using MALDI-TOF mass spectrometry. Our end goal is to determine which of these isolated microbes is most beneficial to potato growth and its resistance to pathogens, and eventual assembly of synthetic microbial communities (SynComs), which will have a positive impact on potato growth and yield and represent an important innovation in the field of sustainable agriculture, as they offer an environmentally friendly plant protection system.

References

1. Petrushin IS, Filinova NV, Gutnik DI (2024). Potato Microbiome: Relationship with Environmental Factors and Approaches for Microbiome Modulation. *International Journal of Molecular Sciences*, 25(2), 750. <https://doi.org/10.3390/ijms25020750>



Effect of endophytic bacterial isolates on the regrowth of shoot tips of apple cv. Gala after cryopreservation

Jurgita Vinskienė, Inga Tamošiūnė, Šarūnė Morkūnaitė-Haimi, Perttu Juhani Haimi and Rytis Rugienius

Lithuanian Research Centre for Agriculture and Forestry, Institute of Horticulture, Laboratory of Cryobiology, Babtai, Lithuania

*jurgita.vinskiene@lammc.lt

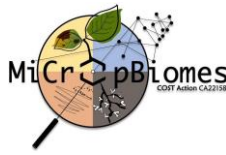
Keywords: Bacterial endophytes; Cold acclimation; Cryofreezing; *In vitro* shoot culture; Meristem; Preconditioning

Cryopreservation at liquid nitrogen temperature (-196 °C) is one of the most effective and safe methods for long-term storage of plant genetic resources. However, not all genotypes of horticultural plants withstand the harsh conditions of cryogenic freezing well enough, which leads to insufficient survival and recovery of explants after cryopreservation. This is being solved by improving cryopreservation technologies, such as changing the conditions of hardening and freezing, or the application of cryoprotectants used for explant preparation. So far, little is known about the potential of microorganisms, including endophytic ones, to increase plant survival after the cold stress experienced by cryoprotected shoot tips. However, it has been proven that some endophytic microorganisms have a positive effect on the growth of microshoots of apple and other species *in vitro* and *ex vitro*. Therefore, the aim of the present study was to evaluate the impact of cold hardening and endophytic bacteria inoculum on improving shoot tip viability parameters of the apple cv. Gala after cryopreservation. A longer preconditioning duration (4 weeks and longer) was found to improve shoot tip survival after cryogenic freezing. In contrast, the effect of *Bacillus* spp. isolates on microshoot regrowth depended on the duration of cold hardening. Inoculation with endophytic bacteria did not have a significant positive effect on the viability of unhardened *in vitro* shoots. Therefore, *in vitro* shoot culture co-cultivation with bacterial inoculum prior to 2 and 4 weeks of cold hardening increased microshoot survival after cryopreservation by 36.4% and 30.3%, and regeneration by 42.8% and 48.8%, respectively. Ongoing research focuses on identifying endophytic bacterial isolates to effectively enhance the regeneration of various horticultural plants following cryopreservation.

References

1. Białoskórska M, Rucińska A, Boczkowska M (2024). Molecular mechanisms underlying freezing tolerance in plants: Implications for Cryopreservation. *Int J Mol Sci.* 25:10110. <https://doi.org/10.3390/ijms251810110>.
2. Vinskienė J, Tamošiūnė I, Andriūnaitė E, Gelvonauskienė D, Rugienius R, Hakim MF, Stanys V, Buzaitė O, Baniulis D (2025). Inoculum of endophytic *Bacillus* spp. stimulates growth of *ex vitro* acclimatised apple plantlets. *Plants* 14:1045. <https://doi.org/10.3390/plants14071045>.

Funding: This research was supported by the Research Council of Lithuania (LMT LT), grant No. S-MIP-25-29.



MICROBES-4-CLIMATE Project: Understanding microbiome-plant-soil-environment interactions for climate-resilient ecosystems

Malek Marian^{1*}, Cintia Mayr¹, Tanja Kostic¹, Angela Sessitsch¹, Livio Antonielli¹, and the Microbes-4-Climate Consortium

¹AIT Austrian Institute of Technology GmbH, Center for Health & Bioresources, Bioresources Unit, Tulln, Austria

*Malek.marian@ait.ac.at

Keywords: Plant microbiome; SynComs; drought stress; sustainable agriculture; Transnational Access programme

Terrestrial biodiversity and ecosystems are being challenged by climate change and environmental degradation with threats to agricultural and forestry ecosystems. Microorganisms constitute the life support system of the biosphere. However, the impacts of climate change-induced stresses on the microbiome assembly, structure, and function, as well as the microbiome contribution to crop stress mitigation and adaptation remain poorly understood.

MICROBES-4-CLIMATE provides the global research community (users) with coordinated access to cluster of complementary, world-class Research Infrastructures offering integrated advanced services, training, and scientific and technical support. Through its excellence-driven Transnational Access programme, the project enables users to conduct curiosity-driven research addressing terrestrial biodiversity and ecosystems, and the complex microbiome-plant-soil-environment interactions underlying climate resilience and mitigation. By fostering high-quality, interdisciplinary research, the initiative advances knowledge on these interactions and supports the development of climate-resilient ecosystems.

Within this framework, Work Package 3 focuses on the establishment and validation of synthetic microbial communities (SynComs) to enhance drought resilience in agricultural systems. Wheat plants and associated soils were collected from drought-affected regions in Greece, Italy, and France, and their microbiomes are being characterized using both culture-dependent and culture-independent approaches. These data will guide the rational design of SynComs aimed at improving wheat drought tolerance under field-relevant conditions.

Funding: Work supported by the awarded Horizon Europe MICROBES-4-CLIMATE Project (Microbial services addressing climate change risks for biodiversity and for agricultural and forestry ecosystems: enabling curiosity-driven research and advancing frontier knowledge; Grant agreement ID: 101131818).

Effect of Direct Plant–Fungus Interaction on Peptaibol Production of *Trichoderma longibrachiatum* f. *bisettii*

Fanni Kovács^{1,2*}, Dóra Balázs¹, Gergő Terna^{1,2}, Henriett Hunkár^{1,2}, Ákos Rozsnyói^{1,2}, Chetna Tyagi¹, András Szekeres¹, Mónika Varga¹, Tamás Papp¹, Csaba Vágvölgyi¹, László Kredics¹, Tamás Marik¹

¹ Department of Biotechnology and Microbiology, Faculty of Science and Informatics, University of Szeged, Szeged, Hungary

² Doctoral School of Biology, Faculty of Science and Informatics, University of Szeged, Szeged, Hungary

*fannikov123@gmail.com

Keywords: *Trichoderma*; *Solanum lycopersicum*; Fungal peptaibol production; Plant-fungus interaction; Host developmental stage

Trichoderma species are soil-borne filamentous fungi widely utilized for their multiple plant health benefits including enhanced plant growth, improved disease resistance, and increased abiotic stress tolerance. Several *Trichoderma* species produce secondary metabolites including peptaibols that are non-ribosomally synthesized peptides with molecular weights from 500 to 2200 Da, typically composed of 5–20 amino acids including the non-proteinogenic α -aminoisobutyric acid and a hydroxylated C-terminus. They exhibit wide range of bioactivities, most notably antimicrobial effects, including antibacterial and antifungal properties, but also antitumor and antiparasitic activities. Their mechanism of action involves the formation of ion channels in the membranes of target organisms, which ultimately leads to cell death. Peptaibols may play important roles in plant–microbe interactions and act synergistically in inducing plant resistance and mediating signaling processes, highlighting their significance in *Trichoderma*-based biocontrol strategies.

We aimed to investigate how the presence and developmental stage of tomato (*Solanum lycopersicum*) plants influence the peptaibol production of *Trichoderma longibrachiatum* f. *bisettii*, and to determine whether this effect is mediated by direct plant–fungus interactions or plant-derived signaling molecules.

Tomato plants were cultivated on Murashige and Skoog (MS) medium, on which *Trichoderma* strains typically produce low levels of peptaibols. The fungus was inoculated at four different time points: at sowing, during germination, at the cotyledon stage, and at the first true leaf stage. To differentiate between the effects of living plants and residual plant-derived compounds, the fungus was also inoculated onto media from which plants had been removed prior to inoculation.

Intensive sporulation of *T. longibrachiatum* f. *bisettii* was observed in the rhizosphere of living tomato plants, a phenomenon associated with peptaibiotic production. This effect was absent on plant-free media, indicating that direct interaction between the plant and the fungus is essential for inducing metabolite production. For quantification of peptaibols, compounds were first extracted using a chloroform–methanol (2:1, v/v) mixture, and the peptaibol content of the extracts was subsequently determined by an agar diffusion bioassay against *Micrococcus luteus*. Peptaibol production was significantly lower on MS medium compared to malt extract medium (MEA). Co-cultivation with tomato plants resulted in significant differences depending on plant developmental stage. The highest peptaibol production was observed when the fungus was inoculated at the first true leaf stage, reaching levels comparable to those measured on MEA. No bioactive compounds were detected in extracts of tomato plants alone.

Our results demonstrate that peptaibol production is strongly influenced by active plant–fungus interactions and the developmental stage of the host plant. These findings provide new insights into *Trichoderma*–plant relationships and may facilitate the optimization of peptaibol production for future field applications in biocontrol strategies.

Funding: This research was supported by the National Research, Development and Innovation Office projects 2025-1.2.4.-TÉT-2025-00035 and 2022-1.2.6-TÉT-IPARI-TR-2022-00009.

Boosting olive drought resilience using *Pseudomonas reactans*

Maria Celeste Dias^{1*} and Paula Lorenzo¹

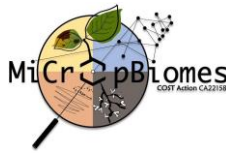
¹ Department of Life Sciences, Centre for Functional Ecology, Associate Laboratory TERRA, Faculty of Sciences and Technologies, University of Coimbra, Calçada Martim de Freitas, 3000-456 Coimbra, Portugal (celeste.dias@uc.pt; paulalorenzo@uc.pt)

*celeste.dias@uc.pt

Keywords: Olive, plant growth-promoting bacteria, photosynthesis, oxidative stress

Agricultural ecosystems are increasingly exposed to extreme climate events driven by climate change, with drought emerging as a major constraint on crop growth and productivity. This challenge extends even to crops traditionally regarded as well adapted to water-limited environments, such as *Olea europaea* L. (olive tree). In this context, the use of eco-friendly strategies, including plant-beneficial microorganisms, represents a promising and sustainable agronomic approach to enhance olive resilience to stress while improving agricultural productivity. In this study, the benefits of pre-treating olive plants with *Pseudomonas reactans* under water deficit conditions were studied. Young potted olive plants were inoculated (in soil) with a solution of *P. reactans* or treated with distilled water (control), and subsequently subjected to two irrigation regimes: well-watered or water deficit. Plant water status, leaf biomass, photosynthesis, pigments, carbohydrate content, oxidative stress biomarkers, and total antioxidant capacity were assessed 61 and 191 days after the onset of the irrigation treatments. The beneficial effects of the *P. reactans* treatment were more pronounced under water deficit conditions, enhancing tolerance to water deficit stress. In particular, *P. reactans* increased leaf dry biomass and improved plant water status, while modulating photosynthesis and antioxidant responses. The treatment promoted net CO₂ assimilation rates and increased carbohydrate accumulation (total soluble sugars and starch). Furthermore, stress-mitigating mechanisms, including enhanced total antioxidant capacity and carotenoid content, were upregulated, contributing to the control of oxidative stress. These findings demonstrate the potential of *P. reactans* to improve olive plant performance and enhance tolerance to drought conditions. This strategy represents a promising approach to increase the sustainability of olive orchards under climate change scenarios. Future studies should further explore the effects of *P. reactans* on different olive cultivars, other (a)biotic stresses, as well as its impact on fruit yield and oil quality.

Funding: This work was supported by FCT - Fundação para a Ciência e Tecnologia, I.P., in the framework of the Project UID/04004/2025 - Centre for Functional Ecology - Science for the People & the Planet, with DOI identifier 10.54499/UID/04004/2025 (<https://doi.org/10.54499/UID/04004/2025>). This presentation is based upon work from COST CA22158, supported by COST (European Cooperation in Science and Technology).



Generational root endophytic enrichment through salinity: Bacterial consortia boost rice growth and resilience

Denise Khouri Chalouhi^{1*}, Iris Bertani¹, Naida Jordamovic¹, Silvano Piazza¹, Cristina Bez¹ and Vittorio Venturi^{1,2*}

¹International Centre for Genetic Engineering and Biotechnology (ICGEB), Trieste, Italy

²African Genome Center, University Mohammed VI Polytechnic (UM6P), Ben Guerir, Morocco

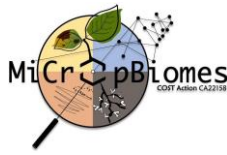
*khouri@icgeb.org

Keywords: Consortia; Endophytes; Enrichment strategy; Rice.

Soil salinity represents a major constraint to global rice (*Oryza sativa*) production, adversely affecting plant growth, physiology, and yield. The root endophytic microbiome plays a critical role in plant adaptation to such abiotic stress, yet strategies to harness these microbial communities remain underexplored. In our previous work (1), we have demonstrated, through bioinformatic analysis, the efficacy of a novel multi-generation enrichment strategy we designed in enriching rice roots endophytes designated as “*super endophytes*” in non stressed and nitrogen starved conditions. In this study, we validated the technique both *in silico* and *in vitro* through a salinity-driven enrichment to select halotolerant bacterial *super endophytes* from rice roots and evaluate their potential as plant growth–promoting inoculants. An initial endophytic community (G0) was serially reinoculated into rice plantlets grown under 50 and 75 mM NaCl across four generations (G1–G4). Community profiling using 16S rRNA gene sequencing, combined with culture-dependent isolation, revealed progressive enrichment of key genera, including *Rhizobium*, *Paenibacillus*, *Pseudomonas*, *Pantoea*, and *Kosakonia*. Selected isolates exhibiting relevant functional traits were assembled into synthetic consortia and evaluated *in planta* under saline and non-saline conditions. Among the tested formulations, an eight-strain consortium (C1) significantly enhanced plant biomass and improved salinity tolerance without disrupting the native root microbiome. A reduced consortium (C5), designed based on strain compatibility and functional complementarity, also demonstrated strong growth-promoting effects. Overall, this study validated that multi-generational enrichment is an effective strategy to select robust endophytes to be tested *in planta*. These findings provide a framework for developing sustainable bioinoculants to enhance rice resilience to salinity.

References

1. Khouri Chalouhi, D., Bertani, I., Esposito, A., Piazza, S., Bez, C., & Venturi, V. (2025). An in Planta Enrichment Route to Identify Bacterial Root Endophytes. *Environmental Microbiology Reports*, 17(3), e70136. <https://doi.org/10.1111/1758-2229.70136>



The rhizosheath microbiome of wild Poaceae across Morocco and its application to drought resistance of wheat

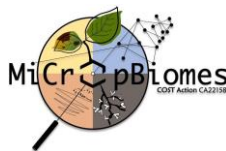
Jean Legeay¹, Mohammed Dahman¹, Mohammed Idbella²

¹ African Genome Center, Université Mohamed 6 Polytechnique, Benguerir, Morocco

² Agricultural Biosciences, Université Mohamed 6 Polytechnique, Benguerir, Morocco

* jean.legeay@um6p.ma

The rhizosheath is a tight agglomeration of soil particles around plant roots, that effects water absorption and retention, thereby increasing the plants resistance to drought. This structure is mostly observed on Poaceae roots ; bacteria play a major rôle in its formation, through the secretion of indole acetic acid and exopolysaccharids. As the rhizosheath is described as typically stronger in wild plants than in crops, this project aims to investigate the feasibility of a transfer of rhizosheath-producing bacteria from wild species to wheat. We are currently in the process of sampling wild Poaceae across Morocco ; we are documenting the thickness of their rhizosheath and we are isolating the associated microbes from the rhizosheath of these plants. Our findings so far show that plants from the species *Hordeum muricum* and *Cynodon dactylon* have the strongest rhizosheath, but even in these species, the presence of rhizosheath seems highly correlated to other environmental factors. Plants with strong and weak rhizosheath from the same species will have their microbiome described through metabarcoding ; once we identified microbes strongly linked to rhizosheath formation, we will perform inoculation tests on wheat in greenhouse, with the aim of increasing drought resistance.



Microbial soil amendments shape the raspberry rhizosphere microbiome and enhance bioactive compounds in fruits

Marijana Pešaković^{1*}, Jovana Todorović¹, Tamara Krstić Tomić¹, Boris Rilak¹, Jelena Tomić¹, Žaklina Karaklajić Stajić¹ and Slobodan Milenković²

¹ Fruit Research Institute, Čačak, Serbia

² The University Educons, Sremska Kamenica, Serbia

*mpesakovic@institut-cacak.org

Keywords: Plant microbiome interaction; Microbial inoculants; Raspberry; Polyphenolics; Antioxidant activity; Sustainable agriculture

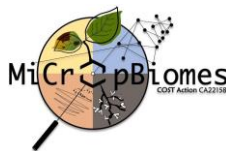
Plant-associated microbiomes play a key role in soil functionality and crop performance in sustainable production systems. This study evaluated the effects of a microbial-enriched vermicompost tea (MeVCT), developed at the Fruit Research Institute Čačak (Serbia), on rhizosphere microbiome dynamics and fruit bioactive compounds in raspberry (*Rubus idaeus* L.).

Field experiments included MeVCT applied alone and in combination with mineral fertilization and soil amendments (humus-based fertilizer and zeolite), alongside conventional fertilization and unfertilized controls. Rhizosphere microbial communities were assessed before trial establishment and after two growing seasons, focusing on total microbial abundance and key functional groups, including nitrogen-fixing and phosphorus-solubilizing microorganisms, together with soil chemical properties. Fruit biochemical traits (total phenolics, anthocyanins, and antioxidant activity) were evaluated after each growing season.

Results showed a substantial increase in rhizosphere microbial populations over time, with several-fold increases in total bacteria and functional microbial groups, accompanied by improvements in soil chemical properties, indicating enhanced nutrient availability and overall soil functionality. These microbiome and soil changes were associated with improvements in fruit biochemical traits. While total phenolics and anthocyanins showed moderate increases (up to ~2–4%), antioxidant activity exhibited a pronounced enhancement, particularly in treatments combining MeVCT with mineral fertilization.

The findings highlight a strong link between rhizosphere microbiome modulation, soil functionality, and fruit metabolic responses, demonstrating the potential of microbial soil amendments to improve both soil health and fruit quality. This study supports the development of microbiome-based strategies and microbial inoculants for sustainable berry production.

Funding: Support was provided by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, Contract No451-03-33/2026-03/200215.



Microbial Bioremediation and Chemical Sensors: A Modern Solution for Heavy Metal Pollution in Agriculture

Danka Kiperović^{1*}, Jovana Vunduk¹, Saša Đurović¹, Dimitrije Mara¹, Milica Čalić¹, Vera Karličić², Flavia Artizzu³

¹ Institute of General and Physical Chemistry, Belgrade, Serbia

² University of Belgrade - Faculty of Agriculture, Belgrade, Serbia

³ Department of Sustainable Development and Ecological Transition (DISSTE), University of Eastern Piedmont “A. Avogadro”, Vercelli, Italy

*danka.radic81@gmail.com

Keywords: Remediation, Luminescent sensors, Soil bacteria, Heavy metal pollution, Sustainable agriculture

Preserving healthy, high-quality soil and producing safe food are imperatives for every country. In the Republic of Serbia, 65% of the territory is agricultural land, the quality of which is constantly declining due to the loss of organic matter. Heavy metals such as Copper (Cu), Nickel (Ni), Lead (Pb), Chromium (Cr), Cadmium (Cd) and Arsenic (As) also pose a significant problem, as they are extremely persistent and cannot be degraded by chemical or biological processes, only transformed into less toxic forms. Among the heavy metals, Ni, Pb and Cr have been identified as the most concentrated in Serbian agriculture, while rice crops in Italy also show high levels of Cd and As contamination. Therefore, remediation methods (phyto- and bioremediation) represent an ideal solution. The literature and practice show promising results, probably due to the presence of *in situ* indigenous strains of microorganisms in combination with adequate plant species. At the same time, the development of chemical sensors for the rapid detection of potential heavy metal pollution *in situ* would enable immediate remediation actions.

Minimum Inhibitory Concentration (MIC) of heavy metals was determined on Mueller-Hinton (Merck, USA) using a 96-well microtiter plate. Cu^{2+} ($\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$, Sigma-Aldrich, USA), Cr^{6+} ($\text{K}_2\text{Cr}_2\text{O}_7$, Merck, USA) and Cd^{2+} ($\text{CdCl}_2 \cdot 6\text{H}_2\text{O}$, Merck, USA) were added to the Mueller–Hinton medium, in the following concentrations: 0.15, 0.3, 0.6, 1.25, 2.5, 5, 10, and 20mM. Bacterial strains included *Pseudomonas* sp., *Bacillus* sp and *Serratia* sp., and have shown higher tolerance to increased Cu^{2+} and Cd^{2+} levels. The MIC for Cu^{2+} was 20 mM. In the case of Cr^{6+} , only *Pseudomonas* sp grew at a concentration of 1.25 mM, and for Cd^{2+} , the inhibitory concentration was 10 mM.

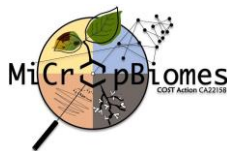
The luminescent sensors were selected for the specified heavy metals. The molecular materials chosen are lanthanide metalorganic frameworks (LnMOFs) with the use of two different Ln ions for ratiometric sensing of the target metal ions. The LnMOFs will later be introduced into the plants by adding them during their growth. Based on the presented results, the hybrid combination of responsive bacterial strains, lanthanoid sensor and adequate plant will be tested in real conditions to demonstrate prospects for this kind of platform, which supports regenerative agriculture.

References

1. Radić D, Pavlović V, Lazović M, Jovičić-Petrović J, Karličić V, Lalević B, Raičević V (2017). Copper-tolerant yeasts: Raman spectroscopy in determination of bioaccumulation mechanism. *Environ. Sci. Pollut. Res.* 24 (27): 21885–21893.
2. Racić G, Vukelić I, Kordić B, Radić D, Lazović M, Nešić L, Panković (2023). Screening of Native *Trichoderma* Species for Nickel and Copper Bioremediation Potential Determined by FTIR and XRF. *Microorganisms* 11: 815.

List of Participants

Full name	Country	email
Ahmed Abdelfattah	Germany	aabdelfattah@atb-potsdam.de
Aleksandra Mesaroš	Serbia	aleksandra.mesaros@bio.bg.ac.rs
Alexandra Pál	Hungary	pal.alexandra@brc.hu
Aliki Kapazoglou	Greece	kapazoglou@elgo.gr
Anna Bonaterra	Spain	anna.bonaterra@udg.edu
Anže Vozelj	Slovenia	anze.vozelj@nib.si
Bogdan Žigić	Serbia	bogdanzigic@gmail.com
Bojana Živanović	Serbia	bojana.zivanovic@imsi.bg.ac.rs
Conceição Santos	Portugal	csantos@fc.up.pt
Claire Prigent-Combaret	France	claire.prigent-combaret@univ-lyon1.fr
Daniel Hoefle	Germany	dhoefle@atb-potsdam.de
Daniele Nicotra	Italy	daniele.nicotra@unict.it
Danka Kiperović	Serbia	dradic@iofh.bg.ac.rs
David Gramaje	Spain	david.gramaje@icvv.es
Davide Bulgarelli	United Kingdom	d.bulgarelli@dundee.ac.uk
Denise Khouri Chalouhi	Italy	khouri@icgeb.org
Dóra Krisztina Balázs	Hungary	balazs.dora.krisztina@szte.hu
Duška Delić	Bosnia and Herzegovina	duska.delic@agro.unibl.org
Elisenda Castellet Godall	Spain	Elisenda.castellet@irta.cat
Elodie Vandelle	Italy	elodigenevieve.vandelle@univr.it
Emilio Stefani	Italy	emilio.stefani@unimore.it
Fanni Kovács	Hungary	fannikov123@gmail.com
Francesco Spinelli	Italy	francesco.spinelli3@unibo.it
Gyorgy Sipos	Hungary	sipos.gyorgy@uni-sopron.hu



Full name	Country	email
Gergő Terna	Hungary	ternag1@gmail.com
Gordana Racić	Serbia	racic@institut-tamis.rs
Hesam Mousavi	Norway	hesam.mousavi@inn.no
Hira Ikram	Italy	hira.ikram@unimore.it
Iglė Vepšaitė-Monstavičė	Lithuania	igle.vepstaite-monstavice@gamtc.lt
Igor Vukelić	Serbia	igor.vukelic@ifvcns.ns.ac.rs
Inga Tamošiūnė	Lithuania	inga.tamosiune@lammc.lt
Irena Budić-Leto	Croatia	irena@krs.hr
Isidora Knezević	Serbia	racic@institut-tamis.rs
Iva Rosić	Serbia	riva@ipb.ac.rs
Ivan Nikolić	Serbia	ivan.nikolic@bio.bg.ac.rs
Ivana Marić	Serbia	mivana@ipb.ac.rs.
Ivana Potočnik	Serbia	ivana.potocnik@pestring.org.rs
Jacob Malone	United Kingdom	Jacob.Malone@jic.ac.uk
Jean Legeay	Morocco	Jean.Legeay@um6p.ma
Jelena Lozo	Serbia	jlozo@bio.bg.ac.rs
Jelena Zindović	Montenegro	jelenazindovic@yahoo.com
Joanna Pulawska	Poland	joanna.pulawska@inhort.pl
Joël Pothier	Switzerland	joel.pothier@zhaw.ch
Jovana Todorović	Serbia	jtodorovic@institut-cacak.org
Juliana Lukša-Žebelović	Lithuania	juliana.luksa@gamtc.lt
Juliana Oliveira-Fernandes	Portugal	juliana.fernandes@univ-rennes.fr
Jurgita Vinskienė	Lithuania	jurgita.vinskiene@lammc.lt
Kamila Bokszczanin	Poland	kamila_bokszczanin@sggw.edu.pl
Katalin Tajti	Hungary	tajti.katalin@brc.hu
Kristina Gruden	Slovenia	Kristina.Gruden@nib.si
Lama Ramadan	Turkey	l.ramadan2021@gtu.edu.tr
Lara Amorim	Portugal	up2001100276@edu.fc.up.pt



Full name	Country	email
Laszlo Kredics	Hungary	laszlo.kredics@gmail.com
Louise Mathier	Switzerland	louise.mathier@zhaw.ch
Luis Alejandro Moll Dos Santos	Spain	ljmoll@ias.csic.es
Manikandan Ariyan	Estonia	manikandanariyan@gmail.com
Maria Celeste Pereira Dias	Portugal	celeste.dias@uc.pt
Maria-Dimitra Tsolakidou	Cyprus	maria-dimitra@hotmail.com
Marian Malek	Austria	Malek.marian@ait.ac.at
Marie Simonin	France	marie.simonin@inrae.fr
Marija Anđelković	Serbia	marija.andjelkovic@bio.bg.ac.rs
Marija Nedeljković	Serbia	marija.nedeljkovic@bio.bg.ac.rs
Marijana Pešaković	Serbia	mpesakovic@institut-cacak.org
Marina Arnaut Stefanović	Serbia	marina@foodscalehub.com
Marina Sokić	Serbia	amarina@ipb.ac.rs
Monika Faruga	Poland	monika.faruga@intermag.pl
Núria Daranas	Spain	nuria.daranas@udg.edu
Nebojša Jasnić	Serbia	jasnicn@bio.bg.ac.rs
Olja Medić	Serbia	olja.medic@bio.bg.ac.rs
Pablo Vargas	Spain	pablo.vargas@irta.cat
Renata Artimová	France	artimova@ife.sk
Salme Timmusk	Sweden	salme.timmusk@slu.se
Stanisavljević Jelena	Serbia	jelena.stanisavljevic@bio.bg.ac.rs
Slaviša Stanković	Serbia	slavisas@bio.bg.ac.rs
Stefan Stošić	Serbia	stefan.stosic@gmail.com
Svetlana Milijašević-Marčić	Serbia	svetlana.milijasevic@pestring.org.rs
Tamara Krstić Tomić	Serbia	m3004_2020@stud.bio.bg.ac.rs
Tamara Ranković	Serbia	tamara.rankovic@bio.bg.ac.rs
Tanja Berić	Serbia	tanjab@bio.bg.ac.rs
Tijana Gordic Jasnic	Serbia	tijana8693@gmail.com

Full name	Country	email
Tina Arnšek	Slovenia	tina.arnsek@nib.si
Walczak Weronika	Poland	weronika.walczak@intermag.pl
Wisnu Wicaksono	Austria	wisnu.wicaksono@tugraz.at
Zisis Vryzas	Greece	zvryzas@agro.auth.gr
Zizi Zafeiro	Belgium	zzi@scientia.be

This brochure is based upon work from COST Action CA22158 MiCropBiomes, supported by COST (European Cooperation in Science and Technology).

COST (European Cooperation in Science and Technology) is a funding organisation for research and innovation networks. Our Actions help connect research initiatives across Europe and beyond and enable researchers and innovators to grow their ideas in any science and technology field by sharing them with their peers. COST Actions are bottom-up networks with a duration of four years that boost research, innovation and careers.

www.cost.eu.



**Funded by
the European Union**

