

2nd BrIAS Conference on Smart Agriculture
BrIAS Agri2025

Book of Abstracts and Conference info



Acknowledgments



Agri2025 Conference presentation and reading key:

Smart agriculture is rapidly transforming the way farming is practiced, revolutionizing traditional agricultural systems through the integration of advanced technologies and data-driven solutions. This shift is not only enhancing productivity but also helping address challenges like resource scarcity, climate change, and the need for sustainable farming practices. The role of smart agriculture is pivotal in both the current and future agricultural systems, as it promises to improve efficiency, sustainability, and resilience. The BrIAS AGRI2025 conference will be dedicated at highlighting the current and future trends in Smart Agriculture, and bridging this to the 5 FAO strategic objective or sustainability goals (reduce hunger, sustainable agriculture, reduce rural poverty, inclusive agricultural systems, increase resilience to biotic and abiotic stresses).

In today's agricultural systems, smart agriculture encompasses a variety of technological innovations that are increasingly being adopted by farmers. Precision agriculture, one of the key components, uses GPS, IoT sensors, drones, and satellite imagery to monitor and manage crops more efficiently. For instance, soil moisture sensors can provide real-time data about soil conditions, enabling farmers to apply water, fertilizers, and pesticides only where they are needed. This results in optimal use of resources, which can lead to higher yields while reducing costs and minimizing environmental impact.

Climate change is another pressing issue, and smart agriculture holds promise for adapting to shifting environmental conditions. Through the use of climate modelling, farmers can receive real-time weather forecasts and adjust their practices to minimize losses due to extreme weather events like droughts, floods, and heatwaves. Moreover, the development of drought-resistant and climate-resilient crops through genetic engineering, combined with data-driven agricultural practices, will allow farmers to maintain productivity even in adverse conditions.

Agri2025 Conference Topics:

- Modelling and control for the smart agriculture of tomorrow.
- Automated remote sensing and estimation for agriculture
- Sustainable approaches for bio-aggressors control: plant protection molecules and biotechnologies
- Plant-omics and bioinformatics for sustainable agriculture
- Policy makers corner: cross-talk among regulatory bodies in agriculture
- Metrology for agriculture
- Crop Protection
- Insect Farming Technologies
- Robotics and technologies for precision farming
- Breeding and automatic phenotyping
- Modelling of agroecological systems
- Automatic support to decisions for agriculture
- Data-driven approaches for smart agriculture

Program chairs and organizing team

- Prof. Emanuele Garone – Université Libre de Bruxelles
- Prof. David Cannella – Université Libre de Bruxelles
- Dr. Luca Rossini – Université Libre de Bruxelles

Logistic chair

- Dr. Anja Garone – BrIAS

Scientific Committee

- Prof. Frédéric Francis – Gembloux Agri-Bio Tech, University of Liege
- Prof. Francesco Lamonaca – Università della Calabria
- Prof. Yael Edan – Ben-Gurion University of the Negev
- Prof. Stefano Speranza – Università degli Studi della Toscana
- Dr. Silvia Turco – Università degli Studi della Toscana
- Dr. Fabrizio Dabbene – CNR-IEIIT
- Prof. Timo Oksanen – Technical University of Munchen
- Prof. Paolo Falcone – Chalmers University of Technology
- Prof. Cécile Thonar – Université Libre de Bruxelles
- Prof. Andrea Gasparri – Università degli studi “Roma Tre”
- Prof. Stefan Gerth – Fraunhofer IIS
- Dr. Renik Van den Eynde – Proefstatoin voor de Groenteteelt
- Dr. Giuseppe Rofrano – IZSM Portici
- Dr. Bas Boom – OnePlanet Research Centre
- Prof. Lorenzo Marconi – Università di Bologna

The Host: BrIAS Brussels Institute of Advanced Studies

The Venue



Institutes for Advanced Studies, IASs, are incubators of ideas, with no philosophical or political restriction, where some of **the very best scientists, artists or designers**, coming from various fields and countries, are given the opportunity to work in an atmosphere of complete freedom, collaboration, mutual emulation and cross-fertilisation. The first IAS was created in Princeton, 1930. Since then, several IASs have been established worldwide.

Despite a considerable number of internationally acclaimed university laboratories, there was no IAS in Brussels or Belgium as of yet. The authorities of ULB and VUB have therefore decided in 2018 to create the Brussels Institute for Advanced Studies (BrIAS) as a joint initiative. Based on submitted projects to mandate biannual programs, **BrIAS sustains fellowships and housing** to a number, typically between 15 and 20, of “BrIASfellows”, for periods of up to 10 months.

BrIAS will stimulate the selected fellows to **a close interaction between science and other fields of creativity**, which are essential **for a harmonious and sustainable future** and which will contribute to the prestige of the Brussels universities, region and zone of influence.

The first program was dedicated to the “Past, Present and Future of food, climate and sustainability”. While the current program is dedicated to “Sustainable Robotics”. The mission of the Brussels Institute for Advanced Studies is:

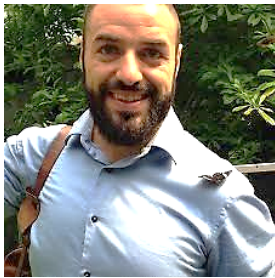
- To contribute to the advancement of science in an interdisciplinary and transdisciplinary spirit by attracting the very best researchers at international level;
- To progress towards a sustainable world;
- To strengthen both the mutual and worldwide collaborations of the founding universities of BrIAS, thanks to the hospitality offered to researchers and postdocs, thereby generating a community of researchers and alumni, part of the global network of IASs;
- To stimulate the interaction between science and creative fields such as arts and design, essential for a harmonious and sustainable future of the socio-economic and cultural environment of the Brussels region and influence zone;
- To contribute to the prestige of the Brussels Region and its constituents.

Conference organizing team



Prof. Dr. Emanuele Garone

Obtained a PhD degree from the University of Calabria (Italy) in 2009. Today is a full professor at the Brussels school of Engineering - école Polytechnique of the Université Libre de Bruxelles (ULB). Here he leads the SAAS - Department of Control Engineering and System. His current research interests include: constrained predictive control, linear parameter varying systems, control reconfiguration for fault tolerant systems, networked control systems, path planning for heterogeneous vehicles, control of switching systems. He is currently the BrIAS program director (2024-2025) on Sustainable Robotics.



Prof. Dr. David Cannella

Obtained a PhD degree from the University of Copenhagen (Denmark) in 2014. Today is associate professor at Brussels school of Bioengineering/Faculty of Science of the Université Libre de Bruxelles (ULB). Here he leads the PhotoBioCatalysis and Biomass Transformation Lab. His current research interests include: bioprocesses, biofuels, light driven biocatalysis with focus on biopolymers and biodegradable polymers, redox enzymes, CAZymes, valorization of lignocellulose into plant active molecules, plant biostimulants, sustainable agriculture, plant immune defenses, mycology of plant pathogens, biochemistry of the plant: pathogen

warfare.



Dr. Luca Rossini

Obtained a Ph.D in Plant and Animal Science (major in Ecological Modelling, minor in Applied Entomology) from Università degli Studi della Toscana. Today is currently working as European Marie Curie Researcher (MSCA-2022-PF), in Ecological Modelling and Applied Entomology at Université Libre de Bruxelles (ULB), at SAAS. His main research topic is the development and validation of mathematical models to describe insect pests and diseases. This includes the integration of sparse field measurements to improve the accuracy of the predictions, pest monitoring, planning of measurement campaigns, field measurements protocols, mathematical and computational biology/ecology, high performance computing.

The Opening Ceremony Interveners



Prof. Dr. Frank Deconinck (VUB) BrIAS Director

He is Professor Emeritus of Medical Physics at VUB. He was research associate at the University of California (UCSF) and research collaborator at Brookhaven National Laboratory. In the nuclear field, he is honorary chairman of the board of governors of the Belgian Nuclear Research Centre (SCK CEN), honorary president of the European Nuclear Society and he coordinates Rad4Med.be, the Belgian network for radiation applications in healthcare.



Prof. Dr. Serge Jaumain (ULB) BrIAS Director

Professor of Contemporary History at the ULB where he is also co-director of AmericaS – the Interdisciplinary Center for the Study of America. He serves as Advisor to the Rector for Development Cooperation and is the President of the NGO ULB-Cooperation and the President of the International Scientific Council of the Institut des Amériques (Paris).



FAO-LOB Director Rashad Al-Khafaji

was appointed Director of the FAO Liaison Office with the European Union and Belgium, effective 1 August 2021. He started his career at the United Nations Office at Vienna (UNOV) in Austria and worked at the United Nations Industrial Development Organization (UNIDO) and the Comprehensive Nuclear-Test-Ban Treaty Organization (CTBTO). In 2003, he joined FAO's Fisheries and Aquaculture Department at headquarters where he worked as Liaison and Meetings Officer. From 2013 to 2019, he served as Attaché de Cabinet in the Office of the Director-General and, subsequently, became Deputy Directeur de Cabinet ad interim. He was Special Assistant to the Director-General since 2019 until he took up his position in Brussels. He holds a Magister in Economics with an emphasis on International Development and Marketing from the Wirtschaftsuniversität Wien

(Vienna University of Economics and Business Administration) in Austria. He is fluent in Arabic and German (both mother tongues) as well as English and French; and has basic knowledge of Italian and Spanish.

Conference schedule

6 February 2025

8:30 - 9:00: Registration

09.00 – 09.30: Opening ceremony and welcome

Prof. Emanuele Garone, Université Libre de Bruxelles

Prof. David Cannella, Université Libre de Bruxelles

Prof. Frank Deconinck, Brussels Institute for Advanced Studies

Dr. Raschad Al-Khafaji, Director FAO Brussels Liaison Office with the European Union and Belgium

09.30 – 10.10: Plenary lecture 1 (Room 1)

Moderator: Emanuele Garone

PT1 Insects need smart promotion ... or eradication.

Prof. Frédéric Francis, Gembloux-Agro Bio Tech.

Parallel Session 1 – Advances in pests and diseases research (Room 1)

Moderators: Luca Rossini and Silvia Turco

10:20 – 10:40

T1 Extracting insect information from entomological museum collections to identify potential insect pests and beneficials using deep learning methods.

G. Noël

10:40 – 11:00

T2 Development of *Bruchus rufimanus* Boheman 1833 (Coleoptera: Chrysomelidae) at different temperatures with special emphasis on rearing and modelling approach.

A. Segers

Parallel Session 2 – Advances in modelling in plant protection (Room 2)

Moderators: Irene Salotti and Yafit Cohen

10:20 – 10:40

T3 A win-win combination in plant disease prediction: field data to update model estimations, estimations to drive field data collection.

O. Benhamouche

10:40 – 11:00

T4 Adaptation of a physiologically based model for predicting the phenology of *Philaenus spumarius*: first validation in Italian olive groves.

Z. Sweidan

11.00 – 11.30: Coffee break

Parallel Session 1 – Advances in pests and diseases research (Room 1)

Moderators: Luca Rossini and Silvia Turco

11:30 – 11:50

T5 Innovations and challenges in black soldier fly farming: Infrastructure, automation, and waste valorization.

H. Luttenschlager

11:50 – 12:10

T6 A novel strain of *Akanthomyces muscarius* as a promising biological control agent against *Toumeyella parvicornis*.

N. Di Sora

12:10 – 12:30

T7 Improving management of emerging and re-emerging pests and diseases of *Prunus persica* (L.) Batsch.

S. Turco

12:30 – 12:50

T8 Characterizing spatiotemporal dynamics of biotic stresses to optimize sampling strategies in agricultural systems.

R. Gafni

Parallel Session 2 – Advances in modelling in plant protection (Room 2)

Moderators: Irene Salotti and Yafit Cohen

11:30 – 11:50

T9 A mechanistic, five-step approach for prediction modelling: Alternaria-tomato pathosystem as case study.

I. Salotti

11:50 – 12:10

T10 AI-Driven pest control: Sustainable agroecosystems through remote monitoring and predictive modeling.

R. Ascolese

12:10 – 12:30

T11 Urban-agricultural interface: Impact of urban habitats on Mediterranean fruit fly dynamics in citrus orchards.

Y. Cohen

12:30 – 12:50

T12 Pest control SDSS – From academy to industry.

A. Cohen

12.50 – 14.00 Lunch break and poster session

Session 3: Advances in plant health sensing (Room 1)

Moderators: Francesco Lamonaca and Valerio Cristofori

14:00 – 14:20

T13 GeoAI, metrology and remote sensing for smart agriculture: Mapping land transformation and climatic impacts to optimize crop resilience and water management in a Mediterranean region.

A. Vitale

14:20 – 14:40

T14 Integrating spatio-temporal vegetation indices with machine learning for dynamic maize field performance monitoring: Development of a real-time crop monitoring framework.

G. Ravid

14:40 – 15:00

T15 Spectral-based weed detection across diverse environmental conditions.

A. Prashar

15.00 – 15.30: Coffee break

Session 4: Advances in plant health sensing (Room 1)

Moderators: Francesco Lamonaca and Valerio Cristofori

15:30 – 15:50

T16 Moving towards regenerative agriculture: Advancements in remote sensing tools to measure soils health regeneration.

M. Silvestri

15:50 – 16:10

T17 How to capture within-field heterogeneity across multi-year crop rotation: High-resolution insights from sentinel-2.

T. Kenda

16:10 – 16:30

T18 A low-cost and AI-integrated imaging device for plant-parasitic nematodes quantification and classification.

G. Bi

16:30 – 16:50

T19 Early detection of nutrient deficiencies: The hazelnut case-study

V. Cristofori

16.50 – 17.40: Plenary lecture 2 (Room 1)

Moderator David Cannella

PT2 Plant defense priming.

Prof. Uwe Conrath, RWTH Aachen University.

19.00: Social dinner at Fondation Universitaire (11 Rue d'Edgemont, 1000 Brussels)

7 February 2025

8:30 – 9:00: Registration

09.20 – 10.10: Plenary lecture 3 (Room 1)

Moderator David Cannella

PT3 Agroecological models explained.

Dr. Niels Holst, Aarhus University.

Parallel Session 5 – Robotics in precision farming (Room 1)

Moderators: Andrea Gasparri and Fabrizio Dabbene

10:20 – 10:40

T20 A control architecture for semi-autonomous robots in agriculture settings.

J. Marino

10:40 – 11:00

T21 A robotic arm design for autonomous kiwi harvesting.

N. Omodei

Parallel Session 6 – Technologies for sensing and phenotyping (Room 2)

Moderators: Luca Bascetta and Christian Hermans

10:20 – 10:40

T22 Automated X-ray plant phenotyping from seedlings to the field.

G. Lehretz

10:40 – 11:00

T23 Uncovering the role of *Serendipita williamsii* volatiles in establishing its own plant beneficial endophytic colonization: A parallel study of the headspace composition and mode of action.

J. Van Vooren

11.00 – 11.30: Coffee break

Parallel Session 5 – Robotics in precision farming (Room 1)

Moderators: Andrea Gasparri and Fabrizio Dabbene

11:30 – 11:50

T24 A distributed framework for task allocation and safe coordination in networked multi-robot

systems for precision agriculture.

A. Gasparri

11:50 – 12:10

T25 Motion planning for an autonomous agricultural robot in unstructured terrain.

F. Dabbene

12:10 – 12:30

T26 Motion planning for agricultural tasks with robotic manipulators.

G. Liu

12:30 – 12:50

T27 Self-supervised local NBV planning for 3D plant reconstruction by a robot.

J. Ci

Parallel Session 6 – Technologies for sensing and phenotyping (Room 2)

Moderators: Luca Bascetta and Christian Hermans

11:30 – 11:50

T28 Using a digital twin of a tracked mobile robot for the design and validation of estimation and control algorithms.

L. Bascetta

11:50 – 12:10

T29 RootForce 4.0: a review of the classical image processing pipeline for root system architecture of cereals.

L. A. Torres-Cisneros

12:10 – 12:30

T30 Constellr HiVE – A satellite constellation for monitoring diurnal temperature cycles and enabling smart agriculture.

C. Lerot

12:30 – 12:50

T31 Cellulose-derived oligosaccharides obtained by LPMO oxidation biostimulate tomato weight, inflorescence, and immunity through ethylene and ROS-free signalling

D. Cannella

12.50 – 14.00: Lunch break and poster session

Session 7: Smart irrigation and soil biodiversity (Room 1)

Moderators: Luis Orihuela and José Maria Manzano

14:00 – 14:20

T32 Application and assessment of model-based leak localization methods in an irrigation network.

L. Orihuela

14:20 – 14:40

T33 Harnessing predictive data analytics of soil microbiota for enhanced bio-sustainability in agriculture.

R. Pace

14:40 – 15:00

T34 Design and deployment of a cloud platform for data-driven leak detection in agricultural irrigation systems.

J. M. Manzano

15.00 – 15.30: Coffee break

Session 8: Biostimulants and soil biodiversity (Room 1)

Moderators: David Cannella and Silvia Turco

15:30 – 15:50

T35 Leveraging rhizosphere microbial diversity and drought-tolerant bacterial isolates to enhance soybean resilience in South Africa.

A. S. Ayangbenro

15:50 – 16:10

T36 Tailoring plant roots for enhanced nitrogen capture in soil.

C. Hermans

16:10 – 16:30

T37 Harnessing biostimulants for sustainable agriculture: A case study of Nurspray® in tomato cultivation.

C. Leclef

16.30 – 17.20: Plenary lecture 4 (Room 1)

Moderator: Emanuele Garone

PT4 AgRobotics for smart agriculture.

Prof. Yael Edan, Ben-Gurion University of the Negev.

17.20 – 17.30: Closing remarks (Room 1)

17.30 – Get together with Italian-Belgian aperitive

Plenary session 1

PT1 Insects need smart promotion ... or eradication

Prof. Frédéric Francis, Gembloux AgroBio-Tech, Université de Liège

Insects represent a functional group of animals showing a very large diversity of living environments, adaptations and finally impacts for humans. They are then captivating models for studies, investigations and understanding in tremendous situations with very distinct applications and consequences. In one hand, many insects are very useful and sources of inspiration to provide very positive services in agriculture such as in pollination, biological control but also by contributing to transform organic residues or/and provide alternative food and biobased materials. In the other hand, some others can be very harmful as crop pests, blood feeders until being vectors of diseases for animals including humans. For all kinds of situations, smart developments are needed and developed for insects either to promote or to control and eradicate them. Several researches performed in the entomological department of Gembloux Agro-Bio Tech will be presented to illustrate insect multitrophic interactions and a diversity of smart proposed strategies leading to efficient and sustainable practices in agriculture focusing on insects.



Frederic Francis Biography:

He was graduated in agricultural science engineering and got a PhD in 2003 on plant – aphid multitrophic interactions. He is Full Professor at Gembloux-Agro Bio Tech – University of Liege and is the head of Entomology Department from 2012. He is the Faculty Dean from 2017. He is also visiting Professor at the Chinese Academy of Agricultural Sciences (CAAS) and at the Shandong Agricultural University. He develops teaching and research activities to understand insect interactions with their environment (to host plant, as virus vector, with symbionts, ...) and promote pest biological control with integrated and complementary strategies. For the last 15 years, he also focused on edible insects. He is involved in many projects in developing countries in Africa, south America and Asia to apply practical approaches to manage insect diversity and valorization. He supervised many master and PhD students in their research works leading to a broad range of publications in international journals and many communications in scientific conferences. He is the founder and chairman of Hexapoda museum – Insectarium Jean Leclercq in

Belgium managing an entomological collection of 5 millions of insects. He promotes entomology at different scales, from the discovery of insects to younger peoples to the support to amateur and professional entomologists.

Plenary session 2

PT2 Plant defense priming

Prof. Uwe Conrath, RWTH Aachen University

When locally infected by necrotizing pathogens, plants activate a systemic immune response, called systemic acquired resistance (SAR). In this process, distal leaves become primed to activate a more robust defense response upon reinfection. Defense priming is associated with an elevated level of microbial pattern receptors (e.g., flagellin-sensing 2), accumulation of dormant signaling enzymes (e.g., mitogen-activated protein kinases 3 and 6), and with modification of chromatin. The latter comprises the covalent modification of histones (e.g., histone H3 and H4 acetylation and/or methylation) and the formation of open chromatin indicative of regulatory DNA with a role in defense priming. Together, these events provide a memory to the initial infection and enable the boosted recall defense response. I will summarize these fascinating discoveries and disclose their potential for sustainable agriculture by introducing smart tools and approaches for identifying and employing priming-inducing chemistry and microbes. When plants are locally infected by necrotizing pathogens, they trigger a systemic immune response known as systemic acquired resistance (SAR). This response primes distal leaves to mount stronger defense upon subsequent infection. Defense priming involves an increased presence of microbial pattern receptors (e.g., flagellin-sensing 2), the accumulation of inactive signaling enzymes (e.g., mitogen-activated protein kinases 3 and 6), and chromatin modifications. These chromatin changes include covalent modifications of histones (e.g., acetylation and/or methylation of histones H3 and H4) and the formation of open chromatin, highlighting regions of regulatory DNA that play a role in priming. Collectively, these processes establish an immune memory of the initial infection, enabling a faster and stronger defense response upon reinfection. In my talk, I will present these exciting discoveries and discuss their potential for sustainable agriculture, focusing on innovative tools and approaches to identify and utilize priming-inducing chemicals and beneficial microbes.



Uwe Conrath Biography:

He is a professor of plant biochemistry and molecular biology at RWTH Aachen University, a cofounder of AgPrime GmbH, and a scientific advisor to agricultural and biotech companies. In particular, he's a passionate pioneer and acknowledged world leader in the research of defense priming. The term describes the enhanced capacity of immunized plants to mobilize defense resulting in earlier, faster, and more robust activation of defense which often leads to immunity. Uwe's research also addresses various agbiotech and bioeconomy aspects for translating concepts discovered in model systems to agriculture. They include tools for spotting priming-inducing compounds, defense pathway engineering, and leaf-sticking gels and capsules for the slow release of active ingredients.

Plenary session 3

PT3 Agroecological modelling explained

Dr. Niels Holst – Aarhus University

We build ecological models to grasp the complexity of natural systems but often complexity bites back at us. That's when you realise that the model itself has become so complicated that you are the only person in the world who understands it. Nobody wants to invest the time needed to follow you. You gained insights but they are insights that you cannot convincingly pass on to your peers. That again, makes you wonder whether those insights were real after all? To avoid this scientific impasse, there are basic rules of model design and implementation that should be followed. First of all, base your modelling on well-known concepts from physiology and population dynamics (and related sciences as needed, e.g., chemistry and physics). These are your generic model building blocks. Next rephrase your questions and reformulate the intended application domain, as you build the model and realise how little is actually unknown about the system. Be aware that the modelling software that you choose determines what can be expressed conveniently; it will determine not only the structure of your model but also its essence. I will walk you through the phases of model construction: formulation, parameter estimation, verification, testing, validation, uncertainty analysis, sensitivity analysis and publication. I will present examples using Universal Simulator, an open-source, do-it-yourself modelling tool that I have developed (www.ecolmod.org).



Niels Holst Biography:

Niels Holst is a Senior Scientist working at the Department of Agroecology, Aarhus University, Denmark, where he was recently appointed Head of the Agricultural Biodiversity Section. With an MSc in Biology, a BSc in Computer Science and a PhD combining the two, he has since his student days continued his work in Ecological Modelling with a focus on creating new software modelling tools, inspired by a wide range of modelling applications. He has applied modelling to integrated pest management, biological control, greenhouse microclimate, honeybees and crop production.

Plenary session 4

PT4 AgRobotics for smart agriculture

Prof. Yael Edan – Ben-Gurion University of the Negev

Agricultural robots have been developed for many agricultural applications such as transplanting, cultivating, spraying, trimming and selective harvesting. As advanced computing and sensing technologies and dexterous grasping become more capable and cost effective these robots are penetrating into market. By equipping these robots with advanced sensor technologies, real-time accurate and timely crop data can be collected providing improved spatial and temporal crop monitoring and management. With the advent of IoT (internet of things) and cloud computing, AI (artificial intelligence) systems can then integrate the online sensory information with remote sensing data, historical data, Information Communication Technologies (ICT) [e.g., cellular technology, global positioning system (GPS), geographic information systems (GIS)], and biological knowledge of the crop and its environment (e.g., crop weed and pest growth models, weather models). AI models developed for the different crop growth phases: cultivation (e.g., selecting crops to be planted, planning and preparation of land, irrigation planning, seed preparation, seed sowing), monitoring and controlling the growth (crop health monitoring, fertilizer use and application, disease/weed identification, and pesticide spraying), and harvesting (e.g., crop cutting, storing, and selling to the market) can be linked to the robots operating in the field. Farmer feedback can be incorporated ‘on-the-go’ to enable continuous improvement of decisions and provide the robots with a ‘green thumb’. These intelligent systems should be advanced to include also social, environmental and economic parameters to optimize decisions. The AI system output can then provide on-the-go controls for the smart farm robot to apply the optimal precision technology at the optimal time and the optimal location (e.g., water and fertilization application, harvesting timing, disease/pest management) leading to improved production costs, yield and quality and enabling better crop control and management. Equipping these autonomous robots with intelligence and connectivity will enable to provide the operational smart farming solutions. Current Digital Farming (also known as Agriculture 4.0) enabled by precision agriculture aims to optimize the agricultural processes by adapting the operations to apply what is needed, when and where is needed. Although information is provided at the plant, crop, soil and environmental level, overall control is mostly at the field level only (not enabling individual plant treatments). Farmers are overwhelmed with data, what is currently missing is the closed loop control which can be provided by the robots. Smart agriculture (defined as Agriculture 5.0), will empower these data-driven farms linking the sensors, IoT and AI to robots that can provide ultrahigh-precision farming (providing ‘phytotechnology’=precise decisions related to how, where and when at the plant level). The concepts of multi-robots, human-robot collaboration, and environment reconstruction from aerial images and ground-based sensors and robots working together will advance smart farming ensuring sustainable precision agriculture.



Yael Edan Biography:

Yael Edan is a Full Professor in Industrial Engineering at Ben-Gurion University of the Negev (BGU). She has a B.Sc in Computer Engineering and a M.Sc in Agricultural Engineering both from Technion, Israel Institute of Technology and a Ph.D from Purdue University. For the last 30 years she has led research in robotics, sensors, simulation, and decision-making systems. Her current robotics research focuses on human-robot cooperation in social assistive robotics. In addition, she has made and is advancing major contributions in the introduction and application of intelligent automation and robotic systems to the field of agriculture with several patents. Her more than 90 graduate students are in leading worldwide positions in academia and industry. Prof. Edan has led many international projects (USA, Japan, Europe). At BGU she is an endowed-chair professor and Director of the Agricultural, Biological and Cognitive Robotics Initiative and has served in several

management functions including Deputy Rector, Chair of the Dept. of Industrial Engineering and Management and of the Paul Ivanier Center for Robotics and Production Management.

List of oral abstracts by order of schedule

T1 Extracting insect information from entomological museum collections to identify potential insect pests and beneficials using deep learning methods

Grégoire Noël^{*,1}, Nicolas Delcommune¹, Gautier Black¹, Didier Vandenspiegel², Patrick Semal³, Frédéric Francis¹

¹ *Functional and Evolutionary Entomology, Gembloux Agro-Bio Tech – University of Liège, TERRA, Passage des Déportés, 2, 5030 Gembloux, Belgium*

² *Biological and Data Management Unit, Royal Museum for Central Africa, Tervuren, Belgium*

³ *Royal Belgian Institute of Natural Sciences, Brussels 1000, Belgium*

*Presenting author e-mail: gregoire.noel@uliege.be

Abstract

While the insect functional biodiversity of our agroecosystems is undermined by the agricultural intensification, their specific identification on the field remains tedious due to the lack of entomological expertise. Entomological collections are invaluable repositories of biodiversity records, crucial for understanding the temporal and spatial distribution of insects, especially insect pests and beneficials in our agroecosystems. Despite ongoing digitization efforts in a lot of natural museums, a significant challenge remains in linking species identification of an insect pest or beneficial from entomological collection boxes to field insects. The automated detection of an insect specimen from a collection box can be a difficult task owing to the remarkable morphological diversity inherent to these organisms. The advent of convolutional neural networks (CNNs) have greatly propelled the field of computer vision, especially in object detection. In this research, deep learning approaches provide a simple basis for carrying out the task of insect detection and classification from high-resolution pictures of entomological collection. Several computer vision algorithms were tested on Lepidoptera and Coleoptera orders by setting-up trained models over more than 80 insect families. Automated detection and classification of insects in entomological collection pictures could be the first step to deeper use in biological control methods. In conclusion, the implementation of deep learning algorithms represents a significant step forward in the digitization and analysis of entomological collections, offering promising avenues for enhanced agricultural research and smart conservation efforts.

T2 Development of *Bruchus rufimanus* Boheman 1833 (Coleoptera: Chrysomelidae) at different temperatures with special emphasis on rearing and modelling approach

Arnaud Segers^{*,1}, Luca Rossini², Rudy Caparros Megido¹, Emanuele Garone², Frederic Francis¹

¹ Functional and Evolutionary Entomology, University of Liège – Gembloux Agro-Bio Tech, Passage des Déportés, 2, 5030 Gembloux, Belgium

² Service d'Automatique et d'Analyse des Systèmes, Université Libre de Bruxelles, Av. F.D. Roosevelt 50, CP 165/55, 1050, Brussels, Belgium

*Presenting author e-mail: arnaud.segers@uliege.be

Abstract

Modelling the thermal response of insect pests is a valuable tool for predicting the stage development of the population, supporting the formulation of more sustainable and effective control strategies. This study focuses on *Bruchus rufimanus*, a specific pest of *Vicia faba* L. responsible for damages caused by larvae that develop inside the seeds. In particular, it tackled the thermal development modelling of this pest in a two-fold approach, given the current lack of information on the cryptic post embryonic development in terms of degree-days. Baseline data were collected by laboratory rearing that considered the insect reproductive diapause and proposed first insights for developing a protocol to rear this pest under controlled conditions. Subsequently, various models were evaluated to describe the effect of different constant temperatures on the embryonic and total development. The effect of temperature on the sex ratio of the next generation was also investigated. The most accurate model for the description of both embryonic and total development was the Briere-2 model. The temperature thresholds obtained for eggs and total pest developments were 8.2 ± 0.5 C and 12 C respectively. Cumulative degree-day requirements were 83 days for eggs and ranged from 550 to 740 -days for total development. Temperature had no effect on sex ratio. These findings provided a better understanding of the annual development of this pest and might support the future formulation of IPM strategies to control *B. rufimanus*.

T3 A win-win combination in plant disease prediction: field data to update model estimations, estimations to drive field data collection

Ouassim Benhamouche^{1,*}, Luca Rossini¹, Nicolás Bono Rosselló², Matthias Pezzutto³, Silvia Turco⁴, Emanuele Garone¹

1 Service d'Automatique et d'Analyse des Systèmes, Université Libre de Bruxelles, Brussels, Belgium

2 Namur Digital Institute, Université de Namur, Namur, Belgium

3 Dipartimento di Ingegneria dell'Informazione, Università degli Studi di Padova, Padova, Italy

4 Dipartimento di Scienze Agrarie e forestali, Università degli Studi della Tuscia, Viterbo, Italy

**Presenting author e-mail: ouassim.benhamouche@ulb.be*

Abstract

This work presents an innovative distributed estimator for the early detection of plant diseases, inspired by an approach initially developed for monitoring human epidemic [1]. The main goal is the identification of the firstly infected plants in a cultivated field, allowing a quick and targeted control action.

The estimator exploits an epidemiological model that describes the spread of infection across the field, taking into account interactions between parcels and environmental factors such as wind direction. This model is formalized as a network where each parcel represents a node, while the interactions, potentially influenced by the wind, constitute the edges. The core of the estimator is based on a Bayesian algorithm that updates the probability distribution of the state of each plant (susceptible, infected, removed) based on available observations. These observations can include diagnostic tests as well as visual inspections.

The estimator is designed to work in a distributed manner, allowing each parcel, or an associated sensor, to locally store and process information about its own state and that of its neighbors. Adapting the estimator, originally designed for human epidemics, to the monitoring of plant infections requires modifications to account for the peculiarities of the agricultural context. The primary objective is to detect the first infected plant, rather than completely eradicating the infection. This results in an adaptation of the cost function used to optimize the resource allocation, prioritizing early detection over comprehensive coverage. The efficiency of the estimator is evaluated through simulations that compare its performance to traditional monitoring strategies, such as sequential row monitoring or a grid-partition hub sampling strategy, which consists of dividing the grid into subgrids and targeting the hub nodes within each subgrid for sampling.

Preliminary results in fig. 1 suggest that the distributed estimator enables faster and more accurate detection of the first infected plants, leading towards more effective and less costly interventions.

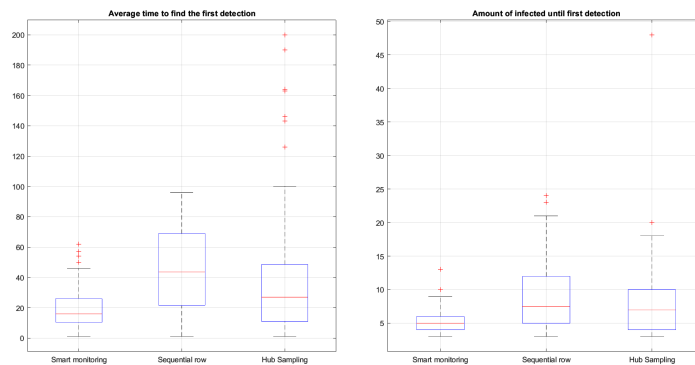


Figure 1: Average elapsed time and number of infected parcels until the first detection

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T4 Adaptation of a physiologically based model for predicting the phenology of *Philaenus spumarius*: first validation in Italian olive groves.

Zeinab Sweidan¹, Marta Corbetta¹, Oussama Bouaicha², Stefania Gualano³, Nuray Baser³, Franco Santoro³, Tito Caffi^{1,4} and Vittorio Rossi⁴

1 Department of Sustainable Crop Production, Facoltà di Scienze Agrarie, Alimentari e Ambientali, Università Cattolica del Sacro Cuore, Piacenza, Italy

2 Faculty of Agricultural, Environmental and Food Sciences, Free University of Bozen-Bolzano, Italy

3 International Centre for Advanced Mediterranean Agronomic Studies of Bari, Valenzano, Italy

4 Research Centre on Plant Health Modelling, Università Cattolica del Sacro Cuore, Piacenza, Italy

**Presenting author e-mail: zeinab.sweidan@unicatt.it*

Abstract

The significance of *Philaenus spumarius* (Hemiptera: Aphrophoridae) has grown considerably due to its high capacity to transmit *Xylella fastidiosa* (Xf), the bacterium responsible for olive quick decline syndrome [1]. Classified as a quarantine organism in 1981 [2], Xf was first detected in 2013 in Apulia [3], a southern Italian region with a long olive- growing tradition, where it has caused significant damage to local production. Effective containment of Xf strongly relies on vector management through chemical insecticides and soil tillage to disrupt vector juvenile stages of *P. spumarius*. To reduce the population capable of transmitting Xf, these measures must be implemented before adult spittlebugs acquire the bacterium from infected plants [4]; this requires precise timing based on pest phenology. In this study, we adapted a physiologically based model [5] to *P. spumarius* to describe its population dynamic. Development temperature-dependent rate functions were fitted and parametrized for each phenological stage, from egg to adult, by using field data derived from literature [6], since no laboratory data were available. The model was validated in different areas of Apulia using two data sets. The first, collected in 2019, comes from a group of seven nearby fields along the Ionian coast; the second, collected in 2024, includes several locations as part of the official monitoring program, with data available online through the regional cartographic service (“Emergenza Xylella”) [7]. In both datasets, data were expressed as number of individuals for each phenological stage on all monitoring dates. Since monitoring activity stopped when no more juvenile stages were observed, no data on adults were incomplete; in addition, few data were available on 1st nymphal instar. Model validation showed a good capacity to predict the 3rd, 4th, and 5th nymphal instars, providing actionable insights for pest management. Indeed, treatments are recommended during peak of emergence 4th nymphal instar, which is the time of highest nymphal abundance, and adults are still not present [7]. Further model improvements should address earlier juvenile stages, since new biological insecticides are going to be developed with potential efficacy on these less mobile phenological stages [8]. Further validation should consider adult population to estimate the lifespan in the field and eventually predict the oviposition period, which would help optimizing soil tillage practices.

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T5 Innovations and challenges in black soldier fly farming: infrastructure, automation, and waste valorization

Hugo Luttlenschlager^{*,1}, Joachim Carpentier¹, Frédéric Francis¹, Sébastien Finet², Rudy Caparros Megido¹

¹ *Functional and Evolutionary Entomology, UR TERRA, Gembloux Agro-Bio Tech, University of Liège, Liège, Belgium*

² *Biowaste Upcycling, Waterloo, Belgium*

*Presenting author e-mail: hluttlenschlager@uliege.be

Abstract

The farming of the black soldier fly *Hermetia illucens* (L. 1758) is gaining popularity across various continents, both in academic and industrial settings. This growing interest stems from the species' remarkable ability to convert organic waste into high-quality protein. A significant portion of current research focuses on larval development, nutritional profiling, and agro-industrial applications. However, a critical yet often overlooked aspect of black soldier fly farming lies in the infrastructure and logistics necessary for efficient rearing. This presentation aims to showcase our facilities, machinery, and the potential pathways for automating black soldier fly farming. Emphasis will be placed on our innovative process for converting organic waste into larval feed. An organic material recycler is utilized to produce a dry, storable, and rehydratable meal that facilitates effective larval development while ensuring precise larval separation through post-development sieving. This process not only optimizes waste valorization but also enhances the overall sustainability of the production cycle. In addition, the broader perspectives and challenges facing black soldier fly farming will be discussed, including scalability, economic viability, and environmental implications. By addressing these issues, we aim to contribute to the development of more efficient and sustainable farming practices for this promising species.

T6 A novel strain of *Akanthomyces muscarius* as a promising biological control agent against *Toumeyella parvicornis*

Nicolò Di Sora^{*1}, Silvia Turco¹, Federico Brugneti¹, Luca Rossini², Mario Contarini¹, Stefano Speranza^{1,3}, Angelo Mazzaglia¹

¹ *Dipartimento di Scienze Agrarie e Forestali, Università degli Studi della Tuscia, Via San Camillo de Lellis snc, 01100 Viterbo, Italy*

² *Service d'Automatique et d'Analyse des Systèmes, Université Libre de Bruxelles, Av. F.D. Roosevelt 50, CP 165/55, 1050 Brussels, Belgium*

³ *Centro de Estudios Parasitológicos y de Vectores (CEPAVE, CONICET-UNLP), Boulevard 120 1900, La Plata B1900, Argentina*

**Presenting author e-mail: nico.disora@unitus.it*

Abstract

Entomopathogenic fungi offer a valuable and sustainable alternative to traditional agrochemicals for crop protection. Species belonging to the genus *Akanthomyces* are widely employed in biocontrol strategies, targeting pests such as aphids, thrips, whiteflies, and mites [1]. Despite its widespread use, the effectiveness of this genus against soft scale insects remains largely unexplored. This study focused on evaluating the potential of a novel strain of *Akanthomyces muscarius* to control *Toumeyella parvicornis*, an invasive pest that has recently threatened European stone pines (*Pinus pinea*) [2] [3]. The fungus was isolated from *Parthenolecanium corni*, another soft scale insect belonging to the same taxonomic family as *T. parvicornis* (Coccidae), on which it demonstrated high infectivity. *Akanthomyces muscarius* has been subjected to molecular characterization and phylogenetic analysis. A series of laboratory bioassays were performed to evaluate the efficacy of the novel strain in comparison to the biological control agents (BCAs) used in commercial formulations. Trials included overwintering females, post-overwintering females, and nymphs of *T. parvicornis*. The findings revealed that this strain of *A. muscarius* effectively colonizes *T. parvicornis*, leading to rapid infection and mortality of the scale insects. Comparison with other available formulations indicates that our strain demonstrates superior pathogenicity against *T. parvicornis*. These results support further investigation into the potential of this *A. muscarius* strain as a biological control agent to mitigate *T. parvicornis* infestations in field conditions.

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T7 Improving management of emerging and re-emerging pests and diseases of *Prunus persica* (L.) Batsch)

Federico Brugneti¹, Luca Rossini², Antonella Cardacino¹, Marco Cirilli³, A. Mazzaglia¹, Silvia Turco^{1,*}

¹Dipartimento di Scienze Agrarie e Forestali, Università degli Studi della Tuscia, 01100 Viterbo, Italy

²Service d'Automatique et d'Analyse des Systèmes, Université Libre de Bruxelles, Av. F.D. Roosevelt 50, 1050 Brussels, Belgium

³Dipartimento di Scienze Agrarie ed Ambientali, Università degli Studi di Milano, 20133 Milano, Italy

*Presenting author: silvia.turco@unitus.it

Abstract

Prunus persica (peach) is one of the most important fruit tree species, renowned for its nutritional value and significant economic impact. Recent estimates highlight that China is leading global peach production, with an output of approximately 18 million tonnes. In the European Union, Spain ranks as the top producer, yielding 1,2 million tonnes per year, closely followed by Italy with 1,0 million tonnes (ISTAT 2024). Considering its impact on the global market, phytosanitary management plays a crucial role in ensuring high-quality products for consumers while striving to minimize the use of synthetic phytosanitary products. Recently, a re-emergence or resurgence of harmful pathogens such as those associated with the Twig Cankers and Shoot Blight disease (TCSB) has been observed in several Italian fields, especially alarming in important peach-producing districts of the Emilia-Romagna region. *Diaporthe amygdali* is considered the main causative agent of the TCSB, inducing rapid drying of shoots, flowers, leaves and branches which can be observed in late winter or early spring and during the season the resin, exudate leakage from the cankers can be observed, probably due to the Fusicoccin A toxin (Hilario et al., 2022). However, the effective causal agent of TCSB is still unclear, since different classes of fungi can induce similar symptoms (i.e. *Botryosphaeria* spp., *L. perooni*, *Cytospora* spp or other *Diaporthe* spp, as *D. eres*) (León et al., 2020). In the framework of the IMPEACHMENT project (PRIN 2022), a series of experiments are being carried out to elucidate the fungal species complex associated with TCSB, based on standard culture-based isolation coupled with advanced metabarcoding analysis of selected peach cultivars. Genomic analysis of *D. amygdali* will provide insights on its mechanism of action and virulence-associated effectors. These results will be reinforced by a massive varietal susceptibility screening, which, through transcriptomics analysis, will allow the characterization of plant-pathogen(s) interactome and, through metagenomics analysis, the characterization of the microbiome associated with varietal tolerance/susceptibility. Different antagonistic fungi and bacteria, mainly belonging to *Trichoderma* and *Bacillus* genera, as well as entomopathogenic microorganisms are currently screened and tested as biological control agents (BCAs) against *D. amygdali*, the fungus deemed as the main causal agent of TCSB, and *H. halys*. The results of these biocontrol tests will be integrated with a dynamic model based on the *D. amygdali* life cycle to develop a precise control strategy involving three key components: plant genetics, monitoring/modeling, and biocontrol agents.

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T8 Characterizing spatiotemporal dynamics of biotic stresses to optimize sampling strategies in agricultural systems

Roni Gafni, Northern R&D, MIGAL – Galilee Research Institute, Kiryat Shmona 11016, Israel,
* Presenting author roni.ga@migal.org.il.

Dana Levanon, Dept. of Industrial Engineering and Management, Ben-Gurion University of the Negev, Be'er Sheva 8410501, Israel, Yafit Cohen, Institute of Agricultural Engineering, Agricultural Research Organization, Bet Dagan 50250, Israel, Yael Edan, Dept. of Industrial Engineering and Management, Ben-Gurion University of the Negev, Be'er Sheva 8410501, Israel

Abstract

Periodic monitoring of pests and diseases in crops is crucial for early detection, enabling preventative agro-technical solutions and minimizing treatments in disease-free areas. However, it is often hindered by resource limitations, leading to late detection and unaddressed outbreaks, resulting in excessive pesticide use, escalating costs, environmental damage, and risks to workers and consumer health. Robotic sensing and proximal data collection systems present a promising solution, facilitating efficient and timely monitoring to enhance decision-making for pest management. However, given the complex nature of agroecosystems, an effective sampling strategy accounting for the spatiotemporal dynamics of pests and diseases, is called for. This study addresses biotic stress in two agroecosystems: [1] the two-spotted spider mite (TSSM, *Tetranychus urticae*), a major pest in greenhouse-grown sweet peppers (*Capsicum annuum*) in southern Israel; and [2] white mold (WM, *Sclerotium rolfsii*), a soilborne disease severely damaging open-field peanuts (*Arachis hypogaea*) in northern Israel. A dynamic sampling algorithm recently simulated for TSSM achieved a 90% detection rate in small fields (<5 ha), though performance decreased as field size increased. To optimize sampling, this study characterizes the spatiotemporal dynamics of these biotic stresses through intensive monitoring and geostatistical analysis. During 2015–2017, TSSM abundance was monitored weekly in four pepper screenhouses by randomly sampling every 20 plants in every fifth row. In 2024, seven WM-infected peanut fields were monitored weekly or bi-weekly for symptoms and pathogen signs using a 20 × 1 m grid. Spatial distributions were analyzed using Average Nearest Neighbor for TSSM and Moran's I Index for WM, with interpolated maps and Hotspot Analysis conducted, respectively. TSSM consistently showed a clustered distribution ($p < 0.001$) across all dates and screenhouses, while WM exhibited a clustered distribution in most fields later along the season, with random distribution or no infestation at early crop stages. TSSM infestations were higher and occurred earlier in the season (around 30 days post-planting) near the screenhouse edges (<20m) but were lower and delayed (70-80 days post-planting) in the center (>30m). Additional results will be presented. Despite the limited number of monitored sites, we identified key infestation patterns consistent across all sites, potentially enabling a monitoring robot to focus on hotspots during critical periods for timely, precise treatments and optimized pest management strategies.

T9 A mechanistic, five-step approach for prediction modelling: *Alternaria*- tomato pathosystem as case study

Irene Salotti, Marco Camardo Leggieri, and Paola Battilani

Department of Sustainable Crop Production, Università Cattolica del Sacro Cuore, 29122 Piacenza, Italy.

**Presenting author e-mail: irene.salotti1@unicatt.it*

Abstract

Predicting the occurrence and development of plant diseases represents one of the main demands for the successful application of crop protection strategies in support of food security and safety. There are numerous ways to develop plant disease models; however, the mechanistic approach has been regularly remarked for its potentialities in providing accurate and robust prediction. Thanks to the process-based method for building the structural and mathematical framework, starting from pathogen life cycle, key weather-pathogen-host interactions are incorporated into the model. On the other hand, lot of information is needed to address such complexity, especially when the disease is caused by a fungal species complex. The current research wants to show the development of a mechanistic, weather-driven model and the management of required information using the *Alternaria*-tomato pathosystem as a case study. *Alternaria* spp. pose a threat to tomato production worldwide and to human health for their ability to produce mycotoxins. Recently, the concept of *Alternaria* disease complex has been introduced to account for the concurrent presence of different *Alternaria* species on the same plants and the misleading symptomatology at early stages of the epidemics. The development of the mechanistic model for *Alternaria* complex disease in tomato was built following five steps. First, a systematic literature review was performed to collect data on each species belonging to the complex on their ecology, biology, and epidemiology, including mycotoxin production. A logical framework was then built to account for the relationship between *Alternaria* spp., tomato, and the environment. Second, knowledge gaps and bottlenecks for model development were identified. Particularly, all *A. tenuissima* biological processes and *Alternaria* spp. mycotoxin production were poorly investigated, highlighting the need for further studies. Third, specific ecological studies were carried out to address the missing information. Experiments were performed under controlled conditions to highlight pathogen response over the tested environmental variables, with little or no interference from uncontrolled factors. Fourth, species-specific equations relating pathogen biological processes and environmental factors were built by pooling quantitative data obtained from literature and set up trials. Fifth, the logical and mathematical framework were joint in a prototype model, which combines *Alternaria* species behavior into the following compartments: i) primary inoculum production, ii) spore borne infection on healthy tomato tissues, iii) latency period, with the transition from latently infected to symptomatic and sporulating tomato sites, and iv) secondary inoculum produced for an infectious period, until the exhaustion of tomato tissues.

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T10 AI-Driven Pest Control: Sustainable Agroecosystems through Remote Monitoring and Predictive Modeling

Roberta Ascolese¹⁻², Giuliano Langella³, and Francesco Nugnes²

¹University of Naples Federico II - Department of Biology, Via Vicinale Cupa Cintia 21, 80126 Naples, Italy; ²Institute for Sustainable Plant Protection (National Research Council) – IPSP (CNR), Piazzale Enrico Fermi 1, 80055 Portici, Italy;

³University of Naples Federico II - Department of Agricultural Sciences, Piazza Carlo di Borbone 1, 80055 Portici, Italy

*Presenting author e-mail: roberta.ascolese@unina.it

Abstract

During the last few years, the planning of phytosanitary management became difficult due to different causes. In particular, agricultural pest management is highly influenced by the recent climate change especially fluctuating temperatures and unpredictable rainfall impact the life cycle of acclimated pest species [1]. As a result, the developmental and flight period of many acclimated pest species no longer correspond with the previously recorded data. Additionally, the rise in average temperature has led the increasing in overwintering insects and their broader geographic distribution [2]. Furthermore, human activities such as trade and travel have also favoured the introduction and the spread of exotic species into new territories [3]. Moreover, pest management has become increasingly challenging due to the banning and reduction of active ingredients that previously enabled effective control but had deleterious effects on the surrounding environment [4]. Entomological monitoring and agrometeorological data collection are fundamental tools for planning and realizing a targeted phytosanitary interventions [5], which can be further enhanced and optimized through the application of Artificial Intelligence. The present study was conducted in the Campania region (Southern Italy), an area that coincides with the recent detection of the oriental fruit fly, *Bactrocera dorsalis*, in some orchards in the province of Naples [6]. The research aims to update the life-cycle data of the Medfly, *Ceratitis capitata*, and assess its interactions with *B. dorsalis*. In the infested fields a comprehensive monitoring system has been established, combining traditional and electronic traps, enhanced with Deep Learning for species recognition, and smart control units for collecting agrometeorological data. Different Machine Learning models, including Artificial Neural Networks, are also being tested to create predictive models for both tephritids. Remote monitoring with the use of e-traps has provided daily data allowing the identification of specific times of the day when adult flight activity peaks, thereby defining the circadian rhythms of both species. Preliminary analyses revealed a shift in the Medfly life cycle due to climate change and highlighted a delayed emergence of *B. dorsalis* in 2023 and 2024, suggesting the possibility of multiple introductions of the oriental fruit fly. Predictive models are currently being defined and developed as key tools to enhance the planning of phytosanitary activities and to be integrated in an updated Decision Support System.

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T11 Urban-Agricultural Interface: Impact of Urban Habitats on Mediterranean Fruit Fly Dynamics in Citrus Orchards

Carmel Katz^{1,2}, Michael Ben-Yosef³, Eitan Goldstein², Roni Nakar⁴, Yafit Cohen²

¹Department of Horticulture the Robert H. Smith Faculty of Agriculture, Food and Environment, Hebrew university of Jerusalem, Rehovot, Israel

²Agricultural and Biosystems Engineering institute, Agricultural Research Organization, Volcani Institute, Rishon Le'Zion, Israel

³Gilat Research Center for Arid C Semi-Arid Agricultural Research, Volcani Institute, Gilat, Israel

⁴The Israel Cohen Institute for Biological Control, The Plant Production C Marketing Board

Abstract

Urban environments, characterized by unique microclimates and untreated vegetation, can influence pest dynamics in adjacent agricultural lands. This study examines the impact of urban habitat characteristics on the Mediterranean fruit fly (*Ceratitis capitata*), a globally significant agricultural pest, in commercial citrus plots in Israel. Using the ecoinformatics approach, data were analyzed from six consecutive citrus growing seasons (2017–2023), encompassing 2,900 orchards, 320 urban settlements, and over 14,000 trap locations monitored across diverse landscapes.

The findings validate earlier studies showing that proximity to urban areas fosters higher *C. capitata* populations in citrus orchards. Fly trap captures were 1.5 times higher within 250 meters of settlements compared to plots located farther away, particularly during the fall population peak (e.g., 2.71 ± 0.16 flies per trap per day, FTD, within 250m vs. 1.82 ± 0.12 FTD beyond 250m in November 2022). The seasonal peaks in pest activity, observed from October to December, underscore the role of settlements as a source of infestations in adjacent orchards. Settlement characteristics, particularly relative vegetation cover, extracted from Sentinel-2 satellite images, significantly influenced *C. capitata* dynamics. Settlements with high vegetation cover (50–84%) resulted in consistently higher trap captures in nearby citrus plots, with increases of up to 2.3-fold compared to plots near settlements with low vegetation cover (0–25%). Conversely, built-up area metrics, such as impervious surface and building volume, presented mixed results. Low-density urban areas with ample vegetation supported greater pest populations, while highly urbanized settlements with impervious cover exceeding 80% occasionally amplified pest presence. Socioeconomic indices of settlements, serving as proxies for relative vegetation cover, corroborated these findings. Citrus plots adjacent to high socioeconomic settlements experienced elevated pest activity, consistent with the vegetation cover effect.

Risk maps generated from these analyses revealed that while 39% of citrus plots are at risk based solely on proximity to urban habitats, incorporating vegetation cover reduces this high-risk area to 12.8%. These results emphasize the importance of integrating urban landscape features into pest management strategies. Incorporating settlement characteristics into decision- support tools could enhance control programs, minimize pesticide applications, and mitigate economic losses. This study highlights the

ecological and economic significance of urban-agricultural interfaces and advocates for proactive, landscape-specific pest management approaches.

T12 Pest Control SDSS- From Academy to Industry

A. Cohen^a, Y. Cohen^b, G. Gefen^c

a Medva GIS, 3 HaBarzel st. Tel Aviv, Israel

b Institute of Agricultural Engineering, Agricultural Research Organization (ARO), Volcani Center, P.O. Box 6, 50250 Bet Dagan, Israel

c The Israel Cohen Institute for Biological Control, PPMB – Citrus Division, Israel

*Presenting author e-mail: avihu@mdvia.net

Abstract

MedCila, a spatial decision support system (SDSS), was developed to address the challenge of controlling the Mediterranean fruit fly (Medfly) in Israeli citrus orchards. Its development followed four main phases: acquiring expert knowledge, identifying and modelling relevant decision-making criteria, integrating the system into a GIS environment, and conducting an initial performance evaluation. Key criteria for control decisions included fly populations, the presence of a "blue eye" in the nearest trap, host susceptibility, Medfly developmental stages (modelled using an accumulative day-degree model), historical trapping data, and medfly populations in nearby traps. Decision-making was guided by Stanford Certainty Theory, combined with a rule-based decision tree. Early evaluations revealed that MedCila provided recommendations generally accepted by experts, minimizing the number of plots requiring coordinator decisions (time saving), and may reduce unnecessary spray actions.

In 2017, the Agri-Insight platform was introduced by Medva GIS for the Israeli Ministry of Agriculture, to manage Medfly control across all Israeli citrus orchards— encompassing 15,000 plots and monitoring 2,000 traps throughout the citrus season. Agri-Insight integrates diverse datasets, including real-time and historical surveys, meteorological data, and plot susceptibility metrics. The platform generates actionable insights for decision-making, enabling efficient pest control through tools for monitoring plot conditions, generating spray maps, and managing GPS-guided spray routes. It also facilitates comprehensive data management for traps, plots, and stakeholders, contributing to the goal of achieving zero Medfly infestation.

Building on MedCila, PestDecide emerged as a refined solution for operational pest control SDSS. PestDecide was developed using long-term field data to optimize its algorithms and provide improved spraying recommendations aligned with expert decisions. The system allows users to select multiple plots, request tailored spraying recommendations, and review and approve these recommendations through intuitive decision-support tools. It further enables users to generate work orders for pest control operations and create tracking files for management and analysis. By storing detailed data on recommendations and decisions for each plot over time, PestDecide supports continuous performance analysis and decision-making improvement. PestDecide has been operational for two years, demonstrating significant advancements in pest control decision-making processes, resource efficiency, and overall effectiveness, establishing itself as a reliable tool for sustainable agricultural risk management. As of today, PestDecide is operational for controlling the Mediterranean fruit fly in citrus orchards. However, since we have developed a comprehensive infrastructure: databases, workflows, algorithms, and a management system—PestDecide can be easily adopted for other pest- host SDSS.

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T13 GeoAI, Metrology and Remote Sensing for Smart Agriculture: Mapping Land Transformation and Climatic Impacts to Optimize Crop Resilience and Water Management in a Mediterranean Region

Alessandro Vitale^{1,2}, and Francesco Lamonaca³

1 Department of Computer Science, Modelling, Electronics and System Science, University of Calabria, Arcavacata di Rende, Italy.

2 National Research Council of Italy, Institute of Nanotechnology (CNR-NANOTEC), Rende, Italy.

3 Department of Civil Engineering, University of Calabria, Rende (CS), Italy.

*Presenting author e-mail: alessandro.vitale@unical.it

Abstract

Integrating GeoAI, metrology, and remote sensing offers transformative potential for addressing agricultural challenges in the context of climate change and land transformation [1]-[3]. This study investigates the interplay between land transformation and climatic variables, including evapotranspiration, maximum and minimum temperatures, and the Drought Severity Index (DSI), to optimize crop resilience and water management in a Mediterranean Region from 1999 to 2024. The research focuses on valuable crop regions across fourteen municipalities along the Tyrrhenian coast of Calabria, Southern Italy, characterized by diverse cropping systems and increasing susceptibility to climatic variability.

To achieve these objectives, the authors utilized the Idaho TerraClimate dataset for climate data, combined with multispectral and multi-temporal satellite imagery from Landsat platforms [4]. A Google Earth Engine (GEE) cloud computing platform was developed to streamline the analysis [5]-[7]. The methodology included employing a Random Forest (RF) classifier to process and classify multispectral satellite images, enabling the interpretation of complex land transformation patterns [8]-[11]. The RF classifier was rigorously trained and validated using georeferenced ground truth elements derived directly from classified multispectral images [12],[13]. The Overall Accuracy (OA) and the Kappa coefficient accuracy metrics confirmed the robustness of the classification process, ensuring reliable insights into spatial and temporal trends.

Results indicate significant land cover changes, with marked reductions in vegetative areas correlating with intensified drought conditions and shifts in climatic variables. Vulnerability zones were identified, particularly in regions experiencing prolonged dry spells and increasing evapotranspiration rates. These findings underscore the urgent need for precision irrigation techniques, adaptive crop management practices, and sustainable land use planning to mitigate the impacts of climate change.

This study further demonstrates the potential of integrating GeoAI and remote sensing with metrological data to enhance agricultural resilience. By providing actionable insights, the research supports policymakers, farmers, and stakeholders in implementing targeted interventions to improve water resource management and crop productivity in Mediterranean cropping systems. Ultimately, this work exemplifies the critical role of advanced geospatial technologies in addressing the intertwined challenges of land transformation and climate change.

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T14 Integrating Spatio-Temporal Vegetation Indices with Machine Learning for Dynamic Maize Field Performance Monitoring: Development of a Real-Time Crop Monitoring Framework

Yafit Cohen¹, Amit Malka², Yonatan Goldwasser¹, Elia Scudiero³, Eitan Goldshtein¹, Gilad Ravid²

1Institute of Agricultural Engineering, Agricultural Research Organization, The Volcani Center, Rishon-LeZion, Israel

2 Industrial Engineering and Management Department, Ben Gurion University of the Negev, Israel

3 Department of Environmental Sciences, University of California, Riverside, CA , USA

**Presenting author e-mail: rgilad@bgu.ac.il*

Abstract

Maize (*Zea mays* L.) stands as one of the world's most strategically important cereal crops, with its production playing a pivotal role in global food security and economic stability. Despite its significance, maize cultivation faces substantial challenges due to its heightened sensitivity to water and nitrogen stress during critical phenological stages, which can severely impact biomass accumulation, kernel formation, and ultimate grain yield. The agricultural sector urgently requires sophisticated tools capable of providing real-time assessment of field functionality throughout the growing season to optimize crop management decisions.

This research presents a comprehensive data-driven methodology utilizing multi-temporal satellite imagery to develop an early warning system for maize crop performance. The study analyzed data from 145 commercial maize fields across seven agricultural enterprises in Israel over four consecutive growing seasons (2018-2021). Field productivity was stratified into three distinct functional categories based on yield outcomes. The methodology leveraged Sentinel-2 satellite imagery, employing its multi-spectral capabilities and frequent revisit period of five days to generate and analyze Spectral Vegetation Indices (SVIs). These indices underwent innovative spatial, temporal, and spatio-temporal transformations to identify robust indicators capable of discriminating between field functionality levels throughout the crop cycle.

The research established Target Development Curves (TDC) and Inhibited Development Curves (IDC) for selected indices, creating a dynamic framework for monitoring crop development.

Following the CRISP-DM (Cross-Industry Standard Process for Data Mining) methodology, we developed and validated a machine learning pipeline incorporating an expanded feature set of 100 derived indices, evolved from six fundamental SVIs. The study evaluated four machine learning algorithms—Random Forest, XGBoost, Multilayer Perceptron (MLP), and Support Vector Machine (SVM)—using both leave-one-year-out validation and traditional 80-20 split with five-fold cross-validation to ensure robust model performance assessment.

The results demonstrated superior classification accuracy using a comprehensive approach incorporating spectral and spatio-temporal features. The optimal model achieved a balanced accuracy of 0.8 at 30 days after sowing (DAS), progressing to 0.9 at 70 DAS using the 80-20 split methodology. The more rigorous leave-one-year-out validation maintained a consistent accuracy of 0.7 from 30 DAS onward. Notably, the integration of our complete index suite yielded a 20% improvement in accuracy compared to traditional NDVI-based approaches, underscoring the significant advantage of incorporating spatial and temporal dimensions in agricultural predictive modeling. These findings establish a robust foundation for developing operational crop monitoring systems that can enhance decision-making in modern maize production systems.

T15 Spectral-based weed detection across diverse environmental conditions

Rina Su¹, Neil Boonham¹ and Ankush Prashar^{1*}

¹*School of Natural and Environmental Sciences, Newcastle University, Newcastle Upon Tyne, NE1 7RU*

*Ankush.prashar@newcastle.ac.uk

Abstract

Herbicide application is a common practice for weed control globally and until recently, emphasis has been mainly on uniform long-term application. This strategy without has led to some negative consequences which include resistance among weed species, suboptimal weed control, increased costs and environmental pollution and food safety concerns. Automation in weed detection and targeted approach for herbicide application represent a promising solution for above concerns. This project study used a machine learning-based workflow build exclusively on spectral features for weed discrimination, thus bypassing the need for shape or texture extraction. In addition, unlike previous research which is confined to similar environmental setups, this study assessed the transferability of these workflows from controlled conditions to variable field environments, offering insights into model performance under both research environments using datasets from a 10 band multispectral camera. Results showed that using the full spectrum of 10 bands outperformed feature selection methods such as RelifF, RFE and Principal Component Analysis (PCA) across all scenarios. Among classifiers, K Nearest Neighbour outperformed Random Forest and Support Vector Machine, in both environments. The experimental set up also helped in identification of optimal weeding times for autonomous approaches, which was validated using statistical analysis. Hence, these findings emphasise the transferability of the workflows across diverse environments and providing practical guidance for management for real- world autonomous applications.

T16 Moving towards Regenerative Agriculture: advancements in remote sensing tools to measure soils health regeneration.

Marco Silvestri

Barilla G. e R. Fratelli S.p.A, via Mantova 166, Parma, Italy

Abstract

Regenerative agriculture focuses on positive environmental outcomes including soil health improvement. Measuring and tracking Soil Organic Carbon (SOC) as soil health indicator is crucial to monitor progresses to encourage implementation of regenerative practices in supply chains but smart, efficient, and reliable system are needed.

Remote sensing technology is a innovative, smart and promising tool to measure and track regenerative practices impact on SOC content, understand the changes that occur over time on soil as well as on farms and in the landscape in which the farm operate.

T17 How to Capture Within-Field Heterogeneity Across Multi-Year Crop Rotation: High- Resolution Insights from Sentinel-2

Tom Kenda¹, Xavier Draye¹, Pierre Defourny¹

¹ *Université catholique de Louvain, earth and life institute, Belgium*

Abstract

Europe faces an urgent need to transition agroecosystems towards agroecological practices to ensure food security, enhance resilience to climate change, restore biodiversity and improve soil carbon stocks. Achieving this transition will require advances in phenotyping to identify optimal combinations of species, genotypes and management practices that can withstand projected climate scenarios. One of the major challenge is to address the spatial and temporal variability of environmental conditions within fields, which have a significant impact on plant growth in farmers' fields. This study aims to characterise the within-field spatial and temporal variability of crop growth. To achieve this, it will (1) develop a method to represent the spatial heterogeneity of crop growth across different seasons and crop types, (2) establish criteria to distinguish heterogeneous fields from homogeneous ones, and (3) identify some of the drivers of heterogeneity (4) while investigating how these patterns evolve over time. For each year of Sentinel-2 (S2) acquisition (2017-2024) and each parcel of the study area (Wallonia), the S2-derived LAI time series was used to (1) infer the growing season of the main crop and (2) produce a spatial indicator of vegetation growth heterogeneity based on this in-season time series. An expert-based qualitative validation was carried out. The resulting maps effectively capture the homogeneity or heterogeneity observed both in the LAI profiles and by the experts on the field, regardless of the crop. A method has been developed to assign an annual and crop-specific heterogeneity score to each plot. The score is calculated by comparing all heterogeneity maps of a given region and ranking them by their standard deviation. These standard deviations were also used as target variables for a linear mixed effects model and a random forest regressor (RF) to try to understand the main drivers of spatial heterogeneity. The input features included namely the crop type, the year (accounting for weather conditions), and variable related to topographic and soil characteristics of each parcel. Finally, to study the potential change in spatial patterns across time, 45 000 parcels (with fixed boundaries over 8 years) were selected. Pairwise correlation coefficients were calculated between all pixels of the heterogeneity maps of each year. For a given parcel, higher correlations were found for two years with similar heterogeneity patterns, while negative or low correlation coefficients were found for two years with opposite or different heterogeneity patterns. Again, a linear mixed effects model was fitted with the correlation coefficient as the target variable and the parcel ID as a random effect. The analysis showed a significantly higher correlation for two years with the same crop (mean correlation of 0.50 ± 0.001) than for two years with different crops (0.39 ± 0.001). Among the observations for two years with the same crop, chicory, winter wheat and sugar beet appeared to be the crops with the highest average coefficient (0.59 ± 0.001 , 0.56 ± 0.001 and 0.55 ± 0.001 respectively). On the other hand, fallow land had the lowest average coefficient (0.30 ± 0.024). The method of Blackmore (2000) has been adapted to delineate management zones. These zones correspond to the following: (1) high productivity stable zone across years, (2) low productivity stable zone or (3) unstable zone across years. Blackmore classified these zones combining annual yield maps. Here, the latter are replaced by the LAI-derived heterogeneity maps using several maps of similar crops for a given field. This allows to overcome the lack of available and good quality yield maps for most farmers. The versatility of the method extends its applicability to different agricultural settings and crops at very low (or no) cost to the end user. The resulting maps could guide dynamic agricultural practices towards greater sustainability, including irrigation, fertilisation and spraying management, and could also provide opportunities for new soil sampling designs and targeted in-field phenotyping. The maps will be made available for Walloon farmers on the Belcam website.

T18 A Low-cost and AI-integrated Imaging Device for Plant-parasitic Nematodes Quantification and Classification

G. Bi¹, Zhipeng Yuan¹, Peng Yue¹, Nasamu Musa², and Po Yang¹

1 School of Computer Science, University of Sheffield, Sheffield, S10 2TN, United Kingdom

2 Department of Soils, Crops and Water, RSK ADAS Ltd High Mowthorpe, Malton, YO17 8BP, United Kingdom

**Presenting author e-mail: g.bi@sheffield.ac.uk*

Abstract

Plant-parasitic nematodes (PPNs) are widespread microscopic roundworms that have parasitic relationships with their host plants. Economically important PPNs, such as root-knot (*Meloidogyne spp.*) and cyst (*Globodera spp.*) nematodes, seriously threaten the yields of crops and woody plants through direct parasitising host plants or indirectly transmitting diseases as pathogens, which are responsible for 8.8%-14.5% annual losses of global crop production [1]. In response to this threat, growers are encouraged to detect the presence of PPNs in plant or soil samples through PPN testing for guiding preventive and sustainable PPN management practices [2]. Multiple PPN testing methods have been proposed, including morphological [3], molecular [4], and AI image [5] testing. Morphological testing relies on manual microscopic examination by trained taxonomists, which is time-consuming and subjective. Molecular methods, including qPCR, high-throughput sequencing, and meta-barcoding, achieve higher accuracy with automatic workflow for PPN testing. However, this type of method is cost-prohibitive [5]. With the advancement of AI technology, AI-driven methods, especially the application of convolutional neural networks, have been proposed to identify PPN species from microscopic images [5]. Although AI image testing has demonstrated advantages in terms of testing speed and cost, an efficient and easy-to-use AI-based PPN testing solution is under-explored due to the reliance on multiple devices, including imaging and computing devices. In this work, we develop a micro-imaging device with computation ability that utilises a PPN detection model to achieve PPN counting and genus classification. Specifically, the developed micro-imaging device consists of Raspberry Pi 5, HQ camera module, microscope lens, uninterruptible power supply, screen, and 3D printed case to provide computational resources, imaging capabilities, and user-friendliness for PPN testing. A PPN detection model optimised by channel attention mechanisms and model quantification technology is integrated into this device for PPN genus classification and instance counting. The contribution of this work is fourfold. firstly, we construct a PPN microscopic image dataset covering five genus of PPNs and two life stages. Secondly, we propose an object detection model for PPN testing, which achieved 53.3% mean average precision. Thirdly, we design an imaging device based on Raspberry Pi 5 as a real-time PPN testing device. Last, the proposed PPN detection model is deployed on the device with model quantification, which achieves a detection speed of 8 frames per second for PPN quantification. This work can provide a low-cost AI-based PPN testing solution for sustainable PPN management.

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T19 Early Detection of Nutrient Deficiencies: The Hazelnut Case-Study

Fabio Fuoti¹, Martina Lippi¹, Andrea Rabbai², Cristina Carletti³, Andrea Gasparri¹, Valerio Cristofori^{2,*}

¹ Department of Civil, Computer Science and Aeronautical Technologies Engineering, Roma Tre University, Roma (Italy); ² Department of Agricultural and Forest Sciences, Università degli Studi della Tuscia, Viterbo (Italy); ³ Sigma Consulting s.r.l., Roma (Italy)
*Presenting author e-mail: valerio75@unitus.it

Abstract

The early detection of nutritional deficiencies in the European hazelnut orchard is a crucial activity to optimize plant growth and yielding, since it ensures fast interventions with targeted foliar nutrition in cases of verified deficiencies [1]. To achieve this aim, we propose a data-driven early detection model to detect nutrient deficiencies that appear in commercial hazelnut orchards. To design and validate the early detection algorithm under varying levels of difficulty, a dataset of thousands of pictures of healthy and damaged leaves were collected in the orchards during the growing season 2024, and two operational contexts are identified.

The first represents a baseline scenario with simple, controllable conditions, where each image captures a single hazelnut leaf on a controlled background, such as a solid color or graph paper. This scenario supports initial algorithm calibration and baseline issue identification. The second involves more complex, less controlled conditions, representative of real-world scenarios. Here, each image captures a hazelnut leaf in the foreground against natural backgrounds, such as the sky, ground, or plant, with varying lighting conditions. Examples from both contexts are shown in Figure 1. Two balanced datasets are created using the available images, as detailed in Table 1. These include the following classes: nitrogen, phosphorus, and iron deficiencies, leaves affected by biotic diseases to be discarded by the model, and healthy leaves. As the quantity of images used during training plays a pivotal role in achieving good model performance, various data augmentation techniques are employed. These include rotations, horizontal and vertical flips, and random adjustments to brightness, contrast, saturation, and sharpness. These techniques help improve the model's robustness and generalization to diverse operating conditions, which might occur especially in real-world settings. Examples of resulting augmented images are shown in Figure 2. As a result, the number of training images increased to 5,544 for the dataset in the controlled environment and to 10,527 for real world dataset. The test sets are composed of 126 and 240 nonaugmented images.

After collecting the datasets, we trained and evaluated two state-of-the-art models: MobileNet [2] and ConvNext [3]. The preliminary comparison of their performance on both datasets revealed that ConvNext consistently outperformed MobileNet. In the controlled environment, ConvNext achieved an accuracy of 89% compared to MobileNet's 79%. Similarly, in the real world environment, ConvNext attained an accuracy of 77% versus MobileNet's 65%. These results underscore the potential of data-driven approaches for the early detection of nutrient deficiencies in European hazelnut. Future work focuses on a deeper evaluation of these methodologies.



Figure 1: Hazelnut leaves with nitrogen deficiencies in controlled environment (left) and real environment (right).

	Nitrogen def.	Phosphorus def.	No deficiency	Healthy	Iron def.
# images	158	158	156	158	/
# images	250	250	250	250	198

Table 1: Datasets composition.

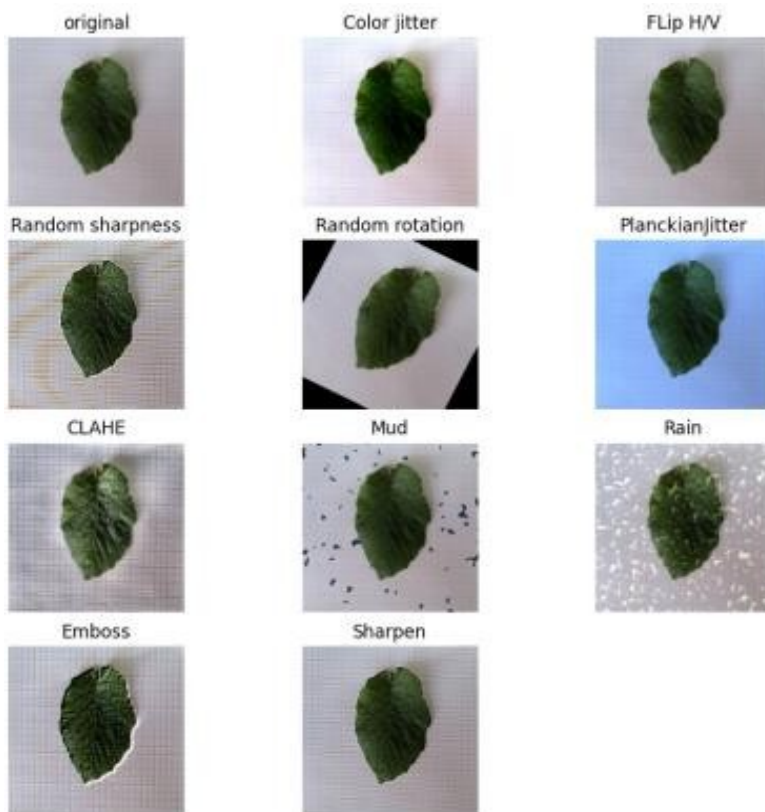


Figure 2: Data augmentation examples.

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T20 A control architecture for semi-autonomous robots in agriculture settings

Jozsef Palmieri¹, Paolo Di Lillo¹, Stefano Chiaverini¹ and Alessandro Marino^{1*}

1 Department of Electrical and Information Engineering, University of Cassino and Southern Lazio, Cassino, Italy.

**Presenting author e-mail: al.marino@unicas.it*

Abstract

Unlike traditional industrial robots operating in structured environments with repetitive tasks, recent advancements have expanded their application to unstructured settings, such as precision agriculture, which requires complex manipulation operations [1]. These scenarios demand robots with enhanced structures, advanced reasoning, rich sensor suites, and sophisticated control architectures, especially for collaborating with humans. Concerning the latter aspect, physical human-robot interaction ensure collaboration by allowing compliance with external forces applied to the robot's structure.

This work presents a unifying and flexible control architecture for mobile dual-arm robotic systems capable of handling kinematic constraints, imposing desired admittance behavior on the end-effectors, and generating internal motions to optimize, in case, multiple objectives. The controller relies on a Hierarchical Quadratic Programming (HQP) framework that incorporates Control Barrier function (CBf) theory to formalize constraints. Admittance constraints at the end-effectors' acceleration level are seamlessly integrated into the HQP, which outputs desired joint velocities, a common interface for many commercial robots lacking joint torque control feature.

The framework is validated within the precision agriculture domain, motivated by the European project CANOPIES¹. In detail, vineyard harvesting serves as the validation scenario, characterized by challenges such as imperfect perception, occlusions, and high dexterity demands. The control architecture (see figure 1) is structured into four modules: (i) Trajectory Generation; (ii) High-Level Layer; (iii) Low-Level Layer; and (iv) Perception System. The Low-Level Layer features the HQP controller, which manages a hierarchy of tasks: safety tasks ensuring system integrity, operational tasks controlling end-effector motion, and optimization tasks for joint configuration. At each time step, the HQP computes joint velocity commands according to tasks' priorities organized in lexicographical order. The Trajectory Generation module provides position and orientation references for autonomous operations, while the Perception System identifies grapes and estimates the 3D position of peduncles using RGB-D data from sensors placed on the robot's head or wrists [2]. Finally, the High-Level Layer, implemented as a finite-State Machine (FSM), adjusts operational tasks in the HQP based on the robot's task performance and the scenario, while maintaining safety and optimization tasks unchanged. This approach allows flexible autonomy, enabling human collaboration for end-effector control while the robot autonomously handles safety and joint configuration.

The overall approach allows the system dynamically to adjust autonomy levels based on task progress and perception outputs, supporting shared control scenarios where human and robot roles are balanced. Robots retain autonomy for behaviors such as collision avoidance, while humans provide direct input, demonstrating effective synergy in complex agricultural tasks.

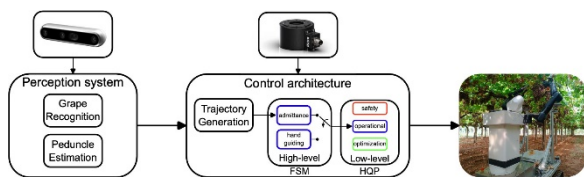


Figure 1: Proposed control architecture for the harvesting procedure.

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T21 A robotic arm design for autonomous kiwi harvesting

Simone Rossi¹, Dario Mengoli¹, Nicolò Omodei^{1,*}, Lorenzo Marconi¹

I Department of Electrica, Electronic and Information engineering - University of Bologna

**Presenting author e-mail: nicolo.omodei@unibo.it*

Abstract

This work presents the design and control of a robotic manipulator intended for kiwi harvesting, addressing the increasing need for automation in agriculture due to labour shortages and the pursuit of precision farming[1]. The research introduces a novel, low-cost robotic solution integrated with a mobile platform to automate the harvesting process in kiwi orchards (figure 1). The system involves the design of a custom anthropomorphic manipulator, including actuator selection, gripper design, and mobile platform integration, specifically adapted for the kiwi harvesting task.

Introduction

As labour shortage is increasing in agriculture and costs are rising, efficiency in tasks became crucial and harvesting is one that is mainly done manually and has to be completed in a defined time-frame. The paper focus on the design of a low-cost robotic arm based on the idea presented by [5], adding some improvements in the gripper mechanism and the integration with the robotic platform of the University of Bologna presented in [3]. The focus on this paper is on the design process of the arm.

Hardware and Perception

The manipulator is a 4 Dof anthropomorphic arm, composed of 4 revolute joints, actuated by Cubemars AK series servo-motors. This design choice is motivated by the shape of the canopy in the kiwi T-bar training system and because it has more flexibility compared to a classical cartesian design. The end-effector is an electrical actuated gripper (inspired by [5]) that is able to grab the kiwi fruit and perform a tilting movement to apply a shear force to the stalk, ensuring a correct detach from the branch.

The perception pipeline is based on computer vision and it lies on two low-cost sensors: an Intel Realsense D435i stereo camera mounted at the robot base in eye-to-hand configuration and a Basler Ace RGB camera mounted on the gripper (eye-in-hand). This double camera configuration was motivated by the lack of precision given by the stereocamera only, especially in outdoor environment, as the Realsense can reach at maximum 2% accuracy in the 1.5m range in laboratory conditions. Therefore, the stereocamera is used to detect and obtain an initial estimate of the kiwi fruits location and the eye-in-hand camera is used in the approaching phase, refining the initial estimate in real-time during the manoeuvre. In both phases, a YOLOv5 ([4]) model has been used to detect the fruits. In addition, during the approach manoeuvre a DeepSort ([7]) model has been used to track the correct object, so the resulting pipeline is depicted in figure (2).

Control

The control architecture is based on an Arduino Portenta H7 microcontroller, which computes a feed-forward torque depending on the trajectory as follow:

$$1. \quad T_{ff}(t) = B(q)\ddot{q} + D(q)\dot{q} + g(q) \quad (1)$$

where q and $\dot{q}$ are the joints position and joints desired position at time t , $B(q)$ is the inertial matrix of the robot, $g(q)$ the gravitation term and $D(q)$ the friction matrix ([5]).

The trajectory is produced by a PC running ROS2 with Moveit2 [2]. As described in the previous paragraph, we developed an algorithm to refine the initial estimate of the trajectory goal in run-time, taking advantage of the Hybrid Planning framework of Moveit2, as described in figure 3: after the first fruit pose estimate, the Global Planner produces the trajectory towards that goal, which is executed by the Local Planner that updates the goal pose estimate and possibly retrigger the Global Planner to produce a new trajectory towards the new estimated goal.

Results and Discussion

The effectiveness of the system has been evaluated through simulations and field experiments, demonstrating its capability to harvest kiwifruits effectively while maintaining fruit quality. future work aims to address challenges related to system robustness in diverse environmental conditions and further improve the adaptability of the harvesting mechanism.

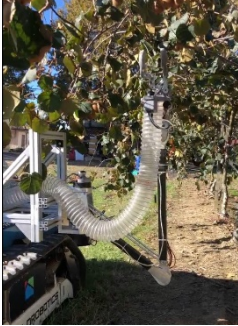


Figure 1: The kiwifruit-picking robotic arm

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T22 Automated X-ray plant phenotyping from seedlings to the field

Günter Lehretz, Thomas, Malzer, Stefan Gerth

Fraunhofer IIS, Flugplatzstraße 75, 90768 Fürth, GERMANY

Presenting author guenter.lehretz@iis.fraunhofer.de

Abstract

For the breeding of plants with a resilience to prevailing environmental factors (nutrients, water, temperature, light), their phenotypic characteristics (color, morphology), in a three-dimensional (i.e. size, shape) and four-dimensional extent (i.e. growth of roots and leaves over time) provide essential information for the selection of new breeding candidates. These characteristics describe the interaction of the genotype of the plants with the above-mentioned environmental factors and allow important estimations on the yield potential under certain environmental conditions or in a certain region. The recording and evaluation of the phenotypic characteristics of plants (underground and above-ground) with various sensors (Xray-CT for tubers and roots, optical 3D sensors for leaves and ears) allows a quantification of the influence of various factors on the appearance of the plant.

The X-ray Technology Development Center (EZRT) of Fraunhofer IIS develops methods and systems in the field of non-destructive testing technologies (NDT) for the agricultural industry: from imaging using optical 3D systems and X-ray-based image acquisition to 3D data reconstruction and 3D image analysis for applications in seed quality control to autonomous weed hoeing in the field. Using these technologies, it is possible to non-destructively record and characterize underground plant parts using X-rays or MRI and above-ground parts using optical scanning methods and to analyze their structures using machine learning methods.

For potato, roots and wheat ears, several Xray CT systems have been integrated for phenotyping under greenhouse conditions. For the detection of above-ground plant parts, AI-based methods based on Neural Radiance Fields (NeRFs) have been developed. Thus, detailed and complete 3D reconstructions of plants including semantic information (e.g. location of fruits) can be generated from a series of 2D RGB camera images. Additionally, a phenotyping infrastructure of the Fraunhofer EZRT in Merkendorf/Triesdorf (“Phenotyping Technology Center”) will enable the cultivation of up to 400 plants under controlled conditions (CO₂, humidity, temperature, lighting). In addition, CT and optical measurement technology are integrated into a conveyor belt system so that automatic sampling is possible.

Altogether, at the EZRT we enable phenotyping all across the plant life cycle and the production process. From seeds over seedlings and mature plants in pots. On the field Xray scanning and yield estimation is done via robotic systems for grain crops like rapeseed, wheat or chickpea. Thus, quantification of phenotypic parameters, especially visually inaccessible ones, enables a precise data-driven breeding of crops with high yield stability for sustainable farming under challenging environments.

T23 Uncovering the role of *serendipita williamsii* volatiles in establishing its own plant beneficial endophytic colonization: a parallel study of the headspace composition and mode of action

Jelle Van Vooren^{1,2}, Marie Blomme¹, Trang Tran Minh¹, Noémie De Zutter¹, Willem Desmedt^{1,3}, Christophe Walgraeve⁴, Sven Mangelinckx², Kris Audenaert¹

¹ Laboratory of Applied Mycology and Phenomics, Department of Plants and Crops, Faculty of Bioscience Engineering, Ghent University, Valentin Vaerwyckweg 1, 9000 Ghent, Belgium

² SynBioC research group, Department of Green Chemistry and Technology, Faculty of Bioscience Engineering, Ghent University, Coupure Links 653, 9000 Ghent, Belgium

³ Flanders Research Institute for Agriculture, Fisheries and Food (ILVO), Entomology unit, Burg. Van Gansberghelaan 96, 9820 Merelbeke, Belgium

⁴ Research group EnVOC, Department of Green Chemistry and Technology, Faculty of Bioscience Engineering, Ghent University, Coupure Links 653, 9000, Ghent Belgium

Presenting author e-mail: jelle.vanvooren@ugent.be

Abstract

Over the past years, there has been a growing interest in plant responses upon exposure to the volatilome of different fungi. However, knowledge on the composition of these fungal volatilomes and how they affect the plant's physiology is scarce. The enigmatic genus of *Serendipita* is a renowned endophytic fungus who can increase the plant's resilience upon abiotic and biotic stress through its volatilome^[1]. A combination of better nutrient uptake through beneficial root colonization and protection against stresses with its volatilome makes *Serendipita* of high potential for advancing sustainable crop production systems^{[2], [3]}. To gain a deeper understanding of how *Serendipita* establishes this beneficial symbiosis with the plant, we developed a new innovative approach to assess the content and bioactivity of the *Serendipita* volatilome: First we assessed the composition of *in vitro* grown *Serendipita* headspace. For this purpose, fungal cultures were grown in closed recipients, allowing for a sterile sampling of their headspace. Then, TD-GC-MS was used to qualitatively identify the most abundant volatile organic compounds (VOC's) emitted by *Serendipita*. In parallel, the role of the whole volatilome of *Serendipita* in establishing root colonization in *Solanum lycopersicum* was studied by using a new experimental setup that allows to rule out the fertilization effect of CO₂ produced by the fungal metabolism when plants are directly exposed to a growing fungus. Tomato plants were exposed to the VOC's produced by *Serendipita* and were compared to plants not exposed to any VOC's. The immunity of the plant was assessed after exposure to the volatiles of *Serendipita* by using a detached leaf assay, allowing us to visualize a difference in pathogen susceptibility. Hyperspectral imaging is additionally used to link the reflectance spectrum of treated plants with their immunity response to a pathogen. Next to this, the colonization of *Serendipita* in the roots of Tomato plants was quantified by using an RNA-based qPCR protocol, to see if exposing tomato plants to *Serendipita* VOC's leads to a higher presence of chlamydospores in the root and thus would facilitate its own colonization.

An overview of the most important volatiles detected will be presented, as well as a detailed outline of the experimental setups with a proposed mode of action.

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T24 A Distributed Framework for Task Allocation and Safe Coordination in Networked Multi-robot Systems for Precision Agriculture

Andrea Miele¹, Martina Lippi¹, and Andrea Gasparri^{1,*}

¹ *Department of Civil, Computer Science, and Aeronautical Technologies Engineering, Roma Tre University, Italy*

*Presenting author e-mail: gasparri@inf.uniroma3.it

Abstract

Coordinating multiple robots to effectively carry out diverse tasks in a real-world environment necessitates addressing several aspects. First, any time new tasks are requested to be executed, they must be allocated to the available robots according to predefined optimality criteria. Second, once the allocation is established, robots must be able to properly coordinate to reach the designated locations to perform the tasks while ensuring safe navigation in dynamic environments. Third, in scenarios where simultaneous execution of all tasks is not feasible, a strategy must be established to prioritize them while ensuring that all tasks are ultimately executed. In addition, achieving coordination in a distributed manner is desirable, i.e., with no central control unit, to promote system scalability, flexibility, and robustness [1]. However, distributed settings are generally significantly more challenging compared to centralized architectures. Indeed, a central control unit orchestrates all robots based on global knowledge of the system, while in a distributed setting, each robot makes its own decisions by solely relying on local data, i.e., gathered from onboard sensors or neighboring robots. Thus, enforcing network connectivity to ensure that each robot can (either directly or indirectly) communicate with every other robot is crucial to achieving effective coordination [2]. We propose a comprehensive distributed framework to achieve online task allocation and coordination of a networked multi-robot system safely, i.e., by ensuring no collision with dynamic obstacles, such as human operators, in the environment and preserving the connectivity of the network. A two-layer architecture, shown in figure 1, is designed where the bottom layer addresses the low-level safe navigation by resorting to Control Barrier functions (CBFs), while the top layer provides the distributed decision-making strategy involving the assignment of the tasks in a distributed manner and the management of possible deadlock situations caused by connectivity constraints. Auction-based and consensus-based algorithms are leveraged in this layer. Moreover, to ensure the proper execution of the assigned tasks, a global finite State Machine (fSM), i.e., with full knowledge of the system, is first designed and then distributed to the robot level, resulting in multiple local fSMs running in parallel. Inspired by the needs of the H2020 European Project CANOPIES1, we demonstrate the framework effectiveness in a precision agriculture setting, as depicted in figure 2, where robots are requested to empty crates filled by harvesters, which can be whether human or robotic, in an agricultural field. Numerical simulations and laboratory experiments are provided to validate the approach.

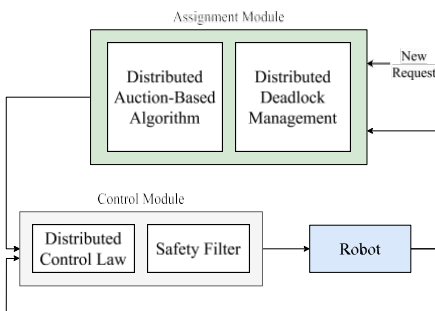


Figure 1: Overview of the distributed framework architecture.



Figure 2: Illustrative example of the

operational scenario.

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Acknowledgment

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T25 Motion planning for an autonomous agricultural robot in unstructured terrain

Matthias Lorenzen¹, Martina Mammarella², Chiara Ravazzi², Mahmoud Ghorab¹ and Fabrizio Dabbene^{2,*}

¹University of Applied Sciences Kempten, Kempten, Germany

²CNR-IEIIT, c/o Politecnico di Torino, Torino, Italy

*Presenting author e-mail: fabrizio.dabbene@cnr.it

Abstract

Despite the wide body of literature on motion planning for autonomous robots targeting structured agricultural environments, e.g., [1, 2], there remains a need for more efficient and reliable approaches for *unstructured* terrains. This work is motivated by a cooperation with the startup Paltech, which develops a weed-removal robot for grasslands, see figure 1. In this work, we employ a typical layered approach for robot navigation, see figure 2. However, in contrast to standard navigation tasks, such as point-to-point navigation, the global planner must solve the more challenging problem of visiting multiple targets in an optimal way while considering the kinematic constraints of the vehicle.

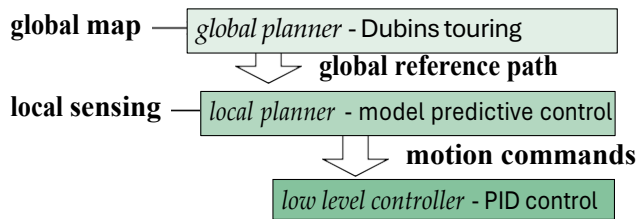


Figure 2: Typical layered approach for robot navigation. unstructured grasslands



Figure 1: Paltech's weed removal robot for grasslands

Specifically, we propose as *global planner* a graph-based Dubins touring algorithm to find a globally near optimal solution. The goal is to define the shortest path that, given a set of target locations, ensures the robot visits each location once, while enforcing the kinematic constraints. We determine the order in which the waypoints should be visited by solving the traveling salesman problem with an Euclidean metric [3]. Then, we design a graph-based solution for the Dubins touring problem [4] to determine the optimal headings in the ordered sequence of targets. The *local planner* is based on a novel model predictive control (MPC) scheme designed for non-holonomic systems to guarantee convergence to a desired target without getting stuck in local minima. Instead of a classical path following, the MPC algorithm takes the path generated in the first layer only as a reference, to then compute a locally optimal solution in real-time based on the current state of the vehicle, a more detailed dynamic model, and the perceived environment. The overall outcome of this work is a near-optimal motion planning algorithm that enables the UGV to visit points of interest in unstructured grassland and, in our specific application, perform autonomous weed treatment. *Ongoing and future work* will focus on several application-driven aspects. first, we will include the energy consumption into the optimization problem, to improve the battery run-time. Then, we will employ the DTSP with neighborhoods to tackle the case where the treatment can be applied even if the vehicle is not perfectly located above the weed, thus leading to reduced path in case the neighborhood region covers multiples plants. Last, we will investigate the adoption of a sampling-based DTSP approach to optimize the waypoints ordering and the headings, combined with the additional complexity introduced by field boundaries and possibly moving obstacles.

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T26 Motion Planning for Agricultural Tasks with Robotic Manipulators

Gaoyuan Liu^{1,4,*}, Bas Boom³, Naftali Slob³, Ann Nowe⁴ and Bram Vanderborght^{1,2}

¹ *Brubotics, Vrije Universiteit Brussel*

² *imec, Belgium*

³ *imec, the Netherlands*

⁴ *AI Lab, Vrije Universiteit Brussel*

*Presenting author e-mail: gaoyuan.liu@vub.be

Abstract

Robotic manipulators provide alternative solutions for various agricultural tasks, such as harvesting, pruning, and thinning. A complete agricultural robotic system requires multiple capabilities, including perception, reasoning, and control. Our work focuses on pruning, an essential orchard management treatment. Most previous work has focused on perception using computer vision techniques but has simplified the robot's behavior [1, 2, 3]. This simplification limits the capabilities of agricultural robotic systems in certain types of plants, such as grapevines, or plants with planar structures [4]. Our effort aims to extend the use cases of robotic manipulators in agricultural scenarios. Our contributions are summarized as follows:

- With the point cloud data of the real orchard, we build a dataset for testing robotic planning methods. This dataset contains the (filtered) point cloud for each tree and a geometric model with the *Adtree* modeling method [5].¹
- Our work addresses the behavior planning challenge for a robotic pruning system, which entails a multi-level planning problem in environments with complex collisions. We formulate the planning problem for a high-dimensional robotic arm in a pruning scenario, investigate the system's intrinsic redundancies, as shown in figure, and propose a comprehensive pruning workflow that integrates perception, modeling, and holistic planning.²³
- We identify the efficiency challenge in planning for pruning tasks. By leveraging the flexibility inherent in pruning tasks, such as arbitrary approach angles, and utilizing the robot's redundancy, we design a customized planner specifically for pruning.



Figure 1: Robotic pruning with possible Cartesian space poses.

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T27 Self-Supervised Local NBV Planning for 3D Plant Reconstruction by a Robot

Jianchao Ci^{a,*}, Xin Wang^a, Eldert J. van Henten^a, Gert Kootstra^a

^a*Agricultural Biosystems Engineering Group, Department of Plant Sciences, Wageningen University and Research, P.O. Box 16, Wageningen, 6700AA, the Netherlands.*

**Corresponding author. E-mail address: jianchao.ci@wur.nl*

Abstract

Robotic perception is essential for agricultural operations, as it gathers necessary information for downstream operations such as harvesting, de-leafing, and phenotyping. However, achieving accurate perception in complex agricultural environments is challenging due to significant plant occlusion, mainly caused by leaves. This occlusion prevents essential information from being captured by sensors, increasing uncertainty in robotic operations. To address this challenge, the use of active perception has been widely explored, enabling robots to actively reposition the camera to maximize information gain (IG), and thereby facilitating efficient perception with the fewest number of views. However, current active perception approaches relying on ray-casting for IG estimation are computationally and memory-intensive. This research proposes a method that utilizes a neural network for efficient IG prediction. Notably, a self-supervised learning framework is integrated, allowing the robot to automatically collect training data for itself and continuously improve and adapt to dynamic agricultural environments in a lifelong manner.

The proposed method was evaluated on 3D plant reconstruction tasks but, with minimal modifications, can be extended to other agricultural robotic tasks facing similar occlusion challenges. Comprehensive evaluations were conducted in both simulation and real-world environments, showing that the proposed method outperforms a random view planning method in terms of plant reconstruction efficiency and quality. Compared to state-of-the-art ray-casting-based methods, it achieves competitive performance in plant reconstruction while improving IG prediction speed by 171 times. Furthermore, due to the use of self-supervised learning, the method continuously fine-tunes and adapts to dynamic agricultural environments and plant structures.

T28 Using a digital twin of a tracked mobile robot for the design and validation of estimation and control algorithms

Luca Bascetta^{*}, Alessandro Febbraro, and Gianni ferretti

^I*Politecnico di Milano, Dipartimento di Elettronica, Informazione e Bioingegneria, Milano, Italy*

^{*}*Presenting author e-mail: luca.bascetta@polimit.it*

Abstract

Mobile robots play a crucial role in supporting Agriculture 4.0 technologies, with tracked mobile robots being especially well- suited for agricultural applications [1]. This paper describes the development of a 3D, multibody dynamic model, i.e., a digital twin, of a vehicle for agricultural applications characterized by flexible tracks, exploiting the modular approach provided by the declarative, multi-domain and object-oriented modelling language Modelica, that allows to describe, with a high level of accuracy, the complete suspension system as well as the interaction of tracks and grousers with the agricultural soil. In particular, the flexibility that is inherent in a modular object-oriented modelling language allows to develop different soil models that can be easily exchanged, and to model the flexible rubber track belts with a finite volumes approach, by dividing them into an arbitrary number of discrete segments that is not constrained by the number of grousers, where each discrete element is in turn divided along the transversal direction into two parts.

An extensive experimental campaign has been carried out to validate the model, mainly focused on the steering dynamics of a tracked robot moving on a rigid surface (indoor experiments) and on a deformable surface (outdoor experiments). In indoor experiments the actual position of robot center of mass and its angular orientation were measured very accurately through a VICON motion capture system and an Inertial Measurement Unit (IMU), in outdoor experiments the motion capture system was replaced by a Global Positioning System (GPS), in this case a technique called Real-Time Kinematic (RTK) is used to enhance the accuracy of the position measurements. The validation campaign allows to demonstrate the accuracy of the proposed digital twin in representing the vehicle dynamics and the interaction with soil. for this reason the model represents a suitable tool for the design and preliminary validation of motion planning and control strategies, for the optimization of the locomotion system of a tracked vehicle, and to assess the change to soil mechanical and hydraulic properties produced by different tracks in different soil conditions. In particular, in this paper the use of this digital twin for the design and validation of slip estimation algorithms and of feedback linearizing controllers is described. In fact, an extensive analysis performed simulating the robot allows to accurately characterize the behaviour and the performance of these estimation and control approaches.

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Acknowledgment

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T29 RootForce 4.0: a review of the classical image processing pipeline for root system architecture of cereals

Luis A. Torres-Cisneros, Thomas Lang, Markus Rehak, Thomas Malzer and Stefan Gerth

Fraunhofer Institute of Integrated Circuits IIS, Development Center X-ray Technology, Fürth, Germany

Presenting author: L.A. Torres-Cisneros

Abstract

Cereals as rice, wheat and maize has been the most prominent source of caloric intake for humans during thousands of years. To understand basic functionalities of cereals as anchoring, nutrient uptake and storage functions, Root System Architecture (RSA) is one of the commonly used characterization procedures. However, RSA depends on a proper non-invasive 3D imaging technique and a suitable segmentation algorithm.

X-rays have been in the past years one of most used non-invasive imagine techniques, since X- rays are able to penetrate matter without perturbing its inner structure and making 3D data accesible. However, understanding RSA requires post-processing of X-ray data that provide basic root properties as root length, minimal and maximal root angle, or packing fraction. To this end we present in the current contribution results of X-ray data of different root systems by using the latest version of RootForce algorithm. We sketch the fundamental steps within the image processing pipeline to analyze thick and thin roots. Finally, we present features computed on the analyzed 3D data to illustrate the data accessible by our image processing pipeline.

T30 Constellr HiVE – a satellite constellation for monitoring diurnal temperature cycles and enabling smart agriculture

Mohammad Iranmanesh¹, Daniel Spengler², Elsy Ibrahim¹, Ariadna Pregel-Hoderlein², Jonas Berhin¹, Christophe Lerot¹

¹ *constellr Belgium S.A., Belgium*

² *constellr GmbH, Germany*

*Presenting author e-mail: mohammad.iranmanesh@constellr.com

Abstract

The diurnal temperature cycle (DTC) plays a fundamental role in understanding and managing agricultural systems. Temperature fluctuations across the day influence multiple processes, including crop growth, nutrient uptake, pest dynamics, and yield prediction. By capturing DTC data, farmers and agronomists can develop more precise strategies to adapt to environmental variability, optimize resource allocation, and improve agricultural productivity. As climate variability increases, the ability to monitor these cycles in real time becomes essential for enhancing food security and ensuring sustainable farming practices.

Constellr develops a constellation of state-of-the-art high-resolution thermal infrared (TIR) as well as visible and near-infrared (VNIR) sensors, planned for launch by the beginning of 2025, to monitor land surface temperature (LST). The HiVE (High-precision Versatile Ecosphere monitoring mission) constellation comprises micro-satellites in the 100 kg class, with orbits in a sun-synchronous plane at an altitude of 550 kilometers. With a remarkable 1-day temporal resolution reached starting 2026 with 5 satellites in orbit, 30 meters spatial resolution for the TIR bands, and up to 10m for the VNIR bands, HiVE is uniquely equipped to provide accurate and timely data optimised for agricultural needs.

We will present the technical specification, status of the HiVE mission, and the added value of diurnal temperature cycle data for agricultural practice. By monitoring DTC, farmers gain insights into critical processes such as:

- **Predicting Crop Maturity and Yield:** DTC patterns influence crop development cycles, helping farmers optimize planting schedules and predict harvest times more accurately. [1]
- **Precision Fertilization:** Temperature fluctuations captured through DTC affect nutrient uptake in plants. By aligning fertilization strategies with DTC insights, farmers can improve efficiency and minimize waste. [2]
- **Frost Protection:** Rapid cooling during nighttime in the DTC can lead to frost, damaging sensitive crops. DTC data allows farmers to anticipate frost events and deploy mitigation strategies in advance. [3]

Besides that, an outlook on further LST-based products and their applications in precision agriculture, including regional-scale agricultural planning and adaptive management practices, will also be presented. Finally, other sectors that benefit from Constellr's LST data will be presented including the urban environment and infrastructure monitoring.

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T31 Cellulose-derived oligosaccharides obtained by LPMO oxidation biostimulate tomato weight, inflorescence, and immunity through ethylene and ROS-free signalling

Sonia Lorrai and David Cannella

Crop Production and Biostimulation Lab, PhotoBioCatalysis Unit, Universite Libre de Bruxelles – ULB, Bruxelles School of Bioengineering – EBB

*Presenting author e-mail: david.cannella@ulb.be

Abstract

Plant biostimulation through oligosaccharides, including those derived from cellulose, chitin, and chitosan, has gained considerable attention for its dual role in promoting plant growth and enhancing immunity. Lytic Polysaccharide Monooxygenases (LPMOs), highly conserved across biological kingdoms, are key enzymes used by phytopathogens to degrade cellulose polymers. In plants, these cellulose-derived products generated through LPMO enzymatic activity mimic pathogen-associated molecular patterns (PAMPs), triggering innate immunity and Systemic Acquired Resistance (SAR). This latter is a defense mechanism that provides long-lasting protection against a broad spectrum of pathogens [1].

Recognition of oligosaccharides by pattern recognition receptors (PRRs) on the plasma membrane, rapidly initiates early signaling events associated with biostimulation. Calcium (Ca^{2+}) influx occurs within 30-60 seconds, followed by activation of the mitogen-activated protein kinase (MAPK) cascade within 5-10 minutes. Reactive oxygen species (ROS) bursts are observed shortly thereafter within 30 minutes and peaking in 10 minutes. Subsequently, a durable immune response mediated by salicylic acid (SA), jasmonic acid (JA), and ethylene (ET) signaling pathways is established, with ethylene biosynthesis persisting for approximately six hours [3]. Together, these signaling events lead to SAR-related gene expression and enhanced resistance to biotic stress, among others responses.

Recent studies indicate that biostimulation by cellulose-derived oligosaccharides can activate plant immune responses independently of ROS signaling [2, 4]. In this work, we dug the biostimulatory effects on *Solanum lycopersicum* of native and C1-oxidized cello- oligosaccharides derived by LPMO activity on cellulose, AA9COS oligosaccharides pool, and the shortest native and oxidized oligosaccharides respectively cellobiose and cellobionic acid. Tomatoes are among the most widely cultivated and economically significant crops in the European agro-food sector. Thus, sustainable methods to enhance tomato crop growth and resilience are essential to meet increasing demands. At different concentrations, none of the tested oligosaccharides showed any production of hydrogen peroxide. However, cellobionic acid and AA9COS oligosaccharides activated ethylene signaling, whereas cellobiose did not, suggesting that distinct oligosaccharides target different signalling pathways. Physiological analyses revealed a general enhancement in plant growth, including increases in height, width, and stem diameter, following elicitor treatments. Additionally, early flowering and fruiting were observed, with stronger elicitor effects corresponding to an increased number of treatments per plant. This study highlights the potential of oligosaccharides as biostimulants to simultaneously promote plant immunity, growth, and fruits productivity. These findings contribute to the advancement of sustainable crop management practices, offering innovative strategies to improve plant resilience and agricultural output.

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T32 Application and assessment of model-based leak localization methods in an irrigation network

Neto f.M.¹, Orihuela L.^{1,2,*}, and Manzano, J.M.³

1 Centro de Investigación en Tecnología, Energía y Sostenibilidad (CITES), universidad de Huelva, Palos de la frontera, Spain

2 Departamento de Ingeniería Electrónica, Sistemas Informáticos y Automática, universidad de Huelva, Huelva, Spain

3 Departamento de Ingeniería, Universidad Loyola Andalucía, Dos Hermanas,

**Presenting author e-mail: luis.orihuela@diesia.uhu.es*

Abstract

The availability of water resources in agriculture is under significant pressure due to climate change and global warming. In some regions, including the south of Spain, rainfall has become increasingly scarce and concentrated over shorter periods, reducing the available water allocations, and forcing a maximization of the efficiency of the irrigation system^{1 2}. This situation places emphasis on leaks within irrigation networks, which exacerbate this issue by decreasing the amount of water available for crops. These leaks not only represent a loss of water, but also lead to increased operational costs due to the energy consumption required to maintain the network under pressure and in operation. Detecting and locating leaks is particularly challenging in buried irrigation networks, where root systems and depth complicate interventions, or in highly permeable or rocky soils, where the water loss caused by the leak can quickly move underground [4].

In this context, there is a pressing need to adapt and improve current leak detection techniques, which have traditionally been designed for water distribution networks (WDN), to the unique characteristics of irrigation systems. Unlike standard mesh WDN, irrigation networks exhibit a hierarchical, tree-like structure, with branches feeding drip lines, and with pressure regulating valves to control downstream pressure.

This work addresses the application of model-based methods designed for WDN for leak localization in irrigation networks. This techniques have been reviewed in [3]. The evaluated methodologies rely on sensitivity matrices for leak management, considering pressure or flow variables as tools to determine measurement nodes. These include techniques such as binarization, vector angle, correlation comparison, Euclidean distance, and least squares [2]; linear programming problem-solving [1]; and the residual projection strategy, which monitors virtual leak flow values based on a dual model [5]. These methods are analyzed against various magnitudes and interference sources, including additive and multiplicative noise, leak size, sensor placement, and more. Hydraulic simulations are performed on standardized WDN widely tested in the literature, such as Hanoi, Net3, and Quebra, as well as on a real irrigation network spanning 125 hectares of citrus orchards located in southwestern Spain (see figure 1). This work establishes an initial analysis and assessment of the state-of-the-art leak detection methods in a real irrigation network, highlighting the need for specific solutions for this type of infrastructure.

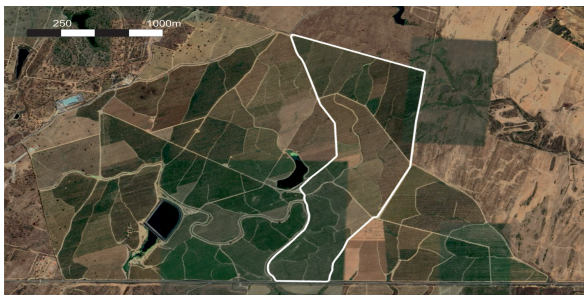


Figure 1: Satellite image of the citrus production farm under study

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T33 Harnessing Predictive Data Analytics of Soil Microbiota for Enhanced Bio-sustainability in Agriculture

Roberta Pace^{1,3,*}, Vincenzo Schiano di Cola², Angelo Napolitano³, Francesca Palomba³, Maurilia M. Monti³, Salvatore Cuomo², Michelina Ruocco³

¹*Department of Biology of the University of the study of Naples "Federico II" – Italy*

²*Department of Mathematics and Applications "Renato Caccioppoli" of the University of the study of Naples "Federico II" – Italy*

³*Institute of Sustainable Plant Protection of National Research Council (IPSP – CNR) – Portici, Naples, Italy*

*roberta.pace@unina.it

Abstract

The dynamic interactions within soil microbiota are fundamental to maintain soil health and fostering bio-sustainability in agricultural ecosystems. However, the complexity and variability of microbial communities present significant challenges in accurately predicting their functional roles and contributions to sustainable agricultural practices [1]. Artificial Intelligence (AI) is transforming the study of soil microbiomes by providing a robust method to analyze complex and high-dimensional data, extract meaningful patterns, and develop predictive models on soil biological health [2-3]. Particularly, Machine Learning (ML) algorithms such as Random Forest (RF), Support Vector Machine (SVM) and Artificial Neural Network (ANN) allow to manage, analyze and interpret microbiome data generated by sequencing technologies. Although existing studies are limited, the potential applications of AI appear highly relevant for developing predictive models of soil fertility based on its biological properties [4].

In our study, we try to pose the basis for the development of an AI forecasting model able to discern patterns of microorganisms beneficial for soil quality under different treatment, also considering correlations with environmental conditions. Soil microbiome data were obtained from soil samples collected at a farm specializing in 'baby leaf' crops grown in greenhouses, located in Bagnolo Mella (Brescia), Italy, during various stages of plant growth. Four fields were chosen to study how microbial community can change under different treatments. The treatments applied were: i) organic farming with application of beneficial microorganisms + Organic Matter (T +OM); ii) organic farming with application of beneficial microorganisms without Organic Matter (T -OM); iii) conventional farming + Organic Matter (C +OM); iv) conventional farming without Organic Matter (C -OM). A metagenomic approach was applied to study the soil microbiome. In the fields where soil samples were collected, a meteorological station was installed to monitor environmental conditions. This station was also equipped with soil sensors to measure soil moisture, temperature and conductance.

Our preliminary results demonstrate that predictive modeling based on comprehensive data analysis can serve as a powerful tool for managing soil health, supporting sustainable and smart agriculture, and fostering long-term ecological balance. By integrating soil microbiome datasets, different treatments and environmental conditions, we identify key microbial indicators and patterns that contribute to soil fertility and ecosystem resilience. These indicators will be used as important feature to construct predictive model thanks to the power of data analytics, combining machine learning, bioinformatics, and statistics, to understand soil microbiota behavior under varying conditions.

The model that will be generated will provide actionable insights for optimizing agricultural practices, enhancing crop yield, and reducing environmental impact. This research underscores the potential of data-driven approaches in advancing bio-sustainability through informed microbiome management.

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T34 Design and Deployment of a Cloud Platform for Data-Driven Leak Detection in Agricultural Irrigation Systems

Manzano, J.M.^{1,*}, Neto, f.M.², Tapia, A.¹, and Orihuela, L.^{2,3}

1 Engineering Department, Universidad Loyola Andalucía. Avda. de las Universidades, s/n, 41704 Dos Hermanas, Sevilla (Spain)

2 Centro de Investigación en Tecnología, Energía y Sostenibilidad (CITES), Universidad de Huelva, Palos de la frontera, Spain

3 Departamento de Ingeniería Electrónica, Sistemas Informáticos y Automática, Universidad de Huelva, Huelva, Spain

*Presenting author e-mail: jmanzano@uloyola.es

Abstract

Efficient management of irrigation systems is crucial for optimizing water use in agriculture, especially in water-scarce regions. In this context, identifying and mitigating leaks in irrigation systems plays a key role in improving resource efficiency. This work presents the DENORI project, which aims to develop an advanced web platform for leak detection in agricultural irrigation networks, specifically for a 500-hectare citrus farm. The platform integrates flow meters and pressure sensors that continuously monitor the system's performance, transmitting real-time data to a cloud-based platform. The importance of leak detection in irrigation systems is well-established in the literature. Early detection of leaks can significantly reduce water waste and enhance system efficiency [1], which is a growing priority in agriculture due to increasing water scarcity and climate change [2]. Several studies have proposed different methods for leak detection, ranging from physical models of water distribution networks [3] to statistical and machine learning-based techniques [4]. The DENORI project proposes three approaches for leak detection, based on (i) satellite imagery and (ii) ground-based sensors. The second approach is further divided into two sub-methods: (ii.1) model-based approaches and (ii.2) data-driven detectors. This paper focuses on the execution of leak detection algorithms through a web platform that enables visualization, analysis, storage, and real-time processing of sensor data from the field. The platform processes measured data and runs basic anomaly detection algorithms to identify unusual patterns that may reveal leaks in the irrigation network. Although the leak detection algorithms are still under development and final results are not yet available, the current capabilities of the platform are discussed, and practical examples of how sensor data can be used for the preliminary analysis of irrigation efficiency are presented. Figure 1 shows an aerial photograph of the citrus farm, while Figure 2 illustrates an example of the data stored on the platform, including pressure measurements before and after the pressure-regulating valve, as well as the volume of water used during the irrigation cycle. This approach illustrates the potential of cloud-based platforms in supporting leak detection and water management practices in agriculture, offering a scalable solution to improve the sustainability and efficiency of irrigation systems.



Figure 1: Aerial snapshot of the case study farm

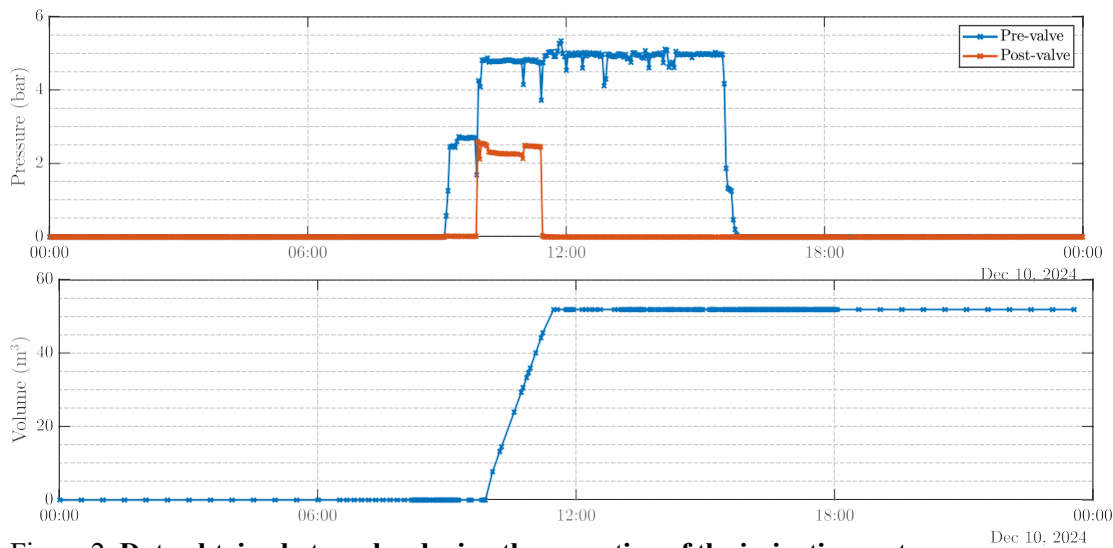


Figure 2: Data obtained at a valve during the operation of the irrigation system

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T35 Leveraging rhizosphere microbial diversity and drought-tolerant bacterial isolates to enhance soybean resilience in South Africa

Ayansina S. Ayangbenro^{1,2}, Funso R. Kutu¹, Olubukola O. Babalola²

1School of Agricultural Sciences, Faculty of Agriculture and Natural Sciences, University of Mpumalanga, Mbombela 1200, South Africa

2Food Security and Safety Focus Area, Faculty of Natural and Agricultural Sciences, North-West University, Mmabatho, 2735, South Africa

**Presenting author e-mail: ayansina.ayangbenro@ump.ac.za*

Abstract

Soybean production in South Africa faces significant challenges, including soil degradation, persistent drought, poor nodulation, diseases, and pest infestations, which have collectively resulted in reduced crop quality and yield losses [1,2]. While the importance of the plant microbiome in enhancing plant health and development is widely recognized, effectively harnessing microbial interactions to mitigate biotic and abiotic stresses remains a major challenge [3]. This study explored the microbial diversity in the rhizosphere of soybean to enhance drought tolerance in two soybean genotypes using a climate-smart synthetic microbial community. A shotgun sequencing approach was employed to analyze the structural and functional diversity of rhizosphere microbial communities, while a culture-dependent method was used to isolate and screen drought-tolerant bacterial species. The dominant phyla identified across all samples were Pseudomonadota, Actinomycetota, Acidobacteriota, and Chloroflexota, with prevalent genera including Pseudomonas, Rubrobacter, Limnobacter, Sphingobium, Sphingomonas, Streptomyces, Solirubrobacter, and Bradyrhizobium. After eight weeks of drought stress trial, no significant ($p > 0.05$) difference in taxonomic abundance was observed between the two genotypes. The bacterial strains isolated and characterized through whole genome sequencing belong to Bacilli genus. In vitro assays revealed these isolates showed robust growth under high concentrations of polyethylene glycol (PEG) 8000, indicating drought tolerance. Ongoing investigations aim to evaluate the efficacy of these isolates as part of a synthetic community, in enhancing drought resilience in soybean.

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T36 Tailoring plant roots for enhanced nitrogen capture in soil

Loïc Haelterman and [Christian Hermans](#)

Crop Production and Biostimulation Laboratory, Brussels Bioengineering School, Université libre de Bruxelles – ULB

Presenting Author : christian.hermans@ulb.be

Abstract

Nitrogen (N) is the most quantitatively important nutrient in cropping systems. However, a large fraction of N is lost through runoff, leading to detrimental consequences for both the environment and human health. Enhancing plant N uptake by optimizing root branching to explore a larger soil volume for mobile nitrate resources could help limit soil leaching. This research underscores the natural variability of root morphology in Brassicaceae species, particularly the Arabidopsis model and rapeseed crop.

We have demonstrated that natural Arabidopsis accessions from public collections worldwide exhibit substantial genetic variation in root morphological traits. Initially, the role of root phenes in N acquisition and biomass production was evaluated in a core set of contrasting accessions. A method was developed to quantify root hairs at the whole root organ level on vertical agar plates. Greater biomass production could be achieved through an increased root system size or specific root hair characteristics. Root system size was positively correlated with high-affinity nitrate uptake, highlighting the benefits of an exploratory root organ in N acquisition. Subsequently, we conducted a prospection campaign in sandy areas of Belgium and the Netherlands, assembling and sequencing a local panel of 210 accessions. Correlations were examined between (i) the physicochemical characteristics of soil harvesting sites, (ii) root phenotypes, and (iii) ionic profiles in root and shoot organs measured under laboratory conditions. Genome-wide association (GWA) mapping is used to search for genotype-phenotype correlations. Ultimately, this work aims to clarify how plant functional traits differ in adaptability based on their natural ecological niche.

Rapeseed holds significant economic value but requires a substantial N amount. Understanding the mechanisms of lateral root growth stimulation or repression by N will help devise strategies to optimize root system architecture. We are identifying genomic regions (QTLs) associated with biomass production and root morphology. Root organs are phenotyped at an early developmental stage in hydroponics (pouch C wick system) and at later stages in soil. The experimental strategy employs GWA with a diversity panel of 300 inbred lines, Linkage Analyses (LA) with two recombinant inbred line families, and Bulk Segregant Analysis (BSA) with one experimental F2 population after crossing two accessions with contrasting lateral root development. Such genetic resources may prove beneficial for future research focused on reducing N fertilizer dependency.

T37 Harnessing biostimulants for sustainable agriculture: A case study of Nurspray® in tomato cultivation

Claire Leclef,
Fytek SA, Belgium

Abstract

As global challenges such as population growth and climate change intensify, the need for innovative, sustainable agricultural technologies has never been greater. Biostimulants, which enhance crop vitality, yield, and resilience to abiotic stresses like temperature extremes and water scarcity, offer a promising solution. Fytek has developed a new generation of biostimulants based on a unique biosourced active ingredient, derived from oligomers of hydroxycinnamic acids (OAH). While the role of OAH in plant cell walls is well established, Fytek has pioneered its use as a natural biostimulant, demonstrating its potential to protect crops from environmental stresses.

In this presentation, we will present an overview of its field performance across various crops over several years. A key focus will be a case study on Nurspray®, a foliar biostimulant based on OAH, applied to tomato cultivation. This research aims to fill a crucial gap in biostimulant studies by assessing the effectiveness of Nurspray® in improving tomato plant growth and yield under open-field conditions. We will examine optimized application strategies tailored to different growth stages, providing actionable insights for both conventional and organic farming systems. The findings offer valuable guidelines for integrating biostimulants into sustainable agricultural practices, enhancing productivity and fruit quality.

List of posters

1. First detection of bufavirus, cutavirus and tusavirus (Parvoviridae) in bivalve mollusks in Italy.
Y.T.R. Proroga, A. Mancusi, T. Vicenza, O. Di Maro, T. Cardellicchio, A. Balestrieri, E. Suffredini
2. Preliminary findings from a genome-wide association study on genetic loci associated with brucellosis resistance in buffaloes.
A. Rinaldi, M. Georgia Riccardi, B. Cecere, R. Paradiso, G. Rofrano, E. De Carlo, G. Borriello
3. Embryonic development and incubation stages of *B. rufimanus* eggs.
L. Rodrigue, A. Segers, L. Rossini, G. Noël, R. Caparros Megido, E. Garone, F. Francis
4. Integrated model for identifying priority areas in the fight against antibiotic resistance: Spatial analysis and GIS applications.
D. Signorelli, G. Rofrano, M. Esposito, L. J. D'Auria
5. Autonomous vehicle with enhanced kinematics for indoor/outdoor agricultural applications.
G. Manca, L. Bianchi, M. Vulcano, J. Farmani, S. Figorilli, S. Mattogno, R. Masocco, A. Tenaglia, C. Possieri, M. Sassano, F. Pallottino, D. Carnevale
6. LPMO-oxidized cellulose oligosaccharides evoke immunity in *Arabidopsis* conferring resistance towards necrotrophic fungus *B. cinerea*.
D. Cannella
7. Testing a mathematical model for the population dynamic of *Frankliniella occidentalis* in table grape vineyards of Southern Italy.
M. Corbetta, T. Caffi, A. Guarino, V. Lasorella, L. Rossini, V. Rossi
8. Biological control of *Toumeyella parvicornis* with two ladybug species.
N. Di Sora, L. Rossini, M. Contarini, S. Speranza
9. Seed quality, production, agronomic and morpho-physiological characteristics assessment of some minor cereals in Southern Italy.
P. P. Adinolfi, E. De Falco, M. Amato, E. L. Frusciante, A. Porfidia, M. Lami, R. Scorziello, M. Giannatiempo, G. M. Cioffi, S. Del Gaudio, N. Trotta
10. Characterization of local cereals of Vallo di Diano.
P. P. Adinolfi, E. L. Frusciante, M. Mele, D. Zito, Vecchio, P. Giglio, N. Trotta
11. Automated crop field inspection for efficient protection treatment planning and delivery.
P. Falcone
12. Mycotoxins contamination in Campania and Calabria regions: A review.
R. D'Ambrosio, T. Toscano, S. Cavallo, P. Gallo, M. Esposito, L. Ambrosio, G. Lucifora, L. Barca, G. Rofrano, L. J. D'Auria, E. De Carlo, L. Baldi
13. The use of precision agriculture technologies in on-farm experimentation (OFE).
S. Bossuyt, E. Ampe
14. Genomic and pathogenic characterization of *Akanthomyces muscarius* isolated from living mite infesting hazelnut big buds.
S. Turco, M. I. Drais, L. Rossini, N. Di Sora, F. Brugnati, S. Speranza, M. Contarini, A. Mazzaglia
15. Effect of temperature on in vitro germination and growth of *Colletotrichum fioriniae*, a new emerging pathogen of olive fruits.
F. Brugnati, L. Rossini, M. I. Drais, S. Turco, A. Mazzaglia

16. A bud's life: Metabarcoding analysis to characterise hazelnut big buds microbiome biodiversity.
S. Turco, F. Brugnati, I. Giubilei, C. Silvestri, M. Petrović, M. I. Drais, V. Cristofori, S. Speranza, A. Mazzaglia, M. Contarini, L. Rossini
17. Fire smoke dispersion in rural areas: a tool for official controls.
S. Cavallo, R. Montella, D. Di Luccio, A. Riccio, R. D'Ambrosio, R. Pellicanò, R. Brunetti, F. Gargano, S. Smeraldo, M. Esposito, L. Baldi
18. Advanced irrigation and unrecognised wells mapping tools.
S. Cavallo, O. R. Belfiore, R. D'Ambrosio, R. Pellicanò, R. Brunetti, F. Gargano, M. Esposito, L. Baldi, G. D'Urso
19. Underground timekeepers: Exploring the interplay between circadian clock and root nutrient uptake for chronoculture.
S. Porco, S. A. Kay, C. Hermans
20. Cellulose-derived oligosaccharides obtained by LPMO oxidation biostimulate tomato growth, inflorescence and immunity through ethylene and ROS-free signalling.
S. Lorrain, D. Cannella

Poster abstracts

First detection of bufavirus, cutavirus and tusavirus (Parvoviridae) in bivalve mollusks in Italy

Y.T.R. Proroga¹, A. Mancusi¹, T. Vicenza², O. Di Maro¹, T. Cardellicchio¹, A. Balestrieri¹, E. Suffredini¹

¹Department of Food Safety Coordination, Istituto Zooprofilattico Sperimentale del Mezzogiorno, Portici, Naples, Italy

²Department of Food Safety, Nutrition and Veterinary Public Health, Istituto Superiore di Sanità, National Reference Laboratory for Foodborne Viruses, Rome, Italy

Corresponding author: andrea.mancusi@izsmportici.it

Protoparvoviruses are small, non-enveloped, single-stranded DNA viruses belonging to the Parvoviridae family. Over the past decade, advancements in metagenomic sequencing have identified three human-infecting members of the Protoparvovirus genus: bufavirus (BuV), first discovered in 2012 in diarrhoeic faeces of children in Burkina Faso; tusavirus (TuV), detected in 2014 in the faeces of a Tunisian child with unexplained diarrhea; and cutavirus (CuV), initially identified in 2016 in faecal and cutaneous samples and subsequently linked to cutaneous T-cell lymphoma. While investigations into the presence of these viruses have been conducted in several European countries, data on their circulation in Italy remains limited. Bivalve mollusks, such as mussels, are filter feeders that can accumulate microorganisms from their marine environment, including those introduced via wastewater discharge. Consequently, they are frequently used as environmental indicators for monitoring microbiological contamination. This study aimed to investigate the presence of protoparvoviruses in bivalve mollusks as a proxy for their circulation within the human population. A total of 43 bivalve mollusk samples (*Mytilus galloprovincialis*) were collected between January and April 2022 from eight coastal locations in Campania, Italy: Bacoli (8 samples), Castellammare di Stabia (4), Ercolano (4), Giugliano in Campania (6), Monte di Procida (4), Napoli (11, including Nisida and Santa Lucia), and Torre Annunziata (6). Digestive tissue was processed according to ISO 15216 guidelines, and real-time PCR was performed to detect BuV, TuV, and CuV using established primers and probes (Väisänen et al., 2014; 2019). Protoparvoviruses were detected in 4 out of 43 samples (9%). BuV and CuV were each identified in two samples, with TuV found in one sample already positive for BuV. All positive samples exhibited high Cq values (>38) and were collected between late February and early March. Notably, both CuV-positive samples originated from consecutive samplings in the same shellfish growing area, suggesting either persistent or recurrent contamination. These findings provide initial evidence of protoparvovirus presence in marine environments in Italy and underscore the need for broader investigations to evaluate their prevalence at a national scale.

Preliminary Findings from a Genome-Wide Association Study on Genetic Loci Associated with Brucellosis Resistance in Buffaloes

Antonio Rinaldi¹, Marita Georgia Riccardi¹, Bianca Cecere¹, Rubina Paradiso¹, Giuseppe Rofrano³, Esterina De Carlo², Giorgia Borriello¹

Istituto Zooprofilattico Sperimentale del Mezzogiorno - U.O.S.D. Genetica Bioinformatica e Biobanca

2Centro di Riferenza Nazionale sull'Igiene e le Tecnologie dell'Allevamento e delle Produzioni Bufaline

3Centro di Riferenza Nazionale per l'Analisi e Studio di Correlazione tra Ambiente, Animale e Uomo

**Presenting author e-mail: giuseppe.rofrano@izsmpartici.it*

Brucellosis is a highly contagious zoonotic disease caused by *Brucella* spp., leading to significant economic losses in livestock production and posing public health risks. The control of the disease is particularly challenging due to its chronic nature and limited availability of effective vaccines. Identifying genetic factors associated with susceptibility or resistance to brucellosis in livestock can provide valuable insights into host-pathogen interactions and allow selective breeding strategies to enhance resistance. In this study, we performed a genome-wide association study (GWAS) using the Axiom Buffalo Genotyping Array to identify genetic loci potentially associated with susceptibility or resistance to brucellosis in a population of 739 buffaloes, including 561 negative and 178 positive individuals for the disease. The analysis, conducted using PLINK and the R package bigsnpr, identified 4 significant SNPs ($p\text{-value} < 5 \times 10^{-8}$) and 64 suggestive SNPs ($p\text{-value} < 5 \times 10^{-6}$). Annotation of these loci revealed 84 associated genes, some of which are known for their involvement in immune response and *Brucella* pathogenesis. Key genes include CEBPA, involved in the regulation of inflammatory responses [1]; TGFBR1, implicated in immune tolerance and inflammatory responses [2]; and GLI3, a transcriptional regulator linked to key cellular processes during infections [3]. Additional noteworthy genes include NR3C2, which may influence susceptibility to infectious diseases [4]; E2F8, involved in cell cycle regulation [5]; and FZD1 and FZD8,

Members of the Wnt signaling pathway, crucial for both innate and adaptive immunity [6]. These findings not only provide a comprehensive view of the genetic architecture underlying brucellosis in buffaloes but also highlight potential pathways and targets for further investigation. The identification of loci associated with resistance or susceptibility could serve as the basis for genetic improvement programs aimed at enhancing disease resistance in livestock. Future studies should focus on functional validation of these loci and exploring their roles in modulating host responses to *Brucella*.

Embryonic Development and Incubation stages of *B. rufimanus* eggs

Lugendo Rodrigue¹, Arnaud Segers¹, Luca Rossini², Noel Grégoire¹, Rudy Caparros Megido¹, Emanuele Garone², Frederic Francis¹

1 Functional and Evolutionary Entomology, University of Liège – Gembloux Agro-Bio Tech, Passage des Déportés, 2, 5030 Gembloux, Belgium

2 Service d'Automatique et d'Analyse des Systèmes, Université Libre de Bruxelles, Av. F.D. Roosevelt 50, CP 165/55, 1050, Brussels, Belgium

Abstract

Bruchus rufimanus Boheman, 1833 (Coleoptera: Chrysomelidae) is a significant pest of faba bean crops. Recent studies have modeled the degree-days required for embryonic development and identified four phenotypic stages during egg incubations. The present study builds upon these observations by modeling, using synthetic indices, the distribution of incubation times across eight constant temperatures ranging from 12°C to 40°C. These findings enhance our understanding of the pest's biology, providing essential information for developing targeted management strategies that minimize collateral effects on beneficial organisms in faba bean cropping systems.

Integrated Model for Identifying Priority Areas in the Fight Against Antibiotic Resistance: Spatial Analysis and GIS Applications

Daniel Signorelli¹, Giuseppe Rofrano^{2*}, Mauro Esposito² and Luigi Jacopo D'Auria²

1 University of Salerno - Laboratory of Geographic Information Systems for the Organization of the Territory, Fisciano (Salerno), Italy

2 National Reference Center for the analysis and study of correlations among environment, animals and humans, IZSM - Portici (Naples), Italy

**Presenting author e-mail: giuseppe.rofrano@izsmportici.it*

Abstract

In recent years, the phenomenon of antibiotic resistance (AR) has emerged as one of the most pressing challenges for global public health. This issue, is jeopardizing the ability to effectively treat bacterial infections that were once easily curable. AR not only threatens to undo decades of medical progress but also demands an integrated approach among science, healthcare, and society to develop innovative and sustainable strategies to counter its spread [1]. The study presented aims to develop a preliminary model to identify potential sources of contamination related to AR, with the objective of creating a dynamic and updatable map of priority sampling areas for bioindicators [2]. The model integrates spatial data localized in the Campania region, sourced from various institutional databases, including the region's surface hydrographic network (update to 2020), wastewater treatment plants cataloged by the ARPAC (update to 2024), livestock farming areas from BDN (update to 2021), and the ISPRA land use map (update to 2018). These datasets, allow the identification of areas most vulnerable to the spread of environmental contaminants. To construct the model, the informational layers were analyzed and classified using the "Natural Breaks" (Jenks) method, which ensures optimal data division into statistically significant classes [3]. Each layer was divided into four classes with progressive scores from 1 to 4, representing increasing levels of relevance or vulnerability. Subsequently, the data were integrated through raster calculation in a Geographic Information System (GIS). The analysis of intensive livestock farming in Campania was carried out using point data, which provided detailed information for each farm and individual species. To achieve a continuous spatial representation, the IDW (Inverse Distance Weighting) interpolation algorithm was applied. For the analysis of surface hydrography, the Horton-Strahler classification was used to organize river segments based on their hydrological hierarchy, estimating the dynamic behavior of surface water bodies and integrated with a river density analysis using the Kernel Density method. The localization of civil wastewater treatment plants was optimized through photo-

interpretation. Geostatistical techniques, including IDW interpolation, were also applied using the number of declared equivalent inhabitants for each treatment plant as the parameter. For the land use map, a bibliographic study was conducted to assign numerical values to the different Corine Land Cover categories. The final map, resulting from the integration of these datasets, highlights critical areas for the phenomenon of AR, providing essential support for resource management, environmental risk mitigation, and the definition of targeted intervention strategies.

Autonomous vehicle with enhanced kinematics for indoor/outdoor agricultural applications

Giorgio Manca¹, Lorenzo Bianchi¹, Matteo Vulcano¹, Jaleh Farmani¹, Simone Figorilli¹, Simone Mattogno¹, Roberto Masocco¹, Alessandro Tenaglia¹, Corrado Possieri¹, Mario Sassano¹, Federico Pallottino² and Daniele Carnevale¹

¹Dipartimento di Ingegneria Civile e Ingegneria Informatica, Università di Roma Tor Vergata, viale del Politenico 1, 00133 Rome, Italy

² Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria (CREA) - Centro di ricerca Ingegneria e Trasformazioni agroalimentari - Via della Pascolare 16, 00015 Monterotondo (Rome), Italy

**Presenting author e-mail: daniele.carnevale@uniroma2.it*

Abstract

We introduce an UGV appositely designed for agricultural applications with mechanics capable of providing dexterity minimizing wheel dragging and consequently avoid furrows in the tilled soil, a desirable feature especially for greenhouse applications with constrained space and high- density crops. Those kinematics features are provided by a double Ackermann steering system and four independently actuated traction wheels, furthermore, the rover span and its height can be modified according to the target crop. The localization system exploits RTK-GNSS, Ultra-Wide Band (UWB) antennas, optical encoders mounted on the traction wheels and precision potentiometers on the double steering system, IMU and a tracking camera information which are feed to an EKF in order to provide UGV pose estimation outdoor where the GNSS signal is available or within greenhouse where UWB have been appositely placed and GNSS signal is not available or strongly deteriorates. Experimental testing have shown the effectiveness of the estimation system that has a precision (standard deviation) of less than one centimeter when GNSS measurements are available or about 4 centimeters when are not and UWB antennas are used instead. A further system based on the combination of RGB and IR camera, whose data are processed by AI-based algorithms, have been recently mounted on board to estimate the track/route and avoid treading on crops, as well as to robustly recognize operators that are not visible to RGB cameras in case of harsh weather conditions such as fog, increasing safety. The control architecture is based on ROS2 that manages the high level control applications, such as UGV state machine, mission definition, parameter settings, telemetry, UKF and provide wheel speed and steering angle references via serial TTL communication to the low level control scheme, implemented on two microcontrollers that manage the six electrical drivers of

400W brushless motors used to track the four desired wheel speed and two steering angles. Such references are obtained by a nonlinear controller that process online the reference path passing through the waypoints that is automatically generated by a dedicated algorithm which is aware of rover kinematics constraints. The mission definition, telemetry and real-time data visualization and rover control are provided by a Java-based HMI. The rover is currently used to gather multispectral data from crops and identify weeds and leaf diseases with the possibility of acting by localized spraying.

LPMO-oxidized cellulose oligosaccharides evoke immunity in *Arabidopsis* conferring resistance towards necrotrophic fungus *B. cinerea*

David Cannella*

*Presenting author e-mail: david.cannella@ulb.be

Abstract

Lytic Polysaccharide Monooxygenases (LPMOs) are powerful redox enzymes able to oxidatively cleave recalcitrant polysaccharides. Widely conserved across biological kingdoms, LPMOs of the AA9 family are deployed by phytopathogens to deconstruct cellulose polymers. In response, plants have evolved sophisticated mechanisms to sense cell wall damage and thus self-triggering Damage Triggered Immunity responses. Here, we show that *Arabidopsis* plants exposed to LPMO products triggered the innate immunity ultimately leading to increased resistance to the necrotrophic fungus *Botrytis cinerea*. We demonstrated that plants undergo a deep transcriptional reprogramming upon elicitation with AA9 derived cellulose- or cello- oligosaccharides (AA9_COS). To decipher the specific effects of native and oxidized LPMO-generated AA9_COS, a pairwise comparison with cellobiose, the smallest non-oxidized unit constituting cellulose, is presented. Moreover, we identified two leucine-rich repeat receptor-

like kinases, namely STRESS INDUCED FACTOR 2 and 4, playing a crucial role in signaling the AA9_COS-dependent responses such as camalexin production. Furthermore, increased levels of ethylene, jasmonic and salicylic acid hormones, along with deposition of callose in cell wall was observed. Collectively, our data reveal that LPMOs might play a crucial role in plant-pathogen interactions.

Testing a mathematical model for the population dynamic of *Frankliniella occidentalis* in table grape vineyards of Southern Italy.

Marta Corbetta¹, Tito Caffi^{1,2}, Antonio Guarino³, Vito Lasorella³, Luca Rossini⁴, and Vittorio Rossi²

1 Department of Sustainable Crop Production, Facoltà di Scienze Agrarie, Alimentari e Ambientali, Università Cattolica del Sacro Cuore, Piacenza, Italy

2 Research centre on Plant Health Modelling, Università Cattolica del Sacro Cuore, Piacenza, Italy

3 AGROLAB S.c.a.r.l.- SPF South, Noicattaro, Bari, Italy

4 Service d'Automatique et d'Analyse des Systèmes, Université Libre de Bruxelles, Brussels, Belgium

**Presenting author e-mail: marta.corbetta2@unicatt.it*

Abstract

Frankliniella occidentalis (Thysanoptera: Thripidae), commonly known as the western flower thrip (WFT), affects several crops and is listed in the EPPO A2 list [1]. Polyphagia and a spread of approximately 230 km/year [2] facilitated the WFT diffusion in Europe since 1980. Beside the direct damage caused to host plants, WFT has also the ability to transmit tospoviruses, such as the Tomato spotted wilt virus (a regulated non-quarantine in the European Union) [3]. Control of WFT is complex and would benefit from mathematical models able to predict its population dynamics.

In this work we parametrized a general modelling framework based on delay differential equations (DDEs) [4], which has the potential to describe the population dynamics of a large class of insect pests, including those with bisexual and arrhenotokous reproduction, as in WFT [5]. The model was conceptualised based on the typical life cycle of WFT in the field at southern Italian latitudes, with the overwintering facultative diapause in the adult stage [6]. Southern Italy is a major producer of horticultural crops and table grapes, and WFT seriously limits their profitability [7]. For the adaptation of the model to the WFT, temperature-dependent biodemographic rate functions were parametrized with a critical approach to the large available data on *F. occidentalis* reared in controlled conditions, which were retrieved through a systematic literature review.

A preliminary model evaluation was conducted by comparing model predictions and observed populations of nymphs and adults collected in several Apulian locations, in different years, on untreated table grapes. Insects were caught through Berlese funnels technique during blooming period, at two-days interval, because adult females generally appear soon after sprouting and peak at fruit setting [8].

Preliminary model evaluation on table grapes was promising but further work is needed for extending validation to other crops and draw more robust conclusions on model accuracy and robustness. Future works would also include into the model framework the interaction between *F. occidentalis*, host plants, and the vectored viruses.

Biological control of *Toumeyella parvicornis* with two ladybugs species

Nicolò Di Sora¹, Luca Rossini², Mario Contarini¹, Stefano Speranza^{1,3}

1 Dipartimento di Scienze Agrarie e Forestali, Università degli Studi della Tuscia, Via San Camillo de Lellis snc, 01100 Viterbo, Italy

2 Service d'Automatique et d'Analyse des Systèmes, Université Libre de Bruxelles, Av. F.D. Roosevelt 50, CP 165/55, 1050 Brussels, Belgium

3 Centro de Estudios Parasitológicos y de Vectores (CEPAVE, CONICET-UNLP), Boulevard 120 1900, La Plata B1900, Argentina

**Presenting author e-mail: nico.disora@unitus.it*

Abstract

The pine tortoise scale, *Toumeyella parvicornis* (Cockerell, 1897), is an invasive pest for the stone pine (*Pinus pinea* L.) in Europe, where it is enlarging its distribution and rapidly altering the landscape Mediterranean vegetation in urban and coastal areas. Although the main control strategy involves endotherapeutic treatments through the injection of abamectin, this method does not provide long-term protection. To achieve an effective pest containment, alternative approaches need to be explored, especially among the biological control agents, due to their environmentally friendly characteristics.

During a multi-year study, we evaluated the effectiveness of two Coccinellidae predators in controlling *T. parvicornis*. Specifically, we focused on two ladybugs species: *Exochomus quadripustulatus* (Linnaeus, 1758) and *Cryptolaemus montrouzieri* Mulsant, 1850. A series of tests were conducted under laboratory condition using a double-choice test and a semi-field condition using an inclusion cage test. Additionally, *E. quadripustulatus* was also tested under open-field condition, testing the predation impact of adult females ladybugs after their release on affected stone pines. Our observations during the trials allowed us to assess: i) the attraction and timing response of the ladybugs species fed with the pest, ii) the effect of another predator's presence on the prey attraction, iii) the predation rate across different prey densities, and iv) the predation impact under varying predator densities. Our results demonstrated the attractiveness of *T. parvicornis* to the ladybugs, as the predators showed a positive response to varying prey densities, exhibiting a high predation rate. *Exochomus quadripustulatus* outperformed *C. montrouzieri* and, during the open-field trial, confirmed its positive effect in reducing *T. parvicornis* infestations. These findings represent significant progress in the containment of *T. parvicornis*. The use of these biological control agents should be considered for future pest management strategies, aiming to reduce chemical inputs and achieve more sustainable and long-lasting pest control.

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Seed quality, production, agronomic and morpho-physiological characteristics assessment of some minor cereals in Southern Italy

Pietro Paolo Adinolfi¹, Enrica De Falco², Mariana Amato³, Elisabetta Laura Frusciante¹, Antonio Porfidia¹, Massimo Lami¹, Rosita Scorziello³, Maurizio Giannatiempo², Gabriele Maria Cioffi², Sofia Del Gaudio^{2,3} and Nikita Trotta¹

1 Council for Agricultural Research and Economics – Research Centre “Plant Protection and Certification” (Crea DC), Battipaglia office – S.S. 18, km 77,700, n.242 – 84091 Battipaglia, SA, Italy

2 Department of Pharmacy, University of Salerno, Via Giovanni Paolo II n. 132, 84084, Fisciano, SA, Italy

3 School of Agricultural, Forest, Food, and Environmental Sciences University of Basilicata Macchia Romana Campus Buildings: 2DA, 3A, 3B 10, Viale dell'Ateneo Lucano - Potenza PZ 85100, Italy

**Nikita Trotta e-mail: nikita.trotta@crea.gov.it*

Abstract

So-called “minor” cereals, considered in this study, are oats, rye, sorghum, spelt, triticale, millet and fonio. Defined as “minor or underutilized” cereals due to their limited cultivation (88,6 million ha) compared to wheat, corn, rice and barley (634,8 million ha, FAOSTAT 2022). Furthermore, a national and a community register has not yet been established for the millet and fonio, so they can't be intended as variety but genetic lines. Despite this, in recent years these species are acquiring considerable importance due to their strong rusticity and short life cycle which make them appropriate in the context of climate change, reduction of the environmental impact of phytosanitary treatments. They also have peculiar nutritional characteristics and above all for their low gluten content or gluten-free, making them suitable for celiac diets [1]. They are useful for green manure which provide the improvement of nutritional and structural characteristics of the soil. The origin of the seed used for sowing and its quality are the most crucial aspects of this work. After careful research of the genetic lines or varieties to compare, in our seed testing laboratory, seeds will be tested to determine the species, the specific purity: the percentage by weight of pure seed, other seeds, and inert matter; the germination to determinate the maximum germination potential of a seed lot, which can then in turn be used to compare the quality of different lots; other seed determination; 1,000 seeds weight of the sample as submitted, and mass per hectolitre [2].

Subsequently we will proceed with the agronomic and morpho-physiological evaluation in the field to make evident the main peculiarities and differences between these cereals. The experimental trial will be carried out in Battipaglia, in South Italy, 40°57'16"/44°98'60", 72.0 m elevation on a clay loam soil with pH 7.4 and the following content of main nutrients: soil organic matter (3.40 g/kg), total nitrogen (0.40 g/kg), phosphorus (125 mg/kg), potassium (0.58 meq/100g), sodium (0.21 meq/100g). The climate classification is Csa (Hot-summer Mediterranean climate) according to Köppen and Geiger (annual mean air temperature 16.1°C, annual sum of precipitation 1,128 mm) [3]. Finally, we will proceed with the determination of the nutritional components of the harvested material.

The aims of the work are to identify the minor cereal that provides a good seed-quality and yield. The technical staff of the Crea DC will transfer our technical knowledge to the university students of Salerno and Basilicata Universities.

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Characterization of Local Cereals of Vallo di Diano

Pietro Paolo Adinolfi¹, Elisabetta Laura Frusciante¹, Michele Mele¹, Domenico Zito¹, Enrica De Falco², Carmelinda Vecchio³, Paolo Giglio³ and Nikita Trotta¹

1 Council for Agricultural Research and Economics – Research Centre “Plant Protection and Certification” (Crea DC), Battipaglia office – S.S. 18, km 77,700, n.242 – 84091 Battipaglia, SA, Italy

2 Department of Pharmacy, University of Salerno, Via Giovanni Paolo II n. 132, 84084, Fisciano, SA, Italy

3 M. T. Cicerone Institute of Higher Secondary Education Via G. Matteotti, n. 84, 84036 Sala Consilina, SA, Italy

**Presenting author e-mail: nikita.trotta@crea.gov.it*

Abstract

The Council for Agricultural Research and Economics – Research Centre “Plant Protection and Certification” (Crea DC), Battipaglia office- is the leader of the Collective Project named Characterization of Local Cereals of Vallo di Diano, financed by the Types of Intervention 16.7.1 and 10.2.1 of the PSR 2014-2020 Campania Region. The other two partners of the Project are the University of Salerno - Department of Pharmacy (DIFARMA), direct beneficiary and the M. T. Cicerone Institute of Higher Secondary Education of Sala Consilina (SA), indirect beneficiary. The aim of the project is to characterize the cereal biodiversity cultivated in the Vallo di Diano in Campania, to identify the most suitable local genetic resource to provide high-quality flour for quality bread-making connected to the territory. The farmers involved in the project grow local cereals in the municipalities of Atena Lucana, Casalbuono, Padula, Polla, Sala Consilina, San Pietro al Tanagro, San Rufo, Sanza, Sassano and Teggiano of the Campania Region, Italy. The genetic resources of interest are wheat, turanicum wheat, barley, rye, spelt and a mixture of common wheat. The recovery is also expected for cereal resources at risk of extinction. The actions concerning technical assistance to the farmers in implementing eco-sustainable cultivation, with the support of a team of technical experts in the agricultural sector. They will also be provided with an IT App dedicated to the purpose. The information useful for App will concern the physico-chemical aspects of soil, the structural and agronomic characteristics of the cultivated areas, the climatic characteristics, the nutritional needs of the crops and the incidence of threats from abiotic and biotic factors. Seed samples taken before sowing have been analyzed in our seed-laboratory to evaluate their quality [1]. Soil samples were analyzed to know their proprieties [2]. Cultivation in ex-situ and in-situ/on farm methods will be characterized morpho-physiologically and agronomically [3]. The harvested cereal grains will be milled for the subsequent manufacturing process and the evaluation of the final transformed product [4]. The identification of the best quality product will be considered under the aspect of marketing perspective, for the creation of a market niche connected to the local territory. The project includes several training study sessions both national and international addressed to the farmers, university and secondary school students. The progress of the actions will be disclosed using a second dedicated App created by an IT consultancy company with the support of ideas and stimuli coming from the students.

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Automated crop field inspection for efficient protection treatment planning and delivery

Paolo Falcone

*Department of Electrical Engineering, Chalmers University of Technology,
Gothenburg, Sweden*

Dipartimento di Ingegneria “Enzo Ferrari”, Università di Modena e Reggio Emilia, Modena
[*falcone@chalmers.se*](mailto:falcone@chalmers.se), [*falcone@unimore.it*](mailto:falcone@unimore.it)

Abstract

Modern agriculture is evolving toward sustainable practices and technologies that aim at minimizing its environmental impact. Unfortunately, decreasing the environmental impact of agriculture through advanced technologies often comes at unsustainable costs. Hence, agricultural technologies must be developed while jointly minimizing their financial and environmental impacts. For example, while bio-based alternatives to chemical synthetic pesticides promise environmentally sustainable crop protections, they are expensive and a precise and efficient product delivery is necessary that minimizes the treatment costs. Cost-efficient and precise delivery can be achieved by focusing the treatment on those areas of the crop field where a disease (or parasite) has been detected or is likely to be present. While crop field inspections by humans are definitely accurate, they are also time-consuming and costly. For this reason, automated, drone-based monitoring and inspection technologies have been developed and deployed with a discrete success. Nevertheless, the bird-view enabled by aerial drones is ineffective in those cases where the symptoms of the disease are visible only through ground inspections.

In our work, we propose to design an inspection system based on camera-equipped mobile manipulators. In such robotic systems, a nine degrees of freedom manipulator, with a camera mounted at the end effector, is installed on a rover, which can navigate the crop field. Assuming that a knowledge-base is available, which contains descriptions of the disease symptoms, along with their locations on the plant, the robot can be programmed to inspect the plants and search for a specific set of symptoms related to one or more diseases. Natural language programming tools can be used to translate the locations from the knowledgebase into target spatial real-world coordinates and camera poses. Existing motion planning and control algorithms can be deployed to position the camera at the target locations. For example, in the case of the tomato blight, a (for example) minimum-energy trajectory could be planned such that a rover can navigate through the plant lines to capture images from the best possible angles (e.g. tomatoes should be inspected from below), while avoiding collisions with the plants and the surrounding farm infrastructure. Image processing algorithms are necessary that process the images captured by the camera and outputs a match score.

The output of the outlined system is a risk map, which provides a probability map layer describing the likelihood the disease is present in a specific field area. Such a map can be used as the input of a treatment planning layer that decides which areas of the field should be treated and how.

Mycotoxins contamination in Campania and Calabria regions: a review

R. D'Ambrosio¹, T. Toscano¹, S. Cavallo¹, P. Gallo¹, M. Esposito¹, L. Ambrosio¹,
G. Lucifora¹, L. Barca¹, G. Rofrano¹, L. J. D'Auria¹, E. De Carlo¹, L. Baldi¹

I Istituto Zooprofilattico Sperimentale del Mezzogiorno – Portici (NA) – Italy

Abstract

Aflatoxins (AF), toxic mycotoxins produced by fungi belonging to the *Aspergillus* species, pose a serious risk to public and animal health. These fungi are frequently found in plant-based products such as oilseeds, animal feed and cereals in ascending order. This study examines the current status and prevention strategy of aflatoxin contamination in plant-based products analysed by Zooprophyllactic Institute of Southern Italy from 2014 to 2024. Mycotoxins occurring in food are linked to long-term effects on health, including the induction of cancers and immune deficiency. Analysis of 33512 plant-based samples over ten years in both Campania and Calabria regions revealed 5% of samples exceeded aflatoxin limits set by European regulations, with Aflatoxin B1 being the most common (92%) Ochratoxin (4%) DON (3%) T2- HT2 (1%). The samples were analysed with advanced analytical techniques such as HPLC, UHPLC-MS/MS, and ELISA ensure precise detection. Addressing feed contamination necessitates an integrative approach combining prevention, advanced modeling, and effective remediation to safeguard agricultural outputs against escalating mycotoxin risks in a changing global climate. Prevention strategies focus on pre-harvest and post-harvest measures, including genetic resistance, biocontrol using atoxigenic *Aspergillus* strains, and predictive modeling of environmental factors influencing fungal growth and aflatoxin production. These findings underscore the need for integrated control measures across the food chain, leveraging predictive modeling and biological controls to ensure food safety in a changing global climate. The predictive model, using large volumes of data, correlates environmental factors with the potential for *A. flavus* growth and consequently AF production in the entire food and feed chain. In pistachio storage, Marín et al.(1) applied models to predict the growth of *A. flavus* and AF production as functions of moisture and temperature and results show that the model correctly predicts the presence of *A. flavus* in 90% of cases and AFs in 89% of cases. Aldars-García et al.(2) also attempted to model growth and AFB1 production by *A. flavus* in storage and transport in order to support decisions on ventilation timing and refrigeration adequation, respectively; the model correctly predicted the presence of AFB1 in 70% to 81% of cases. While post-harvest modelling is more developed, preventing contamination in pre-harvest is also a good perspective. Kaminiaris et al.(3) developed a mechanistic model considering a tree's phenology and meteorological data which correctly predicted 75% of AFB1 contamination in pre-harvest; the authors suggested that this model could indicate the appropriate time for harvest, supporting agricultural systems.

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The use of precision agriculture technologies in On-farm experimentation (OFE)

Sarah Bossuyt and Eva Ampe

*Inagro, Belgium,
sarah.bossuyt@inagro.be, and eva.ampe@inagro.be*

Abstract

On-farm experimentation empowers farmers to test new ideas and products directly on their own fields. For research purposes, the most promising treatments from small plot trials can be scaled up to farm-level trials to assess their feasibility for practical use. Engaging farmers in these experiments and using their testimonials can enhance the adoption of new treatments.

To draw reliable conclusions, the design of the trials is crucial. Implementing alternating strips across the field with a minimal number of different treatments can yield robust results. When the field has heterogeneities, the strips should run across this field variation. Remote sensing is a valuable tool for planning field designs and collecting full trial data. Other data collection methods include yield mapping, or manual assessments with recorded (RTK) GPS positions. Manual assessments can include yield measurements, soil sampling, plant counts, weed counts and disease assessments. Collaboration between farmers, researchers, and industry is essential for successful on-farm experimentation. These partnerships ensure that the experiments are relevant, well-supported, and effectively implemented.

For data interpretation, growth curves of the crop can be generated for each strip if remote sensing images are acquired at regular intervals. To visualize treatment differences at a specific date, a grid can be overlaid on the remote sensing image. The average of a vegetation index, like NDVI, in each grid cell can then be plotted on a graph with the field length on the x-axis. This method visualizes the treatment differences while accounting for field variation. For comprehensive financial analysis, SYSTERRE provides an environment to keep track of all expenses and profits.

Conclusions from these on-farm experiments will provide valuable insights, ultimately contributing to more sustainable and efficient farming practices.

Genomic and Pathogenic Characterization of *Akanthomyces muscarius* Isolated from Living Mite Infesting Hazelnut Big Buds

Silvia Turco^{1*}, Mounira Inas Drais¹, Luca Rossini², Nicolò Di Sora¹, Federico Brugneti¹, Stefano Speranza^{1,3}, Mario Contarini¹, Angelo Mazzaglia¹

*1*Dipartimento di Scienze Agrarie e Forestali, Università degli Studi della Tuscia, Via San Camillo de Lellis snc, Viterbo 01100, Italy

*2*Service d'Automatique et d'Analyse des Systèmes, Université Libre de Bruxelles, Av. F.D. Roosevelt 50, Brussels 1050, Belgium

*3*Centro de Estudios Parasitológicos y de Vectores (CEPAVE, CONICET-UNLP), La Plata, Argentina

Presenting author: silvia.turco@unitus.it

Abstract

The capability of entomopathogenic fungi to live as plant endophytes is well established. However, their presence in undiscovered environmental niches represents the beginning of a new challenging research journey. Recently, *Akanthomyces muscarius* (Ascomycota, Cordycipitaceae) (Petch) Spatafora, Kepler & B. Shrestha was isolated from hazelnut buds infested by the big bud mite pest *Phytoptus avellanae* Nalepa, which makes the buds swollen, reddish, and unable to further develop. Gall formation is known to be regulated by a consortium of microbes and mites, and to better understand the possible role of *A. muscarius* within the infested gall, its whole genome sequence was obtained using a hybrid approach of Illumina and Nanopore reads. The functional and comparative genomics analysis provided within this study may help answer questions related to the ecology and the entomopathogenicity of this fungus.

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Effect of temperature on in vitro germination and growth of *Colletotrichum fioriniae*, a new emerging pathogen of olive fruits

Federico Brugneti¹, Luca Rossini², Mounira Inas Drais¹, Silvia Turco^{1*}, Angelo Mazzaglia¹

*1*Dipartimento di Scienze Agrarie e Forestali, Università degli Studi della Tuscia, Via San Camillo de Lellis snc, Viterbo 01100, Italy

*2*Service d'Automatique et d'Analyse des Systèmes, Université Libre de Bruxelles, Av. F.D. Roosevelt 50, Brussels 1050, Belgium

Presenting author: silvia.turco@unitus.it

Abstract

Olive anthracnose induced by different *Colletotrichum* species causes dramatic losses of fruit yield and oil quality. The increasing incidence of *Colletotrichum fioriniae* (*Colletotrichum acutatum* species complex) as causal agent of olive anthracnose in Italy, is endorsing new studies on its biology, ecology, and environmental factors such as temperature. Five isolates from different sampling sites in Lazio region (Central Italy) were studied under controlled laboratory conditions aiming to better understand the differences of thermal development among the isolates and to lay the foundations of a future mathematical model able to describe the key aspects of the pathogen's life cycle. The mycelial growth rate and the conidial germination rate were assessed at seven different constant temperatures (5, 10, 15, 20, 25, 30, and 35 °C) and fixed relative humidity (100% RH). The obtained dataset was analysed to estimate the parameters of mathematical functions that connect the mycelial growth rate and the spore germination with the environmental temperature. The parameters set provided as the result of this study constitute a key step forward in the biological knowledge of the species and the basis for future formulations of mathematical models that might be the core of decision support systems in an integrated pest management framework.

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A bud's life: Metabarcoding analysis to characterise hazelnut big buds microbiome biodiversity

Silvia Turco^{1*}, Federico Brugnati¹, Irene Giubilei¹, Cristian Silvestri¹, Miloš Petrović², Mounira Inas Drais¹, Valerio Cristofori¹, Stefano Speranza^{1,3}, Angelo Mazzaglia¹, Mario Contarini¹, Luca Rossini⁴

1 Dipartimento di Scienze Agrarie e Forestali, Università degli Studi della Tuscia, Via San Camillo de Lellis snc, Viterbo 01100, Italy

2 Faculty of Agriculture, University of Novi Sad, Trg Dositeja Obradovića 8, Novi Sad, Serbia

3 Centro de Estudios Parasitológicos y de Vectores (CEPAVE, CONICET-UNLP), La Plata, Argentina

4 Service d'Automatique et d'Analyse des Systèmes, Université Libre de Bruxelles, Av. F.D. Roosevelt 50, Brussels 1050, Belgium

Presenting author: silvia.turco@unitus.it

Abstract

Despite *Corylus avellana* L. being an economically important shrub species known for its resilience to adverse environmental conditions, it constantly faces attacks from a plethora of biotic entities. Among these, the mite pest *Phytoptus avellanae* is gaining importance, causing economic losses every year. This mite colonises the new generative and vegetative buds, leading them to become swollen and reddish, and drastically reducing hazelnut production. The biology behind gall formation is still poorly understood. This study provides a qualitative and quantitative description of the microbiome in both healthy and infested buds of two economically important hazelnut cultivars through metabarcoding of fungal ITS and bacterial 16 S. Potentially pathogenic genera such as *Fusarium* and *Pseudomonas* were predominant in the infested buds, along with the obligate intracellular bacterial genus *Wolbachia*. *Akanthomyces muscarius* was instead isolated from culture-based methods only from the infested buds. These findings could improve the understanding of gall ecology, supporting the management of mite populations, and they could also serve as a milestone for further studies on low-impact, monitoring-driven, and genetically targeted control strategies.

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Acknowledgment

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Fire smoke dispersion in rural areas: a tool for official controls

S. Cavallo¹, R. Montella², D. Di Luccio², A. Riccio², R. D'Ambrosio¹, R. Pellicanò¹, R. Brunetti¹, F. Gargano¹, S. Smeraldo¹, M. Esposito¹, L. Baldi¹.

1 Istituto Zooprofilattico Sperimentale del Mezzogiorno: Portici, Naples, CAMPANIA, IT

2 University of Naples "Parthenope" Naples, Italy

**Presenting author e-mail: stefania.cavallo@izsmportici.it*

Abstract

The Seventh Ministerial Conference on Environment and Health of the World Health Organization (WHO) (European Environment and Health Process EHP) in the “Roadmap For Healthier People, A Thriving Planet And A Sustainable Future 2023–2030” consider “Waste and contaminated sites” as a topic [1]. Waste management is a worldwide problem. In Campania region (South Italy) several epidemiological investigations were carried out since early 2000, highlighting a sub-area particularly affected by the impact of waste sites [2]. This paper aims to introduce Smoketracer [3], a novel workflow-powered on-demand application explicitly designed for fast accidental fire response and effects mitigation. By providing information on the spatial and temporal patterns of smoke dispersion, Smoketracer can support Authorities in prioritizing resource allocation, and implement mitigation measures to minimize the impacts of smoke on affected communities. In collaboration with University of Naples “Parthenope”, a smoke dispersion model (SmokeTracer), based on HPC (High Performance Computing) technologies, has been developed. This model simulates the dispersion of fire-related smoke into the atmosphere and has allowed for the efficient direction of field inspections and sampling carried out by the Competent Authorities in response to the need to understand how atmospheric particulate matter emitted during a fire behaves in relation to atmospheric dynamics. It integrates the daily results produced by the WRF (Weather Research and Forecast) meteorological model that has long been successfully used internationally with simulations from the CALPUFF system.

SmokeTracer can predict the direction of smoke dispersion and the area of greatest emission impact using local-scale meteorological information. To meet computational needs, it was necessary to standardize the parameters related to the combusted material, its quantity and the temperature reached by the flames. This was achieved by creating a standard whose variables, set for each simulation, are related to coordinates, date, time and duration of the fire event.

The model provides a shape file of the smoke dispersion that can be easily loaded into any GIS software to locate the area. From 2020 to 2024, 333 simulations (average: 66 simulations/year) were developed and 1130 strictly targeted inspections in fields and farms (average: 226 inspections/year) were carried out. AI algorithms are planned in order to identify hidden patterns and trends in the data, providing additional supporting tools. Data produced by SmokeTracer's modeling chain could be correlated with data constituting “ground truth” to train a predictive model based on deep neural networks capable of correlating model data with real-world data.

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Advanced irrigation and unrecognized wells mapping tools

S. Cavallo¹, O.R. Belfiore², R. D'Ambrosio¹, R. Pellicanò¹, R. Brunetti¹, F. Gargano¹, M. Esposito¹, L. Baldi¹, G. D'Urso²

1 Istituto Zooprofilattico Sperimentale del Mezzogiorno: Portici (NA) Italy

2 Dept. Agric. Sci. University of Naples Federico II, Portici (NA) Italy

**Presenting author e-mail: stefania.cavallo@izsmportici.it*

Abstract

In 2000, the Water Framework Directive (WFD) adopted for the first time a global approach to the risks to which EU waters are exposed [1]. A critical aspect of water management under this framework is the accurate mapping of irrigated areas, which supports the sustainable management of water resources and prevents unauthorized water usage. Numerous studies have shown that Earth Observation (EO) data are effective for identifying irrigated areas and for estimating irrigation water volumes at varying spatial scales [2]. This study focuses on the Campania in South Italy, specifically within the Caserta (CE) province, covering approximately 68,000 hectares. Much of this area falls within the boundary of the Consortium for Land Reclamation and Irrigation of the Lower Volturno Basin (ConsBiv). Within the ConsBiv districts, irrigation is ensured by a system of pressurized networks, supplemented to a lesser extent by wells. In contrast, outside the consortium areas, irrigation occurs only through irrigation wells.

We have applied an integrated approach for mapping irrigated areas outside ConsBiv's serviced zones, based on Machine Learning classification algorithms of Sentinel-2 (S2) EO temporal series and Geographic Information Systems (GIS). The methodology involved several steps[3]:

- NDVI Mapping: Normalized Difference Vegetation Index (NDVI) maps were used to track crop phenology, distinguishing irrigated crops from those grown under dry conditions;
- Smoothing and Gap-Filling: a filtered, cloud-free time series NDVI with 3-day intervals was developed for the reference period;
- Precipitation Data Integration: gridded precipitation data were integrated with NDVI data for improved accuracy;
- Supervised Classification: four thematic classes were identified using time-series NDVI and precipitation data.

Irrigation wells were analyzed by overlaying their locations with irrigated area maps to classify them as active or inactive. Inside ConsBiv districts, wells were presumed inactive, as collective irrigation systems are generally used. Outside these districts, further analysis was conducted. A 150-meter buffer was created around wells to determine the irrigated areas they serve. Irrigated zones outside these buffers were classified as potentially linked on unregistered wells.

The findings revealed a total of 3,020.9 hectares potentially irrigated using unregistered wells. The project plans to validate this model during the 2025 irrigation season by applying it to another area within the Campania region. This approach underscores the potential of combining EO data and advanced analytics to enhance water resource management and ensure regulatory compliance.

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Underground timekeepers: Exploring the interplay between circadian clock and root nutrient uptake for chronoculture

Silvana Porco^{1,2,*}, Steve A. Kay², Christian Hermans¹

1 Crop Production and Biostimulation Laboratory, Brussels Bioengineering School, Université libre de Bruxelles, Belgium

2 Department of Neurology, Keck School of Medicine, University of Southern California, USA

3 Archaeology, Environmental Changes & Geo-Chemistry, Department of Chemistry, Vrije Universiteit Brussel, Belgium

** Presenting author e-mail: silvana.porco@umons.ac.be*

Present address: Proteomics and Microbiology Unit, University of Mons, Belgium

Abstract

The circadian clock is an internal timekeeping mechanism that allows plants to monitor and adapt to cyclic changes in the environment. For example, plant roots are programmed to absorb soil resources more effectively at certain times of the day. This timing ensures plants have the necessary resources to perform various physiological functions. Our recent study highlighted the interplay between the circadian clock and root nitrate uptake in the model species *Arabidopsis thaliana* [1]. The NITRATE TRANSPORTER_2.1 (NRT2.1) gene, which encodes a key high-affinity nitrate transporter, exhibits a rhythmic expression pattern, with daytime increases and nighttime decreases. The rhythmic activity of the NRT2.1 promoter persists under constant light, indicating circadian regulation. The clock-associated transcription factor LUX ARRHYTHMO (LUX), acts as a repressor to modulate the NRT2.1 expression. Loss-of-function of LUX leads to increased NRT2.1 transcript levels and root nitrate uptake at dusk. Through LUX, nitrate transport can also provide feedback to the central oscillator.

We are currently investigating the natural and mutagenized-induced variations of root clock properties in *Arabidopsis*, and their impacts on root morphology and mineral element transport. Through global transcriptomic profiling of root tissues under continuous light conditions (free-running), we are uncovering clock-regulated pathways specific to roots. This research lays the groundwork for developing agro-chronobiological strategies that align agricultural practices with the innate biological rhythms of crops. For example, targeting the timing of fertilizer application could enhance nutrient absorption and reduce environmental impact.

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Cellulose-derived oligosaccharides obtained by LPMO oxidation biostimulate tomato growth, inflorescence and immunity through ethylene and ROS-free signalling

Sonia Lorrai and David Cannella

Crop Production and Biostimulation Lab, PhotoBioCatalysis Unit, Universite Libre de Bruxelles – ULB, Bruxelles School of Bioengineering – EBB

**Presenting author e-mail: sonia.lorrai@ulb.be*

Abstract

Plant biostimulation through oligosaccharides, including those derived from cellulose, chitin, and chitosan, has gained considerable attention for its dual role in promoting plant growth and enhancing immunity. Lytic Polysaccharide Monooxygenases (LPMOs), highly conserved across biological kingdoms, are key enzymes used by phytopathogens to degrade cellulose polymers. In plants, these cellulose-derived products generated through LPMO enzymatic activity mimic pathogen-associated molecular patterns (PAMPs), triggering innate immunity and Systemic Acquired Resistance (SAR). This latter is a defense mechanism that provides long-lasting protection against a broad spectrum of pathogens [1].

Recognition of oligosaccharides by pattern recognition receptors (PRRs) on the plasma membrane, rapidly initiates early signaling events associated with biostimulation. Calcium (Ca^{2+}) influx occurs within 30-60 seconds, followed by activation of the mitogen-activated protein kinase (MAPK) cascade within 5-10 minutes. Reactive oxygen species (ROS) bursts are observed shortly thereafter within 30 minutes and peaking in 10 minutes. Subsequently, a durable immune response mediated by salicylic acid (SA), jasmonic acid (JA), and ethylene (ET) signaling pathways is established, with ethylene biosynthesis persisting for approximately six hours [3]. Together, these signaling events lead to SAR-related gene expression and enhanced resistance to biotic stress, among others responses. Recent studies indicate that biostimulation by cellulose-derived oligosaccharides can activate plant immune responses independently of ROS signaling [2, 4]. In this work, we dug the biostimulatory effects on *Solanum lycopersicum* of native and C1-oxidized cello- oligosaccharides derived by LPMO activity on cellulose, AA9COS oligosaccharides pool, and the shortest native and oxidized oligosaccharides respectively cellobiose and cellobionic acid. Tomatoes are among the most widely cultivated and economically significant crops in the European agro-food sector. Thus, sustainable methods to enhance tomato crop growth and resilience are essential to meet increasing demands.

At different concentrations, none of the tested oligosaccharides showed any production of hydrogen peroxide. However, cellobionic acid and AA9COS oligosaccharides activated ethylene signaling, whereas cellobiose did not, suggesting that distinct oligosaccharides target different signalling pathways.

Physiological analyses revealed a general enhancement in plant growth, including increases in height, width, and stem diameter, following elicitor treatments. Additionally, early flowering and fruiting were observed, with stronger elicitor effects corresponding to an increased number of treatments per plant.

This study highlights the potential of oligosaccharides as biostimulants to simultaneously promote plant immunity, growth, and fruits productivity. These findings contribute to the advancement of sustainable crop management practices, offering innovative strategies to improve plant resilience and agricultural output.

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