

**UNION OF EUROPEAN ACADEMIES FOR SCIENCES
APPLIED TO AGRICULTURE, FOOD AND NATURE
(UEAA)**

ABSTRACTS e-BOOK

The UEAA “*Best Abstracts Scientific
Competition for 2025*”

Bucharest, 2026

**EDITORS: Cipriana BUDEANU and Ioan JELEV -
Academy of Agricultural and Forestry Sciences
"Gheorghe Ionescu- i e ti" Romania**

CONTENTS

Introduction , Ioan Jelev, UEAA President	7
Foreword , Michel Duclos, French Academy of Agriculture, Coordinator of the UEAA Best Abstract Competition 2025	8
Achieving the Golden Mean of Nutritional Quality and Yield in Greenhouse Vegetables . Authors: Nazim S. Gruda, Giedre Samuolienė, Xun Li, Jinlong Dong.....	10
Acid whey permeate valorisation through bioconversion strategies . Authors: A. Sivacova, I. Ciprova.....	11
A new tool for large-scale analysis of bone weakness in living laying hens . Author: Moh Sallam.....	12
Animal welfare and meat quality: on-farm slaughter of Cinta senese pigs . Authors: R.E. Amarie, J. Goracci, L. Casarosa, S. Tinagli, G. Briganti, G. Giunta, M. Senese, G. Terracciano, F. Campeis, A. Del Tongo, A. Serra.....	13
Atlases to reveal the diversity of French woods, their anatomy and their density . Author: M-C. Trouy-Jacquemet.....	14
Bioremediation of Pathogen-Infested Soils: The Case of Greenhouse Tomatoes . Author: Tzenko Vatchev.....	15
Comparison Between Some Plant Fluids and the Human Blood . Authors: A. Sotirov, S. Yordanov.....	17
Contribution to the Enrichment of Wheat Germplasm in Romania . Authors: R. Kadar, I. Racz, D. Hirișcău, A. Varadi, D. Morar, F. Kadar	18
Developing a system for land assessment and improving soil health in Bulgaria . Authors: M. Banov, V. Kolchakov.....	19
Digitalization and valorization of crop diversity in Bulgaria and Slovakia . Authors: Nikolaya Velcheva, Asya Stoyanova-Doycheva, Pencho Malinov, Ľubomír Mendel, Tsvetelina Stoilova, Iveta Čičová, Erika Zetochová, René Hauptvogel.....	20
Domains of increased genetic polymorphism boost crossover in plant breeding . Authors: M.E. Mikhailov, F. Boideau, M. Szymanska-Lejman, V. Botnari, P.A. Ziolkowski.....	21
Effect of Polyunsaturated Fatty Acid Feed Supplements in Broiler Turkeys . Authors: Mitko Lalev, Pavlina Hristakieva, Magdalena Oblakova, Nadia Mincheva.....	22
Emergence of a new plum pox virus variant in Romanian Prunus domestica Orchards . Authors: A.B. Ruiz-García, L.A. Zagrai, A. Olmos, I. Zagrai.....	23
Exploring Bitter Taste Origins in Faba Beans Using Combined Approaches . Authors: A. Karolkowski, C. Belloir, G. Lucchi, C. Martin, E. Meudec, E. Bouzidi, L. Levavasseur, N. Sommerer, L. Briand, C. Salles.....	24

Early Pregnancy Diagnosis in Bulgarian Murrah Buffaloes by PAGs. Authors: I. Fasulkov, Y. Ilieva, P. Penchev, M. Karadaev, B. Ivanova, R. Nenova, N. Vasilev.....	25
Factors affecting fatty-acid profile of lactic lipids in the water buffalo. A review. Authors: P. Penchev, R. Nenova, Y. Ilieva, S. Enchev, M. Schreiner..	26
Fish Fin Evaluation Using a Convolutional Neural Network: A Pilot Study. Authors: S. Osei, T. Aizhan, M.Z. Mehdi, I. Koliada, S. Warjri.....	27
Framework for the selection of wheat varieties for arid agroecosystems. Authors: Q. Soofizada, A. Pescatore, S. Orlandini, M. Napoli.....	28
From Vines to Ecosystems: Ecological Effects of Grapevine Leafroll Disease. Authors: E. C. Buciumeanu, I. C. Guță, D. E. Vizitiu, L. Dinca, G. Murariu...	30
Genetic bases and comparative genomics of Aphanomyces root rot resistance in legumes. Authors: T. Leprévost, C. Lavaud, A. Sugio, and M-L. Pilet-Nayel.....	31
Genetic Variants Associated with Behavioural Response During Milking in Cows. Authors: M. Mincu-Iorga, A.E. Mizeranschi, D. Gavojdian, I. Nicolae, S. Kusza, D.E. Ilie.....	32
Genome Editing and Cultivar Choice for Nutrient-Dense Vegetables. Authors: Julia Weiss, Nazim S. Gruda.....	34
Histological approach to understand <i>in vitro</i> regeneration ability on sweet basil. Authors: M. Montone, A. Cassetti, B. Ruffoni, L. Pistelli, M. Savona....	35
Introducing genetic diversity in animal populations from germplasm collections. Authors: A. Jacques, M. Tixier-Boichard, G. Restoux.....	37
Landscape Transformation in South-Central Bulgaria (2000–2018). Author: P. Tomov.....	38
Light-Driven Nutritional Quality in Vegetable Protected Cultivation. Authors: Nazim S. Gruda, Giedre Samuolienė.....	39
Micro-farms and territory: a new model of small agroecological farms in France. Author: Damien Toublant.....	40
Natural Biostimulants Strengthen Tomato Response to Nitrogen Shortage. Authors: S. Monterisi, M. Y. Alzate Zuluaga, B. Senizza, M. Cardarelli, Y. Rouphael, G. Colla, L. Lucini, S. Cesco, Y. Pii.....	41
One Health and agriculture: bridging data gaps to tackle environmental chemical loads. Authors: J. Vos, M. Alessandrini, M. Trevisan, Y. Pii, F. Mazzetto, G. Orzes, S. Cesco.....	43
Oxidative stress parameters in water buffaloes supplemented stevia. Authors: Radena Nenova, Galina Nikolova, Stanimir Enchev, Pencho Penchev, Yordanka Ilieva, Matthias Schreiner, Yanka Karamalakova.....	45
Predicting plant phenotypes in the context of global change. Authors: B. Ali, S. Nicolas, M. Blein-Nicolas, M.L. Martin, Y. Djabali, T. Mary-Huard, A. Charcosset, L. Moreau, R. Rincent.....	46

Protected Cultivation as a Pathway to Nutrient-Rich Vegetables. Authors: N. S. Gruda, V. M. Gallegos-Cedillo, C. Nájera, C. Egea-Gilabert, J. Ochoa, J. A. Fernández.....	47
Research Regarding the Carbon Balance in Agricultural Farms. Authors: R. Neamt, N. Dragomir, F. Neciu, Ghe. Săplăcan, C. Mihali, A. Mizeranschi, A. Anton, L. Cziszter.....	48
Smart Irrigation and Water Management Strategies in Eastern European Viticulture. Authors: A.C. Florea, D.I. Sumedrea, S. Rodino, M. Ion, V. Dragomir, A. M. Dumitru, L. Pîrcalabu, D.G. Dinu.....	49
Supporting agroecological transition: pathway and tools for farmers' collectives. Authors: A. Alaphilippe, S. Batard, C. Renaud-Gentié, S. Dernat..	51
Survey of several spoilage agents in Moldovan wines. Authors: I. Mitina, C. Grajdieru, D. Zgardan.....	52
Tackling Weaning Stress in Dairy Calves Using Cannabidiol Oil Supplementation. Authors: M. Enculescu, I. Nicolae, D. Gavojdian.....	53
The affinity of vascular plants and bryophytes to forest microclimate buffering. Authors: E. Gril, Fabien Spicher, Alain Vanderpoorten, Emilie Gallet-Moron, Boris Brasseur, Vincent Le Roux, Marianne Laslier, Guillaume Decocq, Ronan Marrec, Jonathan Lenoir.....	54
The Hidden Burden Limiting Europe's Agricultural Performance. Author: Daniel Petrov.....	56
The potential of biochar to reduce carbon emissions from organic fertilizers. Authors: L. Verdi, A. Dalla Marta, S. Orlandini, A. Maienza, S. Baronti, F. P. Vaccari.....	57
Two decades of Field trials of 'HoneySweet' transgenic plum resistant to plum pox. Authors: I. Zagrai, L.A. Zagrai, M. Ravelonandro, R. Scorza, C. Dardick, N. Minoiu, P. van der Meer.....	59

GRAPHICAL ABSTRACTS

Comparison Between Some Plant Fluids and the Human Blood: Authors: A. Sotirov, S. Yordanov.....	61
Domains of increased genetic polymorphism boost crossover in plant breeding. Authors: M.E. Mikhailov, F. Boideau, M. Szymanska-Lejman, V. Botnari, P.A. Ziolkowski.....	62
Genome Editing and Cultivar Choice for Nutrient-Dense Vegetables. Authors: Julia Weiss, Nazim S. Gruda.....	63
Light-Driven Nutritional Quality in Vegetable Protected Cultivation. Authors: Nazim S. Gruda, Giedre Samuolienė.....	64
Natural Biostimulants Strengthen Tomato Response to Nitrogen Shortage. Authors: S. Monterisi, M. Y. Alzate Zuluaga, B. Senizza, M. Cardarelli, Y. Rouphael, G. Colla, L. Lucini, S. Cesco, Y. Pii.....	65

One Health and agriculture: bridging data gaps to tackle environmental chemical loads. Authors: J. Vos, M. Alessandrini, M. Trevisan, Y. Pii, F. Mazzetto, G. Orzes, S. Cesco.....	66
Protected Cultivation as a Pathway to Nutrient-Rich Vegetables. Authors: N. S. Gruda, V. M. Gallegos-Cedillo, C. Nájera, C. Egea-Gilabert, J. Ochoa, J. A. Fernández.....	67
Supporting agroecological transition: pathway and tools for farmers' collectives. Authors: A. Alaphilippe, S. Batard, C. Renaud-Gentié, S. Dermat..	68
Survey of several spoilage agents in Moldovan wines. Authors: I. Mitina, C. Grajdieru, D. Zgardan.....	69
The affinity of vascular plants and bryophytes to forest microclimate buffering. Authors: E. Gril, Fabien Spicher, Alain Vanderpoorten, Emilie Gallet-Moron, Boris Brasseur, Vincent Le Roux, Marianne Laslier, Guillaume Decocq, Ronan Marrec, Jonathan Lenoir.....	70

INTRODUCTION

The fourth edition of the UEAA Best Abstracts Competition 2025 was characterized, in addition to the high scientific quality of the abstracts submitted by the authors, namely: the largest number of participating abstracts - 41, and the submission of extremely suggestive graphic abstracts, in number of 10 out of the 41 papers. The 41 abstracts covered the following areas: Agri-food and Human Nutrition, 3 abstracts; Agronomy, 21 abstracts; Animal production, 10 abstracts; Economy and Agricultural policy, 1 abstract; Environment and territory, 2 abstracts; Forestry, 2 abstracts; Life sciences, 2 abstracts.

The abstracts come from 9 countries as follows: Albania - 4; Bulgaria - 10; Czech Republic - 1; France - 8; Italy - 6; Latvia - 1; Moldova - 2; Romania - 8; Sweden - 1. We note that the most abstracts were received from Bulgaria, 10, followed by France and Romania with 8 abstracts each and Italy with 6 abstracts.

I would like to take this opportunity to express my special thanks to the jury members who reviewed a large number of abstracts under the impeccable coordination of Michel DUCLOS, from the French Academy of Agriculture. He was excellently assisted by: Baiba RIVZA - Latvian Academy of Agriculture, Zenonas DABKEVIČIUS - Lithuanian Academy of Sciences; Simone ORLANDINI - Georgofili Academy, Italy; Hojka KRAIGHER - Slovenian Academy of Sciences and Arts; Revaz ASATIANI - Georgian Academy of Agricultural Sciences.

The winning paper in this edition was: **One Health and agriculture: bridging data gaps to tackle environmental chemical loads**, Italy, authors: J. Vos, M. Alessandrini, M. Trevisan, Y. Pii, F. Mazzetto, G. Orzes, S. Cesco. Second place, at the first participation in the UEAA Abstracts Competition, was remarkably occupied by the paper: **Domains of increased genetic polymorphism boost crossover in plant breeding** with a group of authors from the Republic of Moldova and Poland formed by: M.E. Mikhailov, F. Boideau, M. Szymanska-Lejman, V. Botnari, P.A. Ziolkowski. Third place was shared by two papers: **Genetic bases and comparative genomics of Aphanomyces root rot resistance in legumes**, France, authors: T. Leprévost, C. Lavaud, A. Sugio, and M-L. Pilet-Nayel and **Framework for the selection of wheat varieties for arid agroecosystems**, Italy, authors: Q. Soofizada, A. Pescatore, S. Orlandini, M. Napoli.

I would like to congratulate all participants and especially the winners for their valuable contribution to the 2025 UEAA Best Abstracts Competition.

Prof. Dr. Ioan JELEV
President of UEAA

FOREWORD

The 4th edition of the UEAA Best Abstract Competition, held in 2025, is now closed. A total of 41 abstracts, selected and submitted by the member academies, were received.

The table below presents their distribution by country and topic:

Academy	Number
Albania	4
Bulgaria	10
Czech Republic	1
France	8
Italy	6
Latvia	1
Moldavia	2
Romania	8
Sweden	1
Topic	
Agrifood and human nutrition	3
Agronomy	21
Animal production	10
Economy and agricultural policy	1
Environment and territories	2
Forestry	2
Life sciences	2

The evaluation was carried out by an international jury, which selected and ranked the six best abstracts. The authors ranked first to third (see below) will receive a certificate from UEAA recognizing this achievement and are invited to deliver a short online presentation during the UEAA Steering Committee meeting on 12 March 2026.

With their consent, the recorded presentations will subsequently be made freely available online.

Corresponding Author	Title and Link	Topic	Academy	Rank
Mazzetto F., Univ. Bolzano, IT	<u>One Health and agriculture: bridging data gaps to tackle environmental chemical loads</u>	Environment territories	Italy	1

Mikhailov M.E., Univ. Chisinau, MD, and Ziolkowski, P.A., Univ. Poznan, PL	<u>Domains of increased genetic polymorphism boost crossover in plant breeding</u>	Life Sciences	Moldovia	2
Leprovost T., Univ. Rennes, FR	<u>Genetic bases and comparative genomics of Aphanomyces root rot resistance in legumes</u>	Agronomy	France	3
Napoli M., Univ. Firenze, IT	<u>Framework for the selection of wheat varieties for arid agroecosystems</u>	Agronomy	Italy	3

The UEAA Steering Committee warmly thanks the member academies for selecting and submitting the abstracts, as well as the members of the jury for their careful evaluation. It also congratulates all authors on the high scientific quality of their contributions.

Michel DUCLOS

**French Academy of Agriculture,
Coordinator of the UEAA Best Abstracts Competition 2025**

Achieving the Golden Mean of Nutritional Quality and Yield in Greenhouse Vegetables

Nazim S. Gruda^{123*}, Giedre Samuolienė⁵, Xun Li⁶, Jinlong Dong⁶

¹ University of Bonn, Bonn, Germany; ² Technical University of Cartagena, Cartagena, Spain; and ³ Academy of Sciences of Albania, Tirana, Albania

⁴ Lithuanian Research Centre for Agriculture and Forestry, Kaunas, Lithuania, and ⁵ Lithuanian Academy of Science

⁶ State Key Laboratory of Soil and Sustainable Agriculture, Institute of Soil Science, Chinese Academy of Sciences, Nanjing, China

Corresponding author: ngruda@uni-bonn.de

Abstract

Modern agriculture faces the dual imperative of producing more food while improving its nutritional quality. This requires moving beyond yield-centric practices to strategies with a “golden mean,” where productivity and health-promoting traits are optimized together.

Controlled-environment agriculture offers unique opportunities to fine-tune growth conditions—encompassing environmental, nutrient supply, and cultural practices—allowing for the precise modulation of plant physiology, growth, and development. Evidence suggests that moderate, targeted stressors, such as controlled salinity, regulated drought, or temperature shifts, can stimulate the accumulation of phytonutrients, including antioxidants, vitamins, and minerals. Similarly, wavelength-specific lighting strategies, by activating photoreceptors, can trigger biosynthetic pathways that enhance nutritional profiles without substantially compromising yields. The challenge lies in identifying the overlap between peak quality and acceptable yield for each crop and cultivar.

However, adoption barriers remain significant. High costs of advanced climate-control systems, limited willingness of markets to pay for nutritional traits, and technological constraints in large-scale operations hinder widespread implementation. Nevertheless, emerging innovations, such as Artificial Intelligence and Internet of Things, enabled monitoring, affordable high-resolution sensors, and novel light-selective greenhouse films—present a pathway toward data-driven, scalable solutions. Integrating these with ecologically grounded practices, such as the use of plant growth-promoting microorganisms, can further strengthen sustainability and resilience.

In conclusion, balancing yield and nutritional quality is both a scientific and economic challenge. Success depends on integrating precise environmental control with crop-specific knowledge, supported by technology adoption and consumer demand for nutrient-rich produce.

Advances in digital agriculture, materials science, and plant biology can enable greenhouse systems to deliver consistently high-quality vegetables at a commercial scale, helping reshape future food systems toward healthier and more sustainable diets. Implement moderate stress management combined with spectrum-optimized lighting and cost-effective sensor-based control systems can synchronize yield objectives with enhanced nutritional value.

Keywords: greenhouse cultivation, nutritional quality, yield optimization, phytonutrients, controlled environment agriculture

Source:

Gruda, N.S., Samuolienė, G., Li, X., & Dong, J. (2025). The golden mean of balancing nutritional quality and yield in greenhouse vegetable cultivation. *International Journal of Vegetable Science*.
<https://doi.org/10.1080/19315260.2025.2538489>

Acid whey permeate valorisation through bioconversion strategies

A. Sivacova*, I. Ciprova

Food Institute, Faculty of Agriculture and Food Technology,

Latvia University of Life Sciences and Technologies, Liela iela 2, Jelgava LV-3001, Latvia

* Corresponding author: alina.sivacova@lbtu.lv

Acid whey is a side-stream in fermented dairy product production and presents a persistent utilisation challenge due to its high organic load and limited processing options. This necessitates the development of alternative processing routes for acid whey. In parallel, the growing demand for sustainable protein sources highlights the potential of converting dairy side-streams into nutritionally valuable products. This study evaluates a bioprocessing approach for converting acid whey permeate into yeast-based mycoprotein, providing a practical route for integrating dairy by-product valorisation into circular food systems.

Two lactose-assimilating yeast strains — *Kluyveromyces marxianus* MSCL 79 and *Cyberlindnera jadinii* MSCL 87 (Microbial Strain Collection of Latvia) — were cultivated on partly concentrated acid whey permeate with 13% and 20% total solids. The effects of lactose hydrolysis, supplementation of $(\text{NH}_4)_2\text{HPO}_4$, KH_2PO_4 , $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ and active biomass addition were examined to identify strain-specific optimisation strategies. The fermentation process was carried out in a batch-type bioreactor for up to 72 hours, maintaining a temperature of 30 °C and pH 5.0, with constant agitation at 70 rpm throughout the process.

Both yeasts were able to grow on acid whey permeate, confirming its feasibility as a carbon source for biomass synthesis. Distinct differences emerged between the strains. *K. marxianus* showed consistently higher substrate utilisation efficiency and achieved the highest biomass yields, particularly in hydrolysed whey with 20% total solids. Under these conditions, biomass formation approached 59 g L⁻¹ when active biomass was added. *C. jadinii* produced lower biomass yields (up to ~31 g L⁻¹), indicating comparatively limited performance under the same conditions.

Increasing substrate solids from 13% to 20% enhanced wet biomass formation for both species but resulted in a proportional decrease in protein concentration, reflecting a shift between biomass accumulation and protein density. Lactose hydrolysis improved fermentation efficiency and supported higher protein concentration in both yeasts, while mineral supplementation further promoted protein synthesis at elevated solids levels.

Optimal fermentation conditions differed between strains. *K. marxianus* achieved the most favourable outcomes in hydrolysed whey with 20% solids in combination with supplementation of $(\text{NH}_4)_2\text{HPO}_4$, KH_2PO_4 , $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$. *C. jadinii* achieved better results in hydrolysed whey permeate with 13% solids without active biomass addition. These strain-specific responses underline the need to tailor process parameters to the physiological characteristics of each yeast.

Overall, the study demonstrates a technically feasible method for converting acid whey into nutritionally valuable mycoprotein. By supporting more efficient use of dairy by-products and providing an alternative protein source, this approach contributes to improved resource management and the development of sustainable food and feed strategies.

Keywords

Acid whey, mycoprotein, yeast fermentation, dairy waste-stream, biomass

A new tool for large-scale analysis of bone weakness in living laying hens.

Moh Sallam

*Department of Animal Biosciences, Quantitative Genetics and Breeding
Swedish University of Agricultural Sciences
Box 7023
750 07 Uppsala
Sweden*

*) Corresponding author: mohammed.abdallah.sallam@slu.se

Key words: Laying hens, fractions, X-ray, machine learning, genomics

There are about 7.8 billion laying hens worldwide, producing 87 million metric tons of eggs annually. Bone fracture is a common problem in laying hens posing welfare issues to the birds and production challenges to the egg industry. In this work advanced genomic and deep learning methods has been used to develop a tool for large- scale analysis of X-ray images from living laying hens. This tool can quickly detect identified phenotypic markers for bone weakness and fractures and that can be used to reduce the risks of these conditions in high-producing laying hens through selective breeding. The work describes the development of the tool to prevent skeletal problems that are common in high-producing laying hens worldwide through selective breeding.

Through extensive genomic studies, genetic markers for bone weakness and a specific X-ray structure on the birds' breast bone are identified as a reliable expression of such conditions. The method is based on machine learning techniques and programming for computer vision measurements of X-ray images, and it can be developed to automate the measurement of other skeletal bones as well. The method is well suited for breeding companies as it can analyze thousands of X-ray images in a few minutes and thus has the potential to monitor and fundamentally improve the welfare of many millions of laying hens worldwide.

Details can be consulted in:

Sallam, M. 2025. Digital and genetic tools to improve bones of laying hens. Doctoral Thesis, Acta Universitatis Agriculturae Sueciae 2025:12. ISBN 978-91-8046-497-0.
<https://doi.org/10.54612/a.q33hkb4fja>

Animal welfare and meat quality: on-farm slaughter of Cinta senese pigs

R.E. Amarie ⁽¹⁾, J. Goracci ^{(2)*}, L. Casarosa ⁽¹⁾, S. Tinagli ⁽¹⁾, G. Briganti ⁽³⁾, G. Giunta ⁽³⁾, M. Senese ⁽⁴⁾, G. Terracciano ⁽⁴⁾, F. Campeis ⁽⁴⁾, A. Del Tongo ⁽²⁾, A. Serra ^(1,5,6)

⁽¹⁾ Department of Agriculture, Food and Environment, University of Pisa, via del Borghetto 80, 56124 Pisa, Italy.

⁽²⁾ Tenuta di Paganico Farm, Via della Stazione 10, 58045 Paganico (GR), Italy.

⁽³⁾ Azienda Unità Sanitaria Locale Toscana sud est, via Piero Calamandrei 173, 52100 Arezzo, Italy.

⁽⁴⁾ Istituto Zooprofilattico Sperimentale del Lazio e della Toscana M. Aleandri, SS Dell'Abetone e del Brennero 4, 56123 Pisa, Italy.

⁽⁵⁾ Center for Research in Agricultural and Environmental Sciences, University of Pisa, via Vecchia di Marina, 6 – 56122 San Piero a Grado, Pisa, Italy.

⁽⁶⁾ Research Center of Nutraceutical and Food for Health, University of Pisa, 56124 Pisa, Italy.

* Corresponding author: jacopogoracci@hotmail.com

Transport and lairage before slaughter are critical stressors for pigs, particularly in extensive systems and local breeds. Stress compromises animal welfare and may affect meat quality and safety. On-farm slaughter (OF) has been proposed as an ethical alternative to traditional slaughter (TS), but evidence on local pig breeds is scarce.

Forty Cinta senese barrows reared outdoors in Tuscany were slaughtered between June 2021 and August 2022 using two methods (TS vs. OF). A mobile on-farm prototype was designed and validated. Physiological stress indicators (cortisol, creatine phosphokinase-CPK, lactate dehydrogenase-LDH), meat quality traits (pH, color, water holding capacity), and carcass/meat microbiological loads were assessed. Climatic effects were considered using the Temperature-Humidity Index (THI).

OF pigs showed significantly lower cortisol (29.1 vs 95.8 ng/mL; $P = 0.041$), LDH (1280.0 vs 1495.8 U/L; $P = 0.014$), and CPK (1548.7 vs 2241.0 U/L; $P = 0.030$) than TS pigs, confirming reduced stress. Meat from OF animals had lower pH 48 h post-mortem (5.84 vs 6.14; $P = 0.041$), suggesting improved glycolysis and preservation. No *Salmonella* or *Listeria monocytogenes* were detected. Carcass microbial loads did not differ significantly, though mesophilic counts tended to be lower in OF carcasses. THI influenced microbial loads in meat but not in carcasses.

On-farm slaughter markedly reduced physiological stress without compromising microbiological safety or technological meat quality. Beyond its scientific outcomes, the project represents a concrete example of participatory innovation, born from an ethical need expressed by a farming enterprise and developed through collaboration with health authorities and university research, with the aim of proposing more sustainable and ethical solutions. In this context, the Regulation (EU) 2021/1422 - which amended provisions on official controls to allow slaughter at the holding of provenance - opens the way to wider implementation of on-farm slaughter. This regulatory shift enhances the social pillar of sustainability by strengthening rural communities, safeguarding animal welfare, and supporting short food chains. Overall, the results highlight the potential of on-farm slaughter to integrate welfare, food safety, and local development objectives, while calling for further research to optimize its adoption under different farming and climatic conditions.

Keywords: animal welfare; local pig breeds; on-farm slaughter; stress biomarkers; meat quality.

Atlases to reveal the diversity of French woods, their anatomy and their density

M-C. Trouy-Jacquemet

Lorraine University, INRAe, LERMaB (Laboratory for Studies and Research on Wood Material), 27 rue Philippe Séguin, 88000 EPINAL, France

Corresponding author: marie-christine.trouy@univ-lorraine.fr

In metropolitan France, forests have experienced spectacular expansion over the past several decades and now cover approximately one-third of the territory. The National Forest Inventory, conducted by the National Institute of Geographic and Forest Information (IGN), highlights a key aspect of French forests: their diversity. The IGN partnered with INRAE (the French National Research Institute for Agriculture, Food and Environment) and the University of Lorraine to carry out the XyloDensMap project, which aims to quantify wood density and its variability in French forests, in order to provide the data necessary for assessing forest carbon stocks and fluxes. These measurements show that the average trunk density (at 1.30 m) varies considerably between species: from approximately 300 kg/m³ for paulownia (*Paulownia tomentosa*) to over 850 kg/m³ for holm oak (*Quercus ilex*). Because wood density is linked to its anatomy, a thorough understanding of interspecific variability required the creation of atlases describing the wood of the 154 species recorded between 2016 and 2019, including 40 softwoods and 114 hardwoods.

Furthermore, given the scarcity of wood anatomy specialists and the outdated nature of existing reference works, the XyloDensMap project has enabled the development of a multi-scale identification tool with unprecedented content. The creation of the atlases required more than five years of work to build an exceptional study collection. Each specimen, of known origin, is precisely botanically identified and carefully prepared to ensure optimal observation conditions. For each species, the macroscopic description of the wood is illustrated by photographs of a 1:1 scale cylinder and of meticulously sanded cross-sections of the wood and bark. At the microscopic level, the wood anatomy is described according to the criteria defined by the IAWA (International Association of Wood Anatomists). Anatomical study is of increasing interest because it explains the drought resistance of certain species. The results of the XyloDensMap study (wood density) are also provided, along with dendrometric measurements (national distributions of tree height, diameter, age and ring width).

The forest species recorded during the study period are presented comprehensively, as some of today's secondary species are likely to become dominant species in the future as a result of climate change. A first atlas dedicated to softwoods was published in 2023, and a second volume dedicated to hardwood in 2025. These atlases constitute, at a specific point in time, a crucial snapshot for assessing the changes that will modify, in the future, not only the specific composition of forests but also tree growth rates, and the quality, anatomy and density of the wood produced.

Keywords: French forest, wood identification, wood anatomy, forest biomass, forest biodiversity

Atlas of hardwoods in France, Multi-scale identification tool (in French) Marie-Christine Trouy-Jacquemet, 594 pp., 2025. Éditions Quae, Versailles, ISBN: 978-2-7592-4056-2

Bioremediation of Pathogen-Infested Soils: The Case of Greenhouse Tomatoes

Author: Assoc. Prof. Dr. Tzenko Vatchev ^{1*}

¹*Institute of Soil Science, Agrotechnologies and Plant Protection, 2230, Kostinbrod, Agricultural Academy, Sofia, Bulgaria*

*Corresponding author: Vatchevtzenko@yahoo.com

Abstract

Problem Definition: Crown and root rot of tomatoes is a widespread disease complex and the main limiting factor for tomato greenhouse production in Bulgaria and beyond. Besides the dominant pathogen, *Fusarium oxysporum* f.sp. *radicis-lycopersici*, the aetiology of the disease involves other soilborne fungi, including *Colletotrichum coccodes*, *Pyrenochaeta lycopersici*, *Rhizoctonia solani*, and *Sclerotinia sclerotiorum*, as well as fungal-like *Phytophthora* spp. and *Pythium* spp. The build-up of these pathogens is associated with decline in soil productivity to the extent that tomato cultivation in greenhouses or elsewhere becomes no longer viable. The pathogens co-exist and persist in soils for extended periods and are difficult to eradicate through conventional or reductionist control strategies.

Remediation Objective: For the bioremediation (“healing”) of heavily infested soils, a holistic systems approach that targets the entire consortium of soilborne pathogens is required in order to effectively restore and maintain soil health and economic productivity.

Integrated Remediation Concept: The objective of this bioremediation technology can be achieved through the implementation of an integrated approach, grounded on economically and ecologically sustainable plant disease management strategies. The technological package consists of three core components – stages of intervention – with synergistic and cumulative effects, as follows:

- Off-season reduction of the inoculum potential of the pathogens-infested soil
- Pre-crop enhancement of natural soil suppressiveness against pathogenic communities and their associated diseases
- On-season protection of infection courts by bio-augmentation of the root zone of cultivated plants with consortium of biocontrol microorganisms.

Empirical Approach: The integrated bioremediation technology outlined here is built in four phases: (1) Site assessment and baseline analysis to identify considerable disease conditions; (2) Selectively killing or weakening soil-borne plant pathogens and pests through the application of non-chemical, environmentally benign disinfestation techniques, including: thermal-assisted soil solarization, biosolarization or anaerobic soil disinfestation, soil inundation, cover crops, green manuring and biofumigation; (3) Enhancing general or specific soil disease suppressiveness. This phase involves pre-plant application of highly suppressive organic amendments, incorporation of aboveground forest floor (O soil horizon) biomass, addition of river silt sediments, use of inorganic amendments, and bio-augmentation with specific biocontrol agents, e.g. consortium of antagonistic *Trichoderma* spp., with the purpose of inducing reversible shifts in soil microbial community towards creating highly competitive biological environment, enhanced microbial diversity and activity; (4) On-season protecting the infection courts – bio-augmentation of the root zone of cultivated plants with specific consortium of antagonistic fungi (*Trichoderma* spp. based biopesticide).

Sustainability, Conclusions and Perspectives: The present integrated bioremediation technology is grounded in extensive empirical evidence, validated through over 120 individual

experiments and series of experiments. It represents a comprehensive strategy for biologically-based remediation of greenhouse soils affected by soil-borne fungal pathogens in tomato production. The conceptual framework provided here offers a solid foundation for implementation and adaptation to other pathosystems, crop plants and consortia of soil-inhabiting pathogenic organisms.

Key words: consortium of soil-borne plant pathogens, disease complex, greenhouse tomatoes, biologically-based remediation strategy, integrated empirical approach.

Comparison Between Some Plant Fluids and the Human Blood

A. Sotirov⁽¹⁾ & S. Yordanov⁽²⁾

⁽¹⁾*Institute of Agriculture-Kyustendil, Agricultural Academy, Sofa, Bulgaria*

⁽²⁾*National Center of Infectious and Parasitic Diseases (NCIPD), Sofa, Bulgaria*

Corresponding author: a_sotir@iz-kyustendil.org

The aim is to establish regularities in the biochemistry of plant fluids and human blood. The work seeks to contribute to efforts of producing of human blood or plasma with plant origin. Digital instrumental methods were used. Statistics was done through computer program XLStat. Reference data on the biochemistry of human blood was used. Some similarities and dissimilarities were found between plant fluids and the human blood. Total sugar in a human's blood is the lowest compared to studied plant fluids. Glucose in human blood is similar to that in a grapevine sap. Fructose is in lowest amount in human blood. The water in human blood is almost the same as that of plant fluids. pH of human blood is low alkaline, but plant fluids are acidic. Fats in vegetables are in greater quantities in vegetables, or they are close to human blood. The electrical conductivity of human blood is the highest compared to the studied plant fluids. The amount of dissolved solids in human blood is close to that of vegetables. There is no complete similarity between the studied liquids, but they are similar in water content and they have similar ratios between biochemical indicators. The biochemistry of human blood, like the biochemistry of plant fluids, there are a number of regularities, such as precisely defined ranges and levels of components, precisely defined relationships between them. There are identical dependencies and ratios. Human blood is similar in biochemical parameters to some plant fluids or to other plants. Human blood is located in the central place in the diagram of the water equilibrium between oxidation and reduction of water in itself and is distinguished most by its place in the TDS-Salt diagram, being located farthest from the equilibrium line between salts and dissolved solids, or in a word, the highest measured electrical conductivity in human blood, compared to plant fluids, is not at the expense of salt as an electrolyte, but due to the higher content of other dissolved organic substances in the blood. In the search for suitable plant fluids as substitutes for human blood or plasma, the rule that the biological optimum of plants (the optimum of living matter) is a natural continuation of the thermodynamic state of weathering crust and soil helps and finding the most suitable plant fluid for this purpose will be an indicator of the connection between man and planet Earth.

Key words: *biochemistry, plant fluids, juices, grapevine sap, human blood*

Source of information:

Sotirov, A., Yordanov, S. (2025). Comparative biochemistry between plant fluids and the human blood. *Trakia Journal of Sciences*, No 3, pp 173-185, 2025 Available online at: <https://trakia-uni.bg> ISSN 1313-3551
(online) doi:10.15547/tjs.2025.03.001. <https://tjs.trakia-uni.bg/index.php/tjs/article/view/126/142>

Contribution to the Enrichment of Wheat Germplasm in Romania

R. Kadar ^{(1)*}, I. Racz ^(1,2), D. Hirişcău ⁽¹⁾, A. Varadi ⁽¹⁾, D. Morar ^(1,2), F. Kadar ⁽¹⁾

⁽¹⁾ Agricultural Research and Development Station Turda, no 27 Agriculturii street, Cluj county, Romania

⁽²⁾ University of Agriculture and Veterinary Medicine Cluj-Napoca, Calea Mănăştur 3-5, Cluj

* Corresponding author: rodica.kadar@scdaturda.ro

The main objective of ARDS Turda wheat breeding program is creating varieties that ensure significant genetic progress for production capacity, resistance to adverse environmental conditions, resistance to the most important diseases, appropriate quality indices for the milling and baking industries, in order to increase the profitability of agricultural holdings. The creation of varieties with superior production potential is largely determined by the genetic value of the germplasm sources used in wheat breeding programs. The most productive wheat breeding programs owe their success to both the large number of hybrid combinations achieved and the size of the hybrid populations subjected to selection. Genetic progress for wheat production capacity was estimated based on the results of multiannual comparative trials carried out during 2013-2024 at SCDA Turda at a value of 54 kg·ha⁻¹·year⁻¹, with no ceiling trend. The genetic progress made in improving wheat for bread quality must be associated with other agronomic traits important for production capacity and crop stability, and it is recommended that in creating the initial selection material, high-performing parents for quality, well adapted to local conditions, be used, and the use of the progress made in previous breeding cycles was a safer way to obtain the expected performances. The need to create a large number of hybrid combinations is imposed by the fact that the value of recombination cannot be predicted with certainty only based on knowing the value of the parental forms used in crossing. Experience has shown that a smaller number of well-planned hybrid combinations can provide more valuable hybrid material than a large number of random crosses. Since 1971, when the first variety was launched, until 2025, twenty wheat varieties have been created and launched into production, of which 17 winter varieties and three spring varieties, with an average success rate of one variety every 2,7 years, with the mention that in the last decade has been more accelerated, namely one variety every 1,6 years. The lifetime of varieties created at ARDS Turda are between 10 and 20 years, with the mention that the Arieşan variety (registered in 1985), due to its appreciation by farmers from Transylvanian Plain area, especially for its quality indicators, is approaching 40 years. Of the twenty registered wheat varieties, ten are found in the Official Catalogue of Varieties: Arieşan, Dumbrava, Andrada, Codru, Taisa, Dumitra, Cezara, Luminiţa, Georgiana and Feleacu. In recent years, in the context of climate change, earliness has been a priority objective in the wheat breeding program at ARDS Turda, the advantage of these genotypes being that by heading earlier avoid the effects of drought that often occurs at the end of May-beginning of June in the conditions of the Transylvanian Plain. We have imposed that the varieties that will be homologated in the future be earlier or closer to Arieşan, and Georgiana variety that was homologated in this year corresponds to this objective, being earlier by 5 days, but the production was 2120 kg·ha⁻¹ higher under the same technological conditions.

Keywords: wheat varieties, genetic progress, breeding, earliness, lifetime

Abstract of the paper presented at the second Conference of Geneticists and Breeders in the Agricultural Field in Timișoara (12-13. 11.2025)

Developing a system for land assessment and improving soil health in Bulgaria

M. Banov^{(1)*}, V. Kolchakov⁽²⁾

⁽¹⁾ *Scientific Department "Genesis, Geography and Classification of Soils", N. Poushkarov Institute of Soil Science Agrotechnologies and Plant Protection, Agricultural Academy, 1080 Sofia, 7 Shose Bankia Str., Bulgaria*

⁽²⁾ *Scientific Department "Physics, Erosion, Soil Biota", N. Poushkarov Institute of Soil Science Agrotechnologies and Plant Protection, Agricultural Academy, 1080 Sofia, 7 Shose Bankia Str., Bulgaria*

* *Corresponding author: banovm@abv.bg*

A simplified and easy-to-use methodology has been developed for assessing soil health on agricultural production farms in Bulgaria. The methodology adheres to the limitation methods recommended by FAO and more precisely to those that take into account the number and degree of existing limitations for a certain set of land characteristics and is tailored to the specifics of agricultural production at the farm level. The research enables dynamic monitoring of the changes in the qualities of the soils in accordance with the measures taken to improve their health.

The land features selected for work are grouped into 4 large groups. When selecting the working characteristics of the lands, we complied with the rule to work with the smallest possible number of characteristics that describe as fully as possible the agro-ecological conditions in relation to the requirements of the plants, while at the same time not allowing double and triple evaluation of the same characteristic.

The four groups cover information for agroclimatic, terrain and stony soils, drainage conditions, and soil fertility. It includes a total of 10 indicators. Also, the study suggests the ranking of all these indicators and algorithms for general evaluation and categorization of lands. The evaluation system allows farmers to determine the risk to soil health and receive specific recommendations for its improvement, leading to more sustainable and efficient agriculture.

The suggested indicators allow dynamic monitoring of changes in soil properties in accordance with the measures taken to improve their health. Furthermore, it is possible to further develop a digital tool that evaluates which soil restoration practices are appropriate for a given soil based on its characteristics and how these practices would affect the income-cost structure.

The methodology is open and allows for the inclusion of additional characteristics that will allow for the assessment of some specific soil indicators, such as heavy metal contamination, acidification, salinization, etc.

The developed methodology for assessing soil health allows:

- Testing the approach with data from different countries to ensure broad applicability;
- Developing a digital platform based on the methodology for easy access and application;
- Creating an automated system to provide specific recommendations based on input data;
- Evaluating how soil restoration practices affect the income-cost structure for farmers.

Keywords: Land assessment, soil health, classification

Reference: 5th Edition of Global Conference on Agriculture and Horticulture, September 08-10, 2025, Valencia, Spain

Digitalization and valorization of crop diversity in Bulgaria and Slovakia

Nikolaya Velcheva^{(1)*}, Asya Stoyanova-Doycheva⁽²⁾, Pencho Malinov⁽²⁾, Ľubomír Mendel⁽³⁾, Tsvetelina Stoilova⁽¹⁾, Iveta Čičová⁽³⁾, Erika Zetochová⁽³⁾ & René Hauptvogel⁽³⁾

(1) *Agricultural Academy, Institute of Plant Genetic Resources “K. Malkov”,
2 Druzhba Str., 4122 Sadovo, Plovdiv region, Bulgaria*

(2) *Plovdiv University “Paisii Hilendarski”, Faculty of Mathematics and Informatics, Department of
Computer Systems, 24 Tzar Asen Str., 4000 Plovdiv, Bulgaria*

(3) *National Agricultural and Food Centre, Research Institute of Plant Production,
122 Bratislavská cesta Str., 921 68 Piešťany, Slovak Republic*

*Corresponding author: nikolaya_velcheva@abv.bg

Plant diversity is essential for food security, sustainable agriculture, and environmental protection. The relevant documents on the genetic resources, adopted by international bodies, underline the need of crop conservation for the future of humanity, and guarantee open access to its diversity. Last decades, more and more landraces have been replaced by modern varieties. Under these circumstances, a holistic approach for biodiversity conservation by using elements of two strategies: *in situ/on farm* and *ex situ* preservation, represents a research priority. International collaboration between genebanks has become crucial in ensuring the global conservation and sustainable use of genetic resources in the framework of maintaining compatibility and interoperability in the European area. The Green Deal promotes ecological practices that have positive impact on protection of bioresources. The applied purpose of the study is to improve visibility of the National genebanks of Bulgaria and Slovakia due qualitatively exchange of experience and establishing joint research plan based on their long-standing mission of storage of plant diversity. The hypothesis is that it helps valorization through better access to local plant diversity for meeting the climate challenges and farmers' needs. By sharing good practices in genebank documentation, collecting landraces through expeditions and germplasm exchange using Standard Material Transfer Agreement, the study increase the diversity of the National collections following the priorities of EU Biodiversity 2030 Strategy. The interdisciplinary approach integrates agricultural sciences and information technologies, that facilitating modernisation of documentation systems and supports practical use of the achievements. In the era of digitalization, the results improve the data management quality and sharing new knowledge through local plant genetic resources cataloguing by FAO/Bioversity descriptors and addressing the Nagoya Protocol, which emphasizes the importance of public awareness of genebanks. Results include the development of optimised databases and web-based tools for public access to the gene pool and equitable sharing of benefits from the use of genetic resources under the International Treaty on Plant Genetic Resources for Food and Agriculture. The data is part from the GeneBank System in Bulgaria (<https://genbank.uni-plovdiv.net>) and Genetic Resources Information System of Slovakia (<http://griss.vurv.sk>). Both collections are published with open access in the European catalogue EURISCO (<http://eurisco.ecpgr.org>). They are presented with valuable seed duplicates in the Svalbard Global Seed Vault. The study has an impact beyond academia, as it contributes to sustainable and diverse food production through valorization of traditional and old varieties facilitating their reintroduction into home gardens and farms. It corresponds landraces and crop wild relatives preservation through inventoring the diversity and exploring the environmental conditions in rural and mountain areas in line with the National conservation programs of Bulgaria and Slovakia. The solutions, achieved by the interdisciplinary team, prove the hypothesis and find their application in the overall process of preserving the biodiversity and nature, increasing the crop resilience in dynamic environmental conditions, and guarantee the production of clean and high-quality food.

Acknowledgements

This research work is carried out under the cooperation project DIGIVALPGR, funded by Bulgarian Science Fund, Contract KP-06-Slovakia/9/13.08.2024 and Slovak Research and Development Agency, Contract SK-BG-23-0005/17.09.2024.

Keywords: plant genetic resources, genebanks, descriptors, information systems, EURISCO.

Domains of increased genetic polymorphism boost crossover in plant breeding
 M.E. Mikhailov^{1,3*}, F. Boideau^{2,3}, M. Szymanska-Lejman², V. Botnari¹, P.A. Ziolkowski^{2*}

¹Laboratory of Plant Resistance, Institute of Genetics, Physiology and Plant Protection, Moldova State University, Chisinau, Moldova.

²Laboratory of Genome Biology, Institute of Molecular Biology and Biotechnology, Adam Mickiewicz University, Poznan, Poland.

³These authors contributed equally: Mikhail E. Mikhailov, Franz Boideau.

* Corresponding authors: mihailerik.150@gmail.com; pzio@amu.edu.pl

Meiotic crossovers, which exchange DNA between homologous chromosomes, are essential for accurate chromosome segregation and generate genetic diversity. In plant breeding, crossovers enable the creation of new haplotypes by combining beneficial alleles. Their distribution along chromosomes is shaped by multiple factors, many of which remain poorly understood. One such factor is local DNA sequence divergence between homologous chromosomes, known as *cis*-acting genetic polymorphism. In most species studied, local polymorphism suppresses crossover formation. However, in the self-fertilizing plant *Arabidopsis thaliana*, crossovers are instead stimulated in heterozygous regions when these are juxtaposed with homozygous regions on the same chromosome.

Here, we report a similar effect in the outcrossing maize. We developed a set of nearly isogenic maize lines carrying distinct patterns of polymorphism and phenotypic markers, enabling precise measurements of recombination frequency. Building on a high-quality PacBio genome assembly combined with high-coverage Illumina sequencing, we discovered that crossover stimulation in heterozygous domains adjacent to homozygous regions occurs even more effectively in maize, reaching up to a threefold increase in crossover frequency. This stimulation occurs in both male and female meiosis and is strongest when heterozygous regions fully span the entire measured interval, consistent with crossover redistribution. Since *Arabidopsis* and maize represent distantly related plant lineages (eudicots and monocots), this shared phenomenon suggests a conserved mechanism.

Enhancing crossover frequency in targeted chromosomal regions remains a major challenge in applied genetics. While global increases can be achieved through mutations in DNA repair pathways, such approaches often compromise chromosomal segregation, particularly in cereals. Directing crossovers to specific chromosomal regions is an attractive alternative, yet no such method currently exists in plants.

Our study demonstrates that a similar outcome can be achieved without genetic modifications, simply by selecting parental lines with defined heterozygosity patterns around genomic regions of interest. Because the effect only manifests when large chromosomal segments are homozygous, this strategy is particularly suited to doubled-haploid technology, which is widely used to generate inbred lines. We envision this as especially valuable when recombination is suppressed between closely linked quantitative trait loci (QTLs). By choosing optimal doubled haploid lines for crossing, breeders can substantially increase the probability of recovering the desired genotype. Moreover, as the effect appears to rely on crossover redistribution from homozygous regions, it may also be exploited to locally suppress recombination, preserving linkage between favorable alleles.

In maize, this approach increased local crossover frequency by up to an unprecedented threefold. Importantly, we did not observe differences between two maize backgrounds differing with the polymorphism density, suggesting that the strength of the effect is not affected by the polymorphism density. We therefore propose integrating this phenomenon into the design of breeding strategies. In the era of high-throughput sequencing, where thousands of fully characterized lines are available, exploiting this juxtaposition effect offers a powerful, non-transgenic tool to accelerate trait introgression and enhance selection efficiency.

Reference: Mikhailov et al., *Nature Plants* 2025, <https://www.nature.com/articles/s41477-025-02085-8>

Keywords: crossover, recombination, polymorphism, maize

Effect of Polyunsaturated Fatty Acid Feed Supplements in Broiler Turkeys

Mitko Lalev¹, Pavlina Hristakieva^{1*}, Magdalena Oblakova¹, Nadia Mincheva¹

¹*Agricultural Academy, Agricultural Institute - Stara Zagora, Radnevsko road 1, 6000 Stara Zagora, Bulgaria*

*Corresponding author: pavlinahristakieva@abv.bg

Growing consumer interest in health and nutrition has intensified the search for strategies to produce foods with enhanced functional value. In recent years, research in functional foods has focused on enriching human diets with omega-3 and omega-6 fatty acids. Long-chain omega-3 fatty acids—particularly eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA)—are associated with numerous health and longevity benefits, increasing interest in foods naturally enriched with these nutrients. In poultry production, essential fatty acids are increasingly emphasized not only for improving bird health and productivity but also to meet consumer demand for nutritionally balanced animal products.

Flaxseed and microalgae have emerged as promising dietary supplements for increasing omega-3 content in poultry meat. This study investigated the effects of supplementing broiler turkey diets with omega-3-rich additives on production performance, slaughter traits, and the fatty acid profile of meat. Turkeys received either microalgae meal (1% or 2%; algae cultivated in a closed, controlled system) or a flaxseed- and cereal-based product (0.5%), and were compared with unsupplemented controls. Live weight, daily weight gain, feed conversion, and slaughter characteristics were recorded. Fatty acid composition of breast and thigh meat was determined using gas chromatography after extraction and conversion to methyl esters, and expressed as a percentage of total identified fatty acids. Total PUFA (polyunsaturated fatty acid) content and the omega-6/omega-3 ratio were also calculated.

Turkeys receiving 2% and 1% microalgae meal achieved the highest final live weights (8.935 kg and 8.418 kg, respectively), outperforming both the flaxseed group (7.903 kg) and controls (7.543 kg). Birds supplemented with 2% microalgae also showed a 14% reduction in feed intake compared with controls and the flaxseed group. Meat from all supplemented groups displayed higher omega-3 fatty acid content and lower omega-6/omega-3 ratios than controls.

Overall, the findings demonstrate that flaxseed and microalgae supplementation effectively enhances growth performance and enriches turkey meat with omega-3 fatty acids, supporting their use as functional feed additives in poultry production.

Key words: Turkey's meat, Productivity, Algae, Linseed, Fatty acid ratio (ω_6/ω_3)

Reference: Original scientific paper UDC 637.5'659.2.043:636.592.087.7(560)

Lalev, M., Hristakieva, P., Oblakova, M., Mincheva, N. (2021). Effect of polyunsaturated fatty acids dietary supplementation of broiler turkeys on growth performance and fatty acid content of meat. *Journal of Hygienic Engineering & Design*, 35, 48-55.

Emergence of a new plum pox virus variant in Romanian *Prunus domestica* orchards

A.B. Ruiz-García⁽¹⁾, L.A. Zagrai⁽²⁾, A. Olmos⁽¹⁾, I. Zagrai^{(2)*}

⁽¹⁾ Instituto Valenciano de Investigaciones Agrarias (IVIA), CV- 315, Km 10.7, Moncada 46113, Valencia, Spain

⁽²⁾ Fruit Research & Development Station Bistrita, 3, Drumul Dumitrei Nou, 420127, Bistrita, Romania

*Corresponding author: izagrai@yahoo.com

Abstract

Plum pox virus (PPV), the causal agent of sharka disease, is the most damaging viral pathogen affecting stone fruits. Among the ten recognized PPV strains (D, M, EA, C, Rec, T, W, An, CR, and CV), PPV-D, PPV-M and PPV-Rec are the most prevalent in Europe, with PPV-M being the most aggressive and epidemic. Despite Romania status is a PPV-endemic country, PPV-M had not been reported in the past two decades, even after extensive surveys. To assess whether PPV-M had been introduced through imported planting material, a post-control survey was conducted in newly established plum orchards using trees imported from Hungary, Germany, Italy, the Netherlands, Austria, and the Czech Republic. PPV monitoring was based on symptom observation, serological testing and molecular strain typing using RT-PCR with strain-specific primers targeting CP and 6K1-CIP genomic regions. PPV-D and/or PPV-Rec were detected in 10 of 11 surveyed orchards. Moreover, PPV-M was identified in one year post-planting symptomatic trees from a new orchard in Vaslui County, Romania, which used planting material from Hungary. Two symptomatic *Prunus domestica* cv. Grossa di Felisio trees were selected for high-throughput sequencing (HTS) using RNA-Seq with ribodepletion on an Illumina platform, leading to the first complete genome sequencing of two Romanian PPV-M isolates. This is the first confirmed molecular identification and characterization of PPV-M in Romania, raising concerns about the potential spread of this aggressive strain. If proper containment measures are not implemented, PPV situation in Romania could significantly worsen, impacting stone fruit production.

Keywords: Sharka, PPV-M, HTS, detection, disease management

Journal of Plant Pathology, <https://doi.org/10.1007/s42161-025-01952-9>

Exploring Bitter Taste Origins in Faba Beans Using Combined Approaches

A. Karolkowski ^{(1)*}, C. Belloir ⁽¹⁾, G. Lucchi ^(1,2), C. Martin ^(1,2), E. Meudec ^(3,4), E. Bouzidi ⁽⁵⁾, L. Levavasseur ⁽⁶⁾, N. Sommerer ^(3,4), L. Briand ⁽¹⁾, C. Salles ⁽¹⁾

⁽¹⁾ *Université Bourgogne Europe, Institut Agro, CNRS, INRAE, UMR CSGA, 21000 Dijon, France*

⁽²⁾ *INRAE, PROBE Research Infrastructure, ChemoSens facility, F-21000 Dijon, France*

⁽³⁾ *SPO, Univ. Montpellier, INRAE, Institut Agro, 34000, Montpellier, France*

⁽⁴⁾ *INRAE, PROBE Research Infrastructure, PFP Polyphenol analysis facility, 34070, Montpellier, France*

⁽⁵⁾ *Vivien Paille (Groupe Avril), 59300 Valenciennes, France*

⁽⁶⁾ *Groupe Soufflet-Invivo, 10400 Nogent-sur-Seine, France*

* *Corresponding author: adeline.karolkowski@inrae.fr*

Faba bean is a promising ingredient for the development of sustainable and nutritionally valuable plant-based foods. However, its wider use is limited by the presence of off-flavours, particularly bitterness, which strongly affects consumer acceptance. While previous research on pulses has mainly examined volatile compounds responsible for off-notes, the role of non-volatile molecules in bitterness remains insufficiently understood. Recent studies on peas, soybeans, and lupins have highlighted the involvement of saponins, phenolic compounds, alkaloids, amino acids, and peptides in bitterness, but such investigations remain scarce for faba beans. This study aimed to identify the non-volatile compounds responsible for bitter taste in faba bean fractions and to better understand the influence of process and cultivar selection on taste quality.

Sensory, metabolomic and cellular approaches were combined to characterize the bitterness of 3 air-classified fractions (flour, starch, and protein) obtained from 3 cultivars. First, 21 trained panellists evaluated the bitter intensity of gels containing the different fractions. Significant differences in bitterness were observed according to both the type of fraction and the cultivar. Second, an untargeted metabolomic approach using ultra-high-performance liquid chromatography coupled with diode array detection and high-resolution mass spectrometry (UHPLC-DAD-HRMS) was applied to investigate the origins of these sensory differences. This comprehensive profiling allowed the detection of a large number of non-volatile compounds and showed clear differences between fractions and between cultivars. Third, the sensory data were correlated with those of the metabolomic approach to identify the non-volatile compounds most closely associated with bitterness. A total of 42 non-volatile compounds were tentatively identified as contributing to bitter taste. They belonged to various chemical families, including alkaloids (such as vicine, convicine and their derivatives), amino acids, phenolic compounds, organic acids, and terpenoids. Although β b and DDMP soyaponins are known contributors to bitterness in peas, these compounds were detected in the faba bean fractions without correlating with bitterness. This suggested that their concentrations were too low to contribute to this off-taste and indicated that the bitterness origins differed among pulses. Fourth, the sensory relevance of several highlighted compounds was carried out through a cellular assay targeting human bitter taste receptors (hTAS2Rs). Bitter compounds are known to activate at least one of these 25 receptors, leading to the perception of bitterness. This approach showed that vicine, a specific alkaloid of faba beans, activated the hTAS2R16 receptor, whereas β b soyaaponin activated 11 receptors, including TAS2R42, for which no agonist had previously been reported.

Finally, this multidisciplinary approach provides new insights into the origins of faba bean bitterness and highlights the effect of cultivar and process on taste quality. These findings offer practical perspectives for the agri-food industry. Identifying the compounds that most strongly influence the faba bean bitterness makes it possible to propose strategies for improving their flavour, such as cultivar selection and process optimization. This will promote the development of plant-based ingredients with improved sensory properties, thereby encouraging wider use of faba beans and other pulses as sustainable a source of proteins.

Keywords: faba beans; bitterness; sensory analysis; metabolomic analysis; cellular assays

Reference A. Karolkowski, C. Belloir, G. Lucchi, C. Martin, E. Bouzidi, L. Levavasseur, C. Salles and L. Briand. Activation of Bitter Taste Receptors by Saponins and Alkaloids Identified in Faba Beans (*Vicia Faba* L. *Minor*). *Food Chemistry*, 2023, 426, 136548. <https://doi.org/10.1016/j.foodchem.2023.136548>

Early Pregnancy Diagnosis in Bulgarian Murrah Buffaloes by PAGs

I. Fasulkov ^{(1)*}, Y. Ilieva ⁽²⁾, P. Penchev ⁽²⁾, M. Karadaev ⁽¹⁾, B. Ivanova ⁽¹⁾, R. Nenova ⁽²⁾ & N. Vasilev ⁽¹⁾

⁽¹⁾ *Department of Obstetrics, Reproduction and Reproductive Disorders, Faculty of Veterinary Medicine, Trakia University (TrU), Stara Zagora, Bulgaria.*

⁽²⁾ *Agriculture Academy (AA), Agricultural Institute, Shumen, Bulgaria.*

* *Corresponding author: i.fasulkov@gmail.com*

Timely and reliable pregnancy diagnosis in productive animals is essential for improving reproductive efficiency by reducing calving intervals and allowing rapid rebreeding of non-pregnant females. Pregnancy-associated glycoproteins (PAGs), produced by the ruminant placenta and measurable in maternal circulation, have become an important tool for early pregnancy detection in cattle and buffaloes. The present study evaluated the diagnostic performance of two commercial ELISA kits for detecting PAGs in blood serum and milk of Bulgarian Murrah buffaloes, aiming to determine their suitability for early pregnancy diagnosis under farm conditions.

Blood samples were collected from 57 buffalo cows and 27 heifers on the 28th day following artificial insemination. Additionally, 55 milk samples were obtained from lactating buffaloes on the same day. Pregnancy status was confirmed seven days later, on day 35 post-insemination, through transrectal ultrasonography. PAG concentrations in serum and milk were measured using a commercial ELISA designed for early pregnancy diagnosis. The results were analysed using a non-parametric Chi-square test to compare proportions, employing Statistica 7 statistical software.

PAG concentrations in serum were significantly higher than those measured in milk ($P < 0.05$). Based on serum S-N values, 17 buffalo cows were diagnosed as pregnant and 40 as non-pregnant, while in heifers 7 were classified as pregnant and 20 as non-pregnant. Both serum and milk tests showed acceptable diagnostic characteristics, but serum PAG analysis consistently outperformed the milk test.

In buffalo cows, sensitivity reached 94.4% for serum and 87.5% for milk, while specificity was 100% for both sample types. In heifers, however, sensitivity was considerably lower (55.6%), although specificity for the serum ELISA remained high (88.9%). Accuracy values reflected similar trends: in buffalo cows the serum and milk tests achieved 98.2% and 96.4% accuracy, respectively, while in heifers the serum assay provided 77.8% accuracy.

Positive predictive values (PPV) in buffalo cows were 100% for both serum and milk tests, indicating that all positive diagnoses corresponded to confirmed pregnancies. Negative predictive values (NPV) were also high, reaching 100% for serum and 95.1% for milk. In heifers, PPV was lower at 71.4%, while NPV reached 80.0%. These results show that PAG-based ELISA testing is a reliable method for early pregnancy diagnosis in buffaloes, with serum testing providing the highest overall performance. However, milk sampling offers a valuable, non-invasive alternative that avoids the stress associated with blood collection. The presence of PAGs in milk also makes routine screening feasible in dairy buffalo operations without interrupting daily milking procedures. Although performance in heifers was lower, especially regarding sensitivity, both tests delivered acceptable specificity and practical value for early herd-level pregnancy monitoring.

Overall, the findings indicate that ELISA tests for PAGs in serum and milk are sufficiently sensitive, specific and accurate for diagnosing pregnancy as early as day 28 after artificial insemination. Their use can support more efficient reproductive management in Bulgarian Murrah buffalo herds.

Keywords: pregnancy-associated glycoproteins, serum and milk, ruminants, buffaloes, ELISA.

Reference: <https://seer.ufrgs.br/index.php/ActaScientiaeVeterinariae/article/view/148745>

FACTORS AFFECTING FATTY-ACID PROFILE OF LACTIC LIPIDS IN THE WATER BUFFALO. A REVIEW

P. Penchev^{(1)*}, R. Nenova⁽¹⁾, Y. Ilieva⁽¹⁾, S. Enchev⁽¹⁾, M. Schreiner⁽²⁾

⁽¹⁾ *Agricultural Academy, Sofia, Agricultural Institute – Shumen, BULGARIA,*

⁽²⁾ *University of Natural Resources and Life Sciences, Vienna, Gregor-Mendel-Straße 33, 1180 Wien, AUSTRIA*

*Corresponding author: pen.penchev@gmail.com

Abstract

The aim of this review was to study how lactic fatty acids (FA) are affected by different factors in the different pathways in the buffalo – a species differing from cattle with its response to feeding strategies, metabolism and specific functional composition of milk. It underlines the role of management to manipulate enzymatic desaturation and bacterial synthesis and that of ripening and pasteurization in dairy technology. The review presents some proofs of effect of season on FAs, but it should be correctly discriminated from the effect of lactation stage, showing improved unsaturation in advanced lactation. Farming system has major impact, and it can include feeding strategies (rumen-inert fats, seeds, bioactive compounds, etc.) to affect rumen biohydrogenation, but it is implied that the doze is important. In fact, the best control over bubaline lactic FAs is via natural grazing, improving omega ratio, conjugated linolenic (CLA) and trans-vaccenic acid (TVA). This is not only because of plants' composition of soluble sugars, vitamins, polyphenols and proteins, but mostly because of the stimulated bacterial synthesis and $\Delta 9$ -desaturase activity, responsible for the de novo synthesis. The results about the transformations in the beneficial fatty acids in the yoghurt production are controversial explaining the predominantly negative impact mostly with pasteurization. Cheese processing generally alters the individual isomers but not the groups of beneficial fatty acids (CLA) as a whole chiefly due to ripening and pasteurization (only if the temperature is high), but not due to renneting.

Key words: Bubalus bubalis, milk, fatty acids, grazing, supplementation

Reference: <https://doi:10.17707/AgricultForest.71.1.14>

Fish Fin Evaluation Using a Convolutional Neural Network: A Pilot Study

Osei. S ⁽¹⁾, Aizhan. T ⁽²⁾, Mehdi. M.Z⁽¹⁾, Koliada. I ⁽¹⁾ & Warjri. S ⁽¹⁾.

⁽¹⁾ *Laboratory of Machine Vision in Aquaculture and Water Protection, Faculty of Fisheries and Protection of Waters, University of South Bohemia in Ceske Budejovice, Zamek 136, Nove Hrady 37 333, Czech Republic.*

⁽²⁾ *Faculty of Science and Technology, University of Debrecen, Egyetem ter 1, Debrecen 4032, Hungary.*

Corresponding author: sosei@frov.jcu.cz

Keywords: Convolutional neural network, data annotation, data extraction, fin damage, pikeperch fish.

Fish fin promises to be a valuable non-invasive welfare indicator especially in aquaculture. Fin damage is a broad term that includes fin erosion and other abrasions. Fins that help make these important decisions are mainly the dorsal fin, caudal fin and anal fin. This article reports on the preliminary findings of a pilot study on evaluating fish fin damage using a convolutional neural network.

Keeping track of fish health is a challenging task, with one critical aspect being the assessment of fish fin. To achieve this objective, video data of pikeperch fish in an aquarium was collected, followed by image extraction and annotation (assigning a class to the part of the fin of interest by put that part in a box). The annotated dataset was then used to train a Convolutional Neural Network (CNN) to see the learning performance.

Results from the learning performance revealed that improving the dataset and adjusting certain classes could help achieve exceptionally significant precision (how the CNN model can identify the correctly identify a fin part), recall (how the model is able to identify all the correct instances), and F1 scores (how the precision and recall balances).

These findings underline the potential of deep learning methods in automating aquaculture health assessment.

Source of the Abstracts

Osei, S., Aizhan, T., Mehdi, Z.M., Koliada, I., Warjri, S. (2026). Fish Fin Damage Evaluation Using a Convolutional Neural Network: A Pilot Study. In: Rojas, I., Ortuño, F., Rojas Ruiz, F., Herrera, L.J., Valenzuela, O., Escobar, J.J. (eds) *Bioinformatics and Biomedical Engineering. IWBBIO 2025. Lecture Notes in Computer Science* (), vol 16050. Springer, Cham. https://doi.org/10.1007/978-3-032-08455-2_7

Framework for the selection of wheat varieties for arid agroecosystems

Q. Soofizada ⁽¹⁾, A. Pescatore ⁽¹⁾, S. Orlandini ^(1,2), M. Napoli ⁽¹⁾

⁽¹⁾ Department of Agriculture, Food, Environment and Forestry (DAGRI), University of Florence, Piazzale delle Cascine 18, 50144 Florence, Italy

⁽²⁾ Fondazione per il Clima e la Sostenibilità, Via G. Caproni 8, 50145 Florence, Italy

* Corresponding author: marco.napoli@unifi.it

Wheat production in arid and semi-arid regions faces critical challenges due to erratic climate conditions, soil degradation, and limited access to inputs such as nitrogen fertilizers. These constraints threaten food security and demand innovative approaches for selecting varieties that can perform reliably under resource-limited conditions. To address this, we developed and tested a multidimensional analytical framework aimed at identifying wheat genotypes that combine high yield, resource-use efficiency, and performance stability across variable environments. The study evaluated 33 bread wheat (*Triticum aestivum* L.) varieties across six environments in Afghanistan (three locations over two seasons). The framework integrated agronomic performance (grain yield, straw yield, thousand kernel weight), nitrogen use efficiency, statistical stability metrics (AMMI, Wricke's ecovalence), and economic return (Net Nitrogen-adjusted Margin, NNaM). This integrated approach allows a nuanced understanding of genotype behavior across diverse agro-ecological conditions, moving beyond average performance to include quality, resilience, and economic feasibility. Environmental conditions explained over 80% of the total variance in grain and straw yields, underscoring the influence of site-specific factors such as temperature, rainfall, and soil fertility. Nonetheless, significant genotype \times environment interactions revealed the potential to identify broadly adapted and resilient genotypes. Varieties Lalmi-15 and Lalmi-17 consistently exceeded 4.0 t ha⁻¹ in grain yield with high stability. Nitrogen uptake efficiency (Nt/Ns) ranged from 0.41 to 0.72, with varieties Muqawim-09, Dehdadi-13, and Amir-10 combining high uptake efficiency with consistent translocation and yield performance. Protein content, though primarily environment-driven, showed remarkable stability in variety MH0304-09, which also ranked among the top economic performers. The NNaM, an original economic index combining yield, grain protein value (via GOST classification), and nitrogen cost, was closely linked to both physiological and agronomic traits. A linear regression model explained 96.5% of NNaM variance, highlighting the critical roles of straw yield and Nt/Ns. Inclusion of stability metrics improved model robustness and interpretability, supporting selection decisions under variable conditions. A composite index, aggregating weighted trait means and stabilities, facilitated final varietal ranking. Only three genotypes, Lalmi-15, Lalmi-17, and MH0304-09, emerged as the most suitable candidates, offering high yield, nitrogen efficiency, and resilience. These results support the broader use of integrative, trait-based frameworks for guiding varietal selection in low-input systems. This approach is scalable and adaptable to dryland areas across Central Asia, the Mediterranean, and parts of Eastern and Southern Europe, where similar agro-climatic constraints exist. By combining physiological, agronomic, and economic indicators, this framework advances both scientific methodology and practical decision-making for sustainable crop improvement. It offers valuable guidance for breeding programs, extension services, and agricultural policy aiming to enhance productivity, profitability, and input-use efficiency in the face of increasing climate variability. Furthermore, the methodology has potential for adaptation to other crops and agro-systems where nitrogen use and stability are critical bottlenecks.

Keywords: Genotype-environment interaction; Nitrogen use efficiency; Nitrogen-adjusted profitability; Trait-based selection; AMMI and Wricke stability

Reference: Soofizada, Q., Pescatore, A., Orlandini, S., & Napoli, M. (2025). A multidimensional analytical framework for the selection of soft wheat varieties for dryland environments based on agronomic productivity, stability, nitrogen use efficiency and economic parameters. *European Journal of Agronomy*, 171, 127786. <https://doi.org/10.1016/j.eja.2025.127786>

From Vines to Ecosystems: Ecological Effects of Grapevine Leafroll Disease

E.-C. Buciumeanu^{(1)*} I.-C. Guță⁽¹⁾, D.-E. Vizitiu⁽¹⁾, L. Dinca^{(2)*} & G. Murariu^(3,4)

⁽¹⁾National Research and Development Institute for Biotechnologies in Horticulture Stefanesti - Arges, 37 Bucharest - Pitesti Road, 117715 Stefanesti, Arges Co., Romania

⁽²⁾National Institute for Research and Development in Forestry “Marin Dracea”, 128 Eroilor, 077190 Voluntari, Romania

⁽³⁾Dunarea de Jos University Galati, Faculty of Sciences and Environmental, Department of Chemistry, Physics and Environment, 47 Domneasca Street, 800008 Galati, Romania

⁽⁴⁾Rexdan Research Infrastructure, “Dunarea de Jos” University of Galati, 800008 Galati, Romania

*Corresponding author: dinka.lucian@gmail.com; ebuciumeanu@yahoo.com

Keywords: grapevine leafroll-associated viruses (GLRaV), occurrence, host responses, biological and epidemiological properties, physiology and yield

Abstract

So far, 102 viral entities are known in grapevine, this being considered one of the most affected crops by various types of viruses. As a vegetatively propagated woody species, it is a model plant for studying virus-plant interactions both under controlled and field conditions. Assessing the effects of a viral disease is not easy because a plant can be simultaneously infected with several viruses, and, in addition, it can be subjected to different abiotic and biotic stress factors at the same time. Grapevine leafroll disease (GLD), caused by a complex of grapevine leafroll-associated viruses (GLRaVs), is among the most widespread and economically damaging viral diseases of grapevine. Six positive-sense RNA viruses belonging to family Closteroviridae are associated with grapevine leafroll-associated viruses (GLRaVs): 4 viruses of genus Ampelovirus (GLRaV-1, GLRaV-3, GLRaV-4, and GLRaV-13), 1 virus of genus Closterovirus (GLRaV-2), and 1 virus of genus Velarvirus (GLRaV-7). Of the 6 leafroll associated viruses, GLRaV-3 is the most prevalent in all grapevine growing countries of the world, and most associated to leafroll effects, together with GLRaV-1. While its physiological and yield impacts are well recognized, the broader ecological implications for vineyard ecosystems remain poorly understood. This review integrates traditional literature analysis with bibliometric approaches to synthesize current knowledge on GLRaV occurrence, diversity, host responses, epidemiology, diagnostics, and management. Data from 729 peer-reviewed articles were categorized into six research clusters: global occurrence and first reports, viral diversity and characterization, host–pathogen interactions, epidemiology and vector dynamics, effects on vine physiology and fruit composition, and diagnostic and management strategies. Our findings highlight GLRaVs as dynamic pathogens shaped by genetic variability, human-mediated plant trade, and ecological interactions with vectors and vineyard biodiversity. Knowledge gaps persist regarding mixed infections, underexplored viticultural regions, ecological impacts, and sustainable management. Future work should prioritize high-resolution genomics, multiomics approaches, improved diagnostics, ecological studies, and innovative management tools. By framing GLD not only as an agronomic but also as an ecological challenge, this review provides a foundation for more holistic strategies to safeguard vineyard health and productivity.

Source of the abstract:

Buciumeanu E.-C., Guță I.-C., Vizitiu D.-E., Dinca L., Murariu G. (2025). From Vines to Ecosystems: Understanding the Ecological Effects of Grapevine Leafroll Disease. *Applied Sciences*, 15(22), 11920. <https://doi.org/10.3390/app152211920>.

Genetic bases and comparative genomics of *Aphanomyces* root rot resistance in legumes

T. Leprévost⁽¹⁾, C. Lavaud⁽¹⁾, A. Sugio⁽¹⁾, and M-L. Pilet-Nayel⁽¹⁾

⁽¹⁾ IGEPP, INRAE, Institut Agro, Univ Rennes, 35653 Le Rheu, France

*Corresponding author: leprevost.theo@hotmail.fr

Grain legumes are valuable crops that provide: (i) protein-rich seeds for human and animal consumption, (ii) nitrogen enrichment of soils through symbiotic root associations with bacteria, and (iii) crop diversification in field rotations. However, significant yield instability is commonly observed in legume-growing regions, which can discourage farmers from cultivating these crops. One of the major stresses affecting legumes is root rot disease, caused by the oomycete *Aphanomyces euteiches*. This disease has been reported worldwide, and total yield loss can occur in highly contaminated fields. Currently, no effective control method is available. The creation of resistant varieties is a major challenge in order to protect legume crops from the disease. Significant research in quantitative genetics has led to the identification of quantitative trait loci (QTL) conferring partial resistance in several legume species, especially pea (*Pisum sativum*). Notably, the first French pea varieties with tolerance to *A. euteiches*, carrying resistance QTL, have been registered in recent years. However, the resistance levels in these varieties remain insufficient to prevent pathogen multiplication in soils and to ensure long-term effectiveness of the deployed QTL. Therefore, farmers are eagerly awaiting the release of new varieties with more effective resistance obtained by combining diverse resistance alleles.

This comprehensive study aimed to explore the diversity of *A. euteiches* resistance QTL in three cool-season legumes, *i.e.* pea, faba bean (*Vicia faba*), and lentil (*Lens culinaris*), to support the development of improved future varieties. Additionally, the genomic conservation of QTL among these three species and the model legume *Medicago truncatula* was investigated to identify potentially conserved orthologous resistance genes, in order to inform QTL deployment strategies in crop rotation systems and to contribute to the long-term durability of resistance.

Using QTL mapping and Genome-Wide Association Study (GWAS) approaches applied to diverse biparental populations and diversity panels, a total of 10 consistent resistance-associated genetic regions were identified in pea, confirming two major-effect QTL (*Ae-Ps4.5* and *Ae-Ps7.6*) previously detected. A high diversity of resistance alleles at consistent QTL was identified in new pea partially resistant lines and an accumulation of resistance alleles at these QTL was confirmed in the most resistant pea lines. In addition, one major-effect QTL (*Ae-Vf3.1*) and three other low-effect loci were associated with resistance in faba bean, while only six minor-effect QTL were identified in lentil. A major-effect resistance locus, *AERI*, was confirmed and fine-mapped in *M. truncatula*, revealing three candidate genes. Comparative genomics analysis based on known QTL locations revealed no conservation of major-effect QTL conferring quantitative resistance to *A. euteiches* across pea, faba bean, lentil, and *M. truncatula*. However, conservation between major-effect QTL, *i.e.* *Ae-Vf3.1* in faba bean and *AERI* in *M. truncatula*, and minor-effect QTL in *M. truncatula* and pea, respectively, was detected in two genomic regions.

This work provided new molecular markers closely linked to *Aphanomyces* root rot resistance QTL to assist breeders in improving their germplasm and led to identify candidate genes for further functional validation. Results will support efficient and durable deployment of quantitative resistance to *A. euteiches* in legume-rich cropping systems.

Keywords: *Aphanomyces euteiches*, QTL mapping, GWAS, orthology, durability

Sources :

Leprévost, T., Imbert, B., Lavaud, C., Boutet, G., Miteul, H., Leduc, A., Kreplak, J., Phung, H.-T., Aubert, G., Carrillo-Perdomo, E., Uhdre, R., Sari, H., Bourland, B., Caron, C.T., Tayeh, N., Ma, Y., Coyne, C.J., Sugio, A., and Pilet-Nayel, M-L. Comparative genomic analysis of QTL for resistance to *Aphanomyces euteiches* between pea, lentil, faba bean and the model species *Medicago truncatula*. *Theoretical and Applied Genetics*. [Accepted for publication, Preprint available at <https://doi.org/10.21203/rs.3.rs-5759185/v1>]

Genetic Variants Associated with Behavioural Response During Milking in Cows

M. Mincu-Iorga ^{(1)*}, A.E. Mizeranschi ⁽²⁾, D. Gavojdian ⁽¹⁾, I. Nicolae ⁽¹⁾, S. Kusza ⁽³⁾, & D.E. Ilie ^{(2)*}

⁽¹⁾ *Research and Development Institute for Bovine, 077015, Balotesti, Romania*

⁽²⁾ *Research and Development Station for Bovine, 310059, Arad, Romania*

⁽³⁾ *Centre for Agricultural Genomics and Biotechnology, University of Debrecen, 4032, Debrecen, Hungary*

* *Corresponding author: madalina.mincu@icdcb.ro*

Abstract

Cattle breeding has traditionally focused on improving production traits; however, recent interest in positive animal welfare has shifted attention toward selecting for more robust animals that balance productivity with health and well-being. The aim of the current study was to assess whether behavioural responses during milking in dual-purpose cattle are associated with genetic markers, previously linked to temperament traits in dairy and beef breeds. We focused on 185 lactating cows belonging to the Simmental strain (Romanian Spotted, national name), which were evaluated for their milking behaviour. Genotyping was performed using an 88-SNP panel selected based on prior associations with dairy and beef cattle temperament. The selected SNPs belong to 24 genes associated with ‘milking temperament’: GAP43 (Growth-Associated Protein 43), KCNJ3 (Potassium Inwardly Rectifying Channel Subfamily J Member 3), CD2 (Cluster of Differentiation 2), IGSF3 (Immunoglobulin Superfamily Member 3), NXNL2 (Nucleoredoxin Like 2), GRIN3A (Glutamate Ionotropic Receptor NMDA Type Subunit 3A), TBC1D32 (TBC1 Domain Family Member 32), RARS2 (Arginyl-tRNA Synthetase 2, Mitochondrial), RPS6KA2 (Ribosomal Protein S6 Kinase A2), NEO1 (Neogenin 1), HCN4 (Hyperpolarization-Activated Cyclic Nucleotide-Gated Channel 4), KCTD3 (Potassium Channel Tetramerization Domain Containing 3), USH2A (Usherin), HSPB8 (Heat Shock Protein Family B Member 8), SRRM4 (Serine/Arginine Repetitive Matrix 4), OTUD7A (OTU Deubiquitinase 7A), ADAMTS7 (A Disintegrin And Metalloproteinase With Thrombospondin Motifs 7), TBC1D2B (TBC1 Domain Family Member 2B), EEFSEC (Eukaryotic Elongation Factor, Selenocysteine-tRNA-Specific), RUVBL1 (RuvB Like AAA ATPase 1), KBTBD12 (Kelch Repeat and BTBDomain Containing 12), ZMAT4 (Zinc Finger, Matrin-Type 4); ‘flight speed’: BTC (Betacellulin); ‘temperament and habituation’: ADCY2 (Adenylate Cyclase 2). Genes were included based on their previously reported associations with behavioural traits in cattle and their involvement in neurobiological processes such as sensory perception, synaptic function and stress response regulation. We identified five SNPs that were significantly associated with milking reactivity in the Romanian Spotted breed, located in genes previously linked to neural development, stress response and behavioural regulation (USH2A, ADAMTS7, TBC1D2B and ZMAT4). Our findings suggest that milking behaviour in dual-purpose Simmental cattle is influenced by genetics, supporting the potential for including behavioural traits in future selection strategies. This study contributes to a better understanding of the genetic mechanisms underlying stress-related behaviours in dual-purpose cattle breeds.

Keywords

animal welfare; genetic markers; milking behaviour; Romanian Spotted

Source of Abstract

Mincu-Iorga, M.; Mizeranschi, A.E.; Gavojdian, D.; Nicolae, I.; Kusza, S.; Ilie, D.E.
Detection of Genetic Variants Associated with Behavioural Response During Milking in
Simmental Dual-Purpose Cows. *Animals* 2025, 15, 1766.

<https://doi.org/10.3390/ani15121766>

Genome Editing and Cultivar Choice for Nutrient-Dense Vegetables

Julia Weiss^{1*}, Nazim S. Gruda¹²³

¹ Technical University of Cartagena, Cartagena, Spain

² University of Bonn, Bonn, Germany, and ³ Academy of Science of Albania

*Corresponding author: julia.weiss@upct.es

Abstract

Feeding Europe well in a warming world requires crops that deliver both high productivity and superior nutritional value.

Drawing on two complementary studies, we synthesize how cultivar selection and modern breeding—including CRISPR-based genome editing—can purposefully enhance health-promoting traits in greenhouse and other protected vegetable systems while preserving commercial performance. From this perspective, tailoring cultivars to defined environments stabilizes vitamin, mineral, pigment, and flavor profiles under managed light, temperature, CO₂, and nutrient regimes. Classical and advanced methods (hybrid breeding, backcrossing, marker-assisted selection, RILS (recombinant inbred lines), MAGIC populations (Multi-parent Advanced Generation Intercrosses)) remain foundational. Yet, innovations in phenomics, GWAS, and high-throughput genotyping accelerate the discovery of loci controlling bioactive compounds and anti-nutritional factors. Genome editing adds precision: CRISPR/Cas can directly modify alleles governing carotenoids, phenylpropanoids, bitterness, or postharvest traits without introducing unwanted linkage drag. Together, these strategies reduce breeding cycles, enhance quality improvements, and better align crops with market and public health objectives (Figure 1).

In conclusion, a dual approach—environment-tailored cultivar choice and targeted genome editing—offers the most efficient pathway to producing nutrient-dense vegetables at a commercial scale. Protected cultivation provides the phenotype stability breeders require, while modern genomics delivers speed and specificity. As multi-omics, rapid phenotyping, and edit-ready pangenomes converge, trait pyramiding for quality, resilience, and efficiency will move from experimental to routine practice in greenhouse vegetables.

The combined insights from these studies show that rapid, precise breeding for nutritional traits is already technically feasible and economically viable. This directly supports the UEAA's call for modernizing EU rules on genome editing—specifically, differentiating precision edits from transgenic GMOs. Such reform would enable the deployment of healthier, climate-resilient vegetables across Europe, while maintaining safety standards and competitiveness in a global market increasingly shaped by advanced breeding technologies.

Keywords: genome editing, CRISPR, protected cultivation, nutritional quality, cultivar choice

Source:

Weiss, J.; Gruda, N.S. *Enhancing nutritional quality in vegetables through breeding and cultivar choice in protected cultivation*. *Scientia Horticulturae* 339 (2025): 113914.

<https://doi.org/10.1016/j.scienta.2024.113914>

Histological approach to understand *in vitro* regeneration ability on sweet basil

M. Montone ^(1,2), A. Cassetti ⁽¹⁾, B. Ruffoni ⁽¹⁾, L. Pistelli ^(2,3) & M. Savona ^{(1)*}

⁽¹⁾ CREA Research Centre for Vegetable and Ornamental Crops (CREA-OF), Corso Degli Inglese 508, 18038 Sanremo, Italy

⁽²⁾ Department of Agriculture, Food and Environment, University of Pisa, Via del Borghetto 80, 56124 Pisa, Italy

⁽³⁾ Interdepartmental Research Centre “Nutraceuticals and Food for Health”, University of Pisa, Via del Borghetto 80, 56124 Pisa, Italy

* Corresponding author: marco.savona@crea.gov.it; Tel.: +39-0184-694829

Abstract

Ocimum basilicum L. (Lamiaceae), commonly known as sweet basil, is an aromatic species economically important worldwide for its food, ornamental and pharmaceutical purposes. Micropropagation represents a powerful technique for the species. New efficient *in vitro* regeneration protocols are strictly required for genome editing applications, for example, to improve resistance to pathogens. Five commercial cultivars (‘Prospera’, ‘Paoletto’, ‘Italiko FT’, ‘Dark Opal’, and ‘Bolloso Napoletano’) were evaluated for *in vitro* germination and regeneration aptitude. Histological detection was conducted to verify the presence of early meristematic activity during *in vitro* regeneration process.

Seeds were surface sterilized with ethanol (70% v/v) and hypochlorite solution (1,5% v/v), cultured at 23 ± 1 °C, for *in vitro* germination, on Petri dishes containing standard basal medium (MS) + 0,3% sucrose + 0,6% agar (pH 5.7). Among the cultivars, ‘Prospera’ ensured the highest germination percentage (96%) combined with the lowest average germination time (0.65 days).

For each cultivar, *de novo* shoot regeneration trial was set up, under different hormonal induction conditions, using roots (MS + 1.0 mg L⁻¹ TDZ), hypocotyls (MS + 2.0 mg L⁻¹ TDZ + 0.1 mg L⁻¹ IBA), cotyledons (MS+ 2.25 mg L⁻¹ BAP) and cotyledonary nodes, i.e. CNs (MS+ 0.5 mg L⁻¹ BAP + 0.25 mg L⁻¹ IAA) as starting plant materials. Significant differences occurred among cultivars and explant types; for example, the best regeneration potential was recorded on roots, through nodule-like meristems (NLMs), precursors of shoots, especially in ‘Prospera’ (100%). CNs also showed a good morphogenic aptitude, reaching 72.5% of direct regeneration events in ‘Paoletto’. Cotyledons ensured the highest cv-related response: ‘Prospera’ (36%) and ‘Paoletto’ (25.50%) were more efficient than ‘FT Italiko’ (3.8%) and ‘Dark opal’ (10%). Hypocotyls were the explants with the lowest regeneration competence in all cultivars tested.

Based on economic and commercial interest, 20-day-old *in vitro* roots and cotyledons of three selected cultivars (‘Prospera’, ‘Paoletto’, and ‘Italiko FT’) were embedded in paraffin and stained with toluidine blue 0.25 M for histological analysis. Microscopic detection was suitable for identifying early meristematic organization in both roots and cotyledons grown in induction substrates, compared to the control without hormonal induction. Among the *O. basilicum* cultivars analyzed, different intensities of meristematic activity were detected. In roots, presence of meristematic centres was observed with the ability to generate shoot primordia; in cotyledons, both direct, with shoot primordia formation, and indirect, through callus, organogenesis pathways were observed.

A strong cultivar-dependent morphogenic aptitude was recorded in *O. basilicum* L., especially in these cultivars with high commercial interest. Up to now, this is the first report on the histological observations of *in vitro* regeneration in sweet basil, as a tool that can improve the understanding of *de novo* morphogenesis and *in vitro* regeneration mechanism. These results represent a valuable starting point for future New Genomic Techniques experiments in *Ocimum basilicum* L.

Keywords: morphogenesis, *Ocimum basilicum*, cultivar response, germination, explant types

Source: Montone, M., Casseti, A., Ruffoni, B., Pistelli, L., Savona, M. Evaluation of *in vitro* regeneration aptitude through histological detection in *Ocimum basilicum* L. *Horticulturae*, 2025, 11, 1060
<https://doi.org/10.3390/horticulturae11091060>

Introducing genetic diversity in animal populations from germplasm collections

A. Jacques^{(1,2)*}, M. Tixier-Boichard⁽²⁾ and G. Restoux⁽²⁾

¹ *Eliance, 75012 Paris, France*

² *Université Paris-Saclay, INRAE, AgroParisTech, GABI, 78350 Jouy-en-Josas, France*

* *Corresponding author: alicia.jacques@eliance.fr*

Keywords: *Biodiversity, cryobank, genetic resources, pigs, ruminants, dogs*

Genetic diversity is essential for the conservation and adaptation of animal populations. However, in a closed population, genetic variability inevitably decreases under the effect of genetic drift, inbreeding or selection. This is the case for domestic animals, where strong selection takes place in a few breeds, drastically reducing their effective population size whereas other breeds become endangered. *Ex situ* genetic resources, particularly cryopreserved ones such as semen or embryos, offer a unique opportunity to reintroduce or manage genetic diversity in domestic animal *in situ* populations. However, these resources are rarely used for this purpose. Indeed, there are no recommendations to help population managers use them in a way that addresses their objectives (e.g. conservation, selection...) and to the species involved. In fact, reintroducing diversity from "old" material might increase inbreeding and decrease performances if not carefully planned.

By combining the analysis of real data with simulations, this thesis aims at i) proposing a framework for evaluating *ex situ* genetic resources in the perspective of using them to manage the diversity of *in situ* populations, ii) understanding the determinants of their effective use and iii) proposing general recommendations for their future use and the setting of new collections. Analysis of data from the French National Cryobank has enabled us to propose several standardized indices for measuring the diversity present in collections at different scales, from the breed to the individual. It has also been shown that the collection effort depends heavily on the species in question, as well as on whether it is accustomed to using artificial insemination. Analysis of a specific case in the Abondance breed, where semen from a bull born in 1977 was re-used between 2004 and 2009, demonstrated the positive impact of using cryopreserved resources on the genetic diversity of *in situ* populations, even when under selection (Jacques et al., 2023). This made it possible to reintroduce genetic variability, as well as to improve certain traits that had deteriorated over time, while limiting the negative impact on production performance, for which a certain lag was expected. This potential of "old" *ex situ* genetic resources has been confirmed in other contexts, by simulating various selection schemes ranging from conservation to selection with changing or unchanging objectives. Whatever the situation, few individuals were used, but this was enough to significantly reintroduce genetic diversity while maintaining the objectives set in each situation. Prolificity, on the other hand, seemed to have little effect on results. Finally, still using simulations, recommendations were made for building up a collection to optimize its use in managing the diversity of *in situ* populations. This was done with a gene bank collection of fixed size to mimic the financial and human limitations inherent in such programs.

This work has therefore provided validation of the long-term usefulness of *ex situ* collections for managing the genetic diversity of *in situ* populations, while also providing recommendations for end-users and managers. These results could be transposed to wild populations in zoos or parks.

Jacques, A., Leroy, G., Rognon, X., Verrier, E., Tixier-Boichard, M., & Restoux, G. (2023). Reintroducing genetic diversity in populations from cryopreserved material: The case of Abondance, a French local dairy cattle breed. *Genetics Selection Evolution*, 55(1), 28. <https://doi.org/10.1186/s12711-023-00801-6>

Landscape Transformation in South-Central Bulgaria (2000–2018)

P. Tomov^{(1)*}

⁽¹⁾ *Agricultural Academy, Institute of Soil Science, Agrotechnologies and Plant Protection “N. Pushkarov”, 7 Bansko shosse, Sofia 1331, Bulgaria*

* *Corresponding author: p.tomov@issapp-pushkarov.org*

Keywords: land use change, land cover mapping, agricultural transformation, landscape dynamics, South-Central Bulgaria

Abstract:

This study examines land use changes in Bulgaria’s South-Central Planning Region from 2000 to 2018, a period marked by post-socialist economic transition and land restitution. The objective was to quantify spatial transformations and identify key environmental and socio-economic trends. CORINE Land Cover data from the European Environment Agency were analyzed at six-year intervals using GIS and statistical methods. Results show a steady decline in mature forest areas, particularly coniferous and broad-leaved types, coupled with an expansion of transitional woodland-shrub formations, reflecting ongoing cycles of deforestation and regeneration. Agricultural land displayed mixed dynamics, with shrinking pastures but expanding vineyards and fluctuating arable areas. Urban and industrial land increased continuously, driven by infrastructure and development pressures. The findings demonstrate how economic restructuring and natural processes have jointly reshaped the regional landscape. This evidence provides valuable guidance for sustainable land management and regional planning in post-transition Bulgaria.

Reference: Comptes rendus de l’Académie bulgare des Sciences, Vol. 78, No. 5, 2025, DOI: 10.7546/CRABS.2025.05.18

Light-Driven Nutritional Quality in Vegetable Protected Cultivation

Nazim S. Gruda^{1,2*}, Giedre Samuolienė^{3,4}

¹ University of Bonn, Bonn, Germany; ²Academy of Sciences of Albania, Tirana, Albania

³ Lithuanian Research Centre for Agriculture and Forestry, Kaunas, Lithuania, and ⁴ Lithuanian Academy of Science

Corresponding author: ngruda@uni-bonn.de

Abstract

Environmental control is central to modern protected cultivation, yet among all growth factors, light is the most decisive driver of nutritional quality in vegetables. Here, we analyze how practical decisions about light intensity, duration (photoperiod), Daily Light Integral (DLI), and spectral composition influence the accumulation of vitamins, minerals, and secondary metabolites in greenhouse-grown vegetables. While temperature, CO₂, and humidity also modulate growth, targeted manipulation of the light environment provides the most precise and energy-efficient lever to enhance produce quality. Specific wavelengths trigger photoreceptors—phytochromes, cryptochromes, phototropins, and UVR8—that regulate photosynthesis, redox status, source–sink allocation, and the biosynthesis of bioactive compounds such as carotenoids, flavonoids, anthocyanins, and phenolic acids.

From a practical standpoint, DLI and intensity set the baseline for photosynthetic carbon supply and antioxidant capacity: raising DLI within crop-specific optima increases vitamin C and phenolics, whereas supra-optimal intensities risk photoinhibition and quality loss. Spectral quality then fine-tunes metabolism: red–blue mixes enhance pigments and antioxidant potential; modest green fractions improve canopy light distribution and can lower nitrates in leafy greens; far-red modulates morphology and carbohydrate partitioning – beneficial in some fruit vegetables, but excessive doses may disrupt flowering/fruit set. UV-A/UV-B pulses upregulate defense pathways and phenolic synthesis without yield penalties when dosed carefully. Photoperiod scheduling is another practical tool for balancing energy use and quality. Continuous or pulsed strategies can maintain photosynthetic efficiency at lower energy cost and align spectral recipes with developmental stages—blue-enriched for seedlings, small green fractions for leafy biomass and mineral balance, and blue/UV-A support during flowering and ripening to bolster flavor and antioxidant profiles.

Integrating spectral management with plant-specific response curves enables real-time, algorithmic control of metabolic pathways that determine the health potential of vegetables. Emerging systems that unite tunable LEDs with canopy sensors, biochemical feedback, and AI control will enable growers to maximize phytonutrient output per kilowatt-hour while increasing yield, making light management a core practical tool in next-generation greenhouse production.

Greenhouse producers should deploy dynamic, spectrum-optimized lighting—centered on a red–blue foundation with crop-specific additions of green, far-red, and UV-A/UV-B—tuned to DLI targets and growth stages, and coupled with real-time monitoring to optimize nutritional quality, yield, and energy efficiency.

Keywords: controlled environment agriculture, greenhouse vegetables, light spectrum, LED technology, photoreceptors, phytonutrients.

Original source:

Gruda, N.S., Samuolienė, G., Li, X., & Dong, J. (2025). Environmental conditions and nutritional quality of vegetables in protected cultivation. *Comprehensive Reviews in Food Science and Food Safety*, e70139. <https://doi.org/10.1111/1541-4337.70139>

Micro-farms and territory: a new model of small agroecological farms in France

Damien Toublant⁽¹⁾

⁽¹⁾ Postdoctoral researcher at UMR TREE – CNRS – University of Pau and Adour Region

Corresponding author: damien.toublant@gmail.com

Keywords: small-scale farms, territory, agroecology, constructivist approach, agricultural and food model

Dominant agricultural model is questioned: soil degradation, loss of biodiversity, dependence on chemical inputs, income crisis and generational renewal blocked. Agroecological transitions are urgent and call for reconsidering the contributions of diverse agricultural models. This study focuses more specifically on small farms and the discreet yet significant innovations of micro-farms in France. Its central aim is to determine whether micro-farms constitute an alternative by offering multiple territorial solutions to complex challenges.

Our geographical, agronomic and socio-anthropological approach opens up a new research field on individual, agricultural and territorial pathways for change. Conducted over ten years and involving 99 farms in the Nouvelle-Aquitaine region, it seeks to identify the characteristic features of this model: practices (archetypal model), aspirations (desired future model) and reference framework (normative model for action).

The study first reviews existing research that contributes to characterise micro-farms, then develops an original methodological approach based on a participatory survey. This survey was implemented within the MicroAgri action-research programme (2017–2020) in Gironde, bringing together researchers, agricultural stakeholders, farmers and local authorities. Farmers were invited to define their identity through a structured set of questions, followed by qualitative interviews to deepen understanding of the social diversity of the group. This collaborative method revealed a much greater heterogeneity than initially expected.

These very small farms, often diversified and committed to agroecology, attract new profiles of farmers. They combine life projects, ecological engagement and territorial embeddedness. Such structures are more accessible to those wishing to establish themselves on a human scale, with better control over costs, labour intensity and the use of inputs. They also help to rebalance the place of women in agriculture.

Behind the term “micro-farm” lies a highly heterogeneous set of situations: from 1,000 square meters of market gardening for a single worker to 70 hectares for four people in mixed crop–livestock systems. Some farms are specialised, while others combine livestock, processing, agroforestry or educational activities. Their legal, economic and human diversity reflects strong adaptation to local contexts: land availability, social networks, markets, territorial culture or economic opportunities. Micro-farms thus appear as deeply rooted territorial constructions. They play an essential social role: creating connections, welcoming citizens, transmitting knowledge and stimulating short supply chains. They are as much places of social experimentation as of agronomic innovation. Ecologically, they develop advanced agroecological practices: reduced tillage, intercropping, autonomy in inputs and energy, frugality, and attention to ecological dynamics.

In conclusion, the study shows that micro-farms outline an agricultural and food model proportionate to a more harmonious balance in human life. This model is expressed in three forms: an archetypal model that gives concrete shape to desires for a change of life; a desired-future model that spreads to initiate a shift towards a peasant agroecological development model; and a normative model for action that experiments to co-construct projects for agricultural and food relocalisation. Supporting any one of these three forms of the micro-farm model means encouraging a network of experiments (farm-places, narrative-places, project-places) that are essential to social, ecological and economic transformations.

Reference : Toublant Damien, *Micro-fermes et territoire : émergence d'un modèle de petites fermes agroécologiques et paysannes en France*, thèse de doctorat en géographie, Université Bordeaux Montaigne, 2024. Français, <https://theses.hal.science/tel-04902795>

Natural Biostimulants Strengthen Tomato Response to Nitrogen Shortage

Monterisi S.¹, Alzate Zuluaga M.Y.¹, Senizza B.², Cardarelli M.³, Rouphael Y.⁴, Colla G.³, Lucini L.², Cesco S.¹, Pii Y.¹

¹Faculty of Agricultural, Environmental and Food Sciences, Free University of Bozen/Bolzano, Piazza Università 1, 39100 Bolzano, Italy

²Department for Sustainable Food Process, Università Cattolica del Sacro Cuore, 29122 Piacenza, Italy

³Department of Agriculture and Forest Sciences, University of Tuscia, Viterbo, Italy

⁴Department of Agricultural Sciences, University of Naples Federico II, Portici, Italy

Corresponding author: stefano.cesco@unibz.it

Improving nitrogen (N) use efficiency in crops is a major challenge in modern agriculture. Farmers often apply large quantities of N fertilizers to maintain yields, but much of this N is lost from the soil, contributing to greenhouse gas emissions, water contamination, and economic inefficiency. Finding sustainable solutions that sustain crops' growth with less N is therefore critical for both food production and environmental protection and is directly aligned with current European agricultural sustainability goals.

This study investigated whether plant-derived biostimulants, specifically a *Malvaceae*-based protein hydrolysate (C) and one of its molecular fractions (F2), can help tomato plants cope with limited N availability. Protein hydrolysates are natural products obtained from plant proteins and are increasingly used in agriculture as biostimulants to improve plant growth, stress tolerance, and nutrient uptake. However, their biological mechanisms and the specific role of different molecular fractions are not well understood, representing a key knowledge gap for their optimized agronomic application.

Tomato plants were grown either under optimal or reduced N supply and periodically sprayed with the unfractionated biostimulant (C), its medium-weight peptide fraction (F2), or with water (control). To understand how these treatments influenced the plants' functioning, the study combined transcriptomics (RNA-seq) and metabolomics, allowing the authors to observe changes in both genes' modulation and metabolic compounds and offering a comprehensive systems-level view particularly valuable for applied crop sciences.

Under optimal N conditions, the C biostimulant modulated genes involved in photosynthesis, stress response, and hormone signalling, suggesting a general strengthening of plant metabolism. Both C and F2 influenced genes linked with plant hormones such as auxins and cytokinins, and with the circadian rhythm, a system that helps plants coordinate growth and stress responses.

Under low N availability, the effects were even more relevant for sustainable agriculture. The biostimulant C activated genes related to N transport, light response, and stress protection, indicating an enhanced capacity to adapt to nutrient shortage. Metabolomic analysis showed that C increased the production of fatty acids, amino acids, and phenolic compounds, all associated with stress tolerance. In contrast, the F2 fraction mostly affected hormonal pathways and had a milder metabolic impact.

When integrating molecular datasets, it was found that C triggered a broader reprogramming of N-related processes, whereas F2 primarily influenced signalling pathways. These findings suggest that the full *Malvaceae*-derived hydrolysate is more effective than its isolated fraction in helping tomato plants use N more efficiently and adapt to low-fertility environments. Although fractionation can facilitate the selection and concentration of peptide groups with specific metabolic targets, this process may also inadvertently remove other bioactive peptide

components, thereby limiting the breadth of molecular pathways that can be modulated. This methodological aspect should therefore be considered when evaluating the comparative performance of whole versus fractionated biostimulants.

Overall, this study demonstrates that plant-based protein hydrolysates can enhance crop resilience while reducing dependency on synthetic fertilizers. Their ability to support tomato growth under N-poor conditions has clear implications for sustainable agriculture, including the possibility of adjusting fertilizer application rates to lower inputs, lower environmental impacts, and improved resource efficiency. In this perspective, the results support strategies consistent with current EU directives promoting reduced-input and environmentally responsible agriculture. Although these results are highly promising, further research is needed to clarify how different biostimulant fractions interact with plant metabolism, identifying key molecular targets and the mechanisms underlying enhanced resilience. Such knowledge is essential for optimizing their effective use in crop management strategies and will be crucial to guide future improvements in their formulation and agronomic deployment, ensuring maximum efficiency within more sustainable farming systems.

Keywords:

Solanum lycopersicum L., Protein hydrolysates, Biostimulant fractionation, RNA-seq, Untargeted metabolomic, Nitrogen deficiency

One Health and agriculture: bridging data gaps to tackle environmental chemical loads

J. Vos^{1,3}, M. Alessandrini¹, M. Trevisan², Y. Pii³, F. Mazzetto^{3,4}, G. Orzes^{4,5}, S. Cesco³

¹Law Group, Wageningen University and Research, Wageningen, The Netherlands

²Department for Sustainable Food Process, Università Cattolica del Sacro Cuore, I-29122 Piacenza, Italy

³Faculty of Agricultural, Environmental and Food Sciences, Free University of Bolzano, Piazza Università 5, 39100 Bolzano, Italy

⁴Competence Center for Plant Health, Free University of Bolzano, Piazza Università 5, 39100 Bolzano, Italy

⁵Faculty of Engineering, Free University of Bolzano, Piazza Domenicani 3, 39100 Bolzano, Italy

Corresponding author: fabrizio.mazzetto@unibz.it

The *One Health* approach seeks to ensure a sustainable balance between the health of people, animals, plants, and ecosystems, recognizing their deep interconnections. Whilst its definition was expanded in 2022 to explicitly include plant health, the agricultural dimension of *One Health* still remains insufficiently developed in practice. This study examines how data gaps and methodological inconsistencies hinder the assessment of the contribution of each domain (*i.e.*, plant, animal and human) to environmental chemical pollution, thereby limiting the design of specific and effective mitigation actions.

Using publicly available datasets from FAO, EUROSTAT, ESVAC, Animal Health Europe and OECD (2010–2020), we compared chemical inputs from agrochemicals, and drugs for and human applications across five EU countries (Italy, Germany, France, Spain and the Netherlands). Data were standardized to kilograms of active substance and normalized by land or residential area to ensure comparability among the plant, animal and human domains.

Results indicate that agriculture is a significant source of environmental chemical inputs, followed by human and veterinary drugs. However, major data limitations persist, particularly for non-antimicrobial veterinary drugs (*animal domain*), over-the-counter human medicines (*human domain*) and emerging (industrial) contaminants such as PFAS or endocrine disruptors. These gaps prevent accurate estimation of total environmental chemical load and the design of targeted mitigation strategies. In the absence of a robust evaluation of the specific contribution of each domain, setting *a priori* limits, such as the EU targets on pesticide or fertilizer reduction, may therefore prove ineffective in achieving the intended objectives. While these objectives are undoubtedly important, they could indeed unintentionally compromise other essential areas, including agricultural productivity (*SDG 12: Responsible Consumption and Production*) and food security (*SDG 2: Zero Hunger*).

Harmonized and transparent data collection across *One Health* domains would therefore enable more precise identification of pollution sources and support evidence-based policymaking. Integrating agricultural professionals (*i.e.*, licensed agronomists, foresters, and animal production specialists) into the *One Health* framework is also crucial to ensure that environmental policies remain compatible with food production and rural sustainability. Moreover, the parallel implementation of precision agriculture, digital monitoring and biotechnological innovation could reduce agrochemical dependence while maintaining productivity.

The work identifies three key priorities for future actions: (i) standardizing national and international data reporting on agrochemicals and medicines; (ii) strengthening cross-sectoral and international regulatory coordination to avoid pollution displacement; and (iii) fostering interdisciplinary collaboration among policymakers, scientists and practitioners. By emphasizing the pivotal role of agriculture within *One Health*, the study contributes to the development of integrated strategies that safeguard ecosystem integrity, food security and public well-being. Ultimately, this approach reinforces the scientific foundation of the EU Green Deal, the Farm-to-Fork Strategy and the UN Sustainable Development Goals, promoting sustainable chemical management and truly integrated vision across all sectors of society.

Keywords:

One Health, agriculture, environmental chemical loads, data standardization, sustainability

Original article:

Vos J, Alessandrini M, Trevisan M, Pii Y, Mazzetto F, Orzes G, Cesco S, 2025. *One Health approach: Addressing data challenges and unresolved questions in agriculture*. Science of the Total Environment, 977, art. no. 179312.

DOI: <https://doi.org/10.1016/j.scitotenv.2025.179312>.

Oxidative stress parameters in water buffaloes supplemented stevia

Radena Nenova⁽¹⁾, Galina Nikolova^{(2)*}, Stanimir Enchev⁽¹⁾, Pencho Penchev⁽¹⁾, Yordanka Ilieva⁽¹⁾, Matthias Schreiner⁽³⁾ & Yanka Karamalakova⁽²⁾

⁽¹⁾ *Agricultural Academy, Agricultural Institute, 9700 Shumen, Bulgaria*

⁽²⁾ *Medical Chemistry and Biochemistry Department, Medical Faculty, Trakia University, 11 Armeiska Str., 6000 Stara Zagora, Bulgaria*

⁽³⁾ *University of Natural Resources and Life Sciences (BOKU), Institute of Food Science, Vienna, Austria*

* Correspondence author: galina.nikolova@trakia-uni.bg ;

Abstract

Objectives: Stevia (*Stevia rebaudiana* Bertoni) is a perennial green plant widely recognized for its intense natural sweetness, primarily derived from the diterpene glycoside stevioside found in its leaves. The extract of Stevia is rich in flavonoids and polyphenolic compounds, including substantial concentrations of chlorogenic acid. This study aimed to evaluate the effects of dietary supplementation with Stevia on the antioxidant status of buffaloes and the principal nutritional composition of their milk. **Methods:** To achieve this objective, a comprehensive assessment and comparative analysis were conducted, encompassing key biochemical parameters, oxidative stress biomarkers, and the concentrations of selected interleukins and cytokines. These measurements were used to determine the systemic impact of Stevia rebaudiana supplementation on oxidative balance and immune modulation in buffaloes. **Results:** The inclusion of Stevia in the buffalo diet did not induce significant changes in the lipid composition of the milk. However, it exerted a pronounced beneficial effect on the animals' oxidative status. Reductions in oxidative damage and pro-inflammatory cytokines, along with a balanced modulation of endothelial (eNOS) and inducible nitric oxide synthase (iNOS) activity, indicated that Stevia rebaudiana supplementation fosters a more favorable redox and inflammatory profile. This integrated physiological response suggests improved endothelial function and enhanced systemic resilience in the supplemented buffaloes.

Keywords: buffaloes; stevia; oxidative stress; ROS; SOD

Predicting plant phenotypes in the context of global change

Keywords: systems genetics, maize, plant breeding, multi-omics, integration

B. Ali ⁽¹⁾, S. Nicolas ⁽¹⁾, M. Blein-Nicolas ⁽¹⁾, M.L. Martin ⁽²⁾, Y. Djabali ^(1,2), T. Mary-Huard ⁽¹⁾, A. Charcosset ⁽¹⁾, L. Moreau ⁽¹⁾, R. Rincent ^{(1)*}

(1) IDEEV, INRAE, GQE - Le Moulon, 12 Rte 128, 91190 Gif-sur-Yvette, France

(2) Université Paris-Saclay, CNRS, INRAE, Université Evry, Institute of Plant Sciences Paris-Saclay (IPS2), 91190 Gif sur Yvette, France

* Corresponding author: renaud.rincent@inrae.fr

In plant breeding, the primary goal is to develop new crop varieties that meet the diverse needs of farmers, processors, and consumers. This endeavour is critical in an era of global change, where agriculture must adapt to reduced inputs and a changing climate. The varieties identified must, for example, be highly adapted or resilient to the specific environmental conditions in which they will be cultivated.

Crop varieties comprise thousands of interacting genes, and their growth and development are influenced by hundreds of environmental factors. As a result, developing a new variety can be a highly complex task. Predictive approaches—integrating knowledge of a variety’s DNA and environmental factors—are essential tools for navigating this complexity. These methods enable breeders to forecast how a given variety will perform in a new environment, even if the variety has never been observed in the field. This capability considerably enhances the speed and screening capacity of plant breeders.

However, the predictive ability of these models remains limited, primarily due to their inability to fully capture the underlying biological processes. In our study (Ali et al. 2025), we introduced novel methods for modelling gene interactions and regulatory mechanisms using gene expression and protein abundance data. By integrating variabilities at the DNA, gene and protein levels, we achieved a 50% improvement in predictive ability compared to the reference model under certain conditions.

Using state-of-the-art statistical models, we also demonstrated that integrating these datasets allowed us to identify far more genetic regions than conventional approaches. Notably, we revealed the substantial contribution of regulatory regions to phenotypic traits and showed that these regions are far more predictive than other regions of the genome.

This work paves the way for the practical application of systems genetics in plant breeding, leading to more accurate predictions and a deeper understanding of the complex biological processes that shape traits of interest. These findings hold significant importance for both fundamental, and applied research in particular in the field of plant breeding in the context of global change. They also have practical implications for guiding varietal recommendations to farmers, taking into account local pedoclimatic conditions.

Ali B, Nicolas S, Blein-Nicolas M, Martin ML, Djabali Y, Mary-Huard T, Charcosset A, Moreau L, Rincent R (2025) Unravelling the Genetic Architecture of Field Traits through Multi-Omics Platform Data integration. Biorxiv.
doi:<https://doi.org/10.1101/2025.10.27.684747>

Protected Cultivation as a Pathway to Nutrient-Rich Vegetables

NS Gruda^{123*}, VM Gallegos-Cedillo¹, C Nájera⁴, C Egea-Gilabert¹, J Ochoa¹, JA Fernández¹

¹ Department of Agronomical Engineering, Technical University of Cartagena, Cartagena, Spain

² Department of Horticultural Sciences, Institute of Crop Science and Resource Conservation, University of Bonn, Germany, ³Academy of Sciences of Albania, Tirana, Albania

³ Department of Agronomy, University of Almería, Almería, Spain

* Corresponding author: ngruda@uni-bonn.de

Abstract

Protected cultivation has become a cornerstone of sustainable agricultural intensification, enabling stable production of nutrient-rich vegetables despite climate variability and resource constraints. Greenhouse-grown vegetables already account for more than 60% of the global market value, offering improved productivity, quality, and a year-round supply.

Here, we analyze how agrotechnological innovations and cultural practices can enhance the nutritional profiles of vegetables within protected environments. Our bibliometric analysis revealed a surge in research over the last decade. Although each category began with a similar number of publications in 2014 (around eight), their trajectories diverged markedly over the following decade. Articles published between 2014 and 2024 revealed striking growth trends: studies on environmental conditions increased by about 8.8-fold. However, those on agrotechnological innovations increased by more than 32-fold, and on cultural practices by nearly 9.5-fold, presenting a high potential for improving nutritional quality.

Practices such as biofortification, controlled eustress, deficit irrigation, grafting, biostimulant use, and precision nutrient management have demonstrated strong correlations ($R^2 = 0.97\text{--}0.98$) with improved levels of vitamins, minerals, and bioactive compounds. These techniques influence plant metabolism by regulating stress-responsive pathways, enhancing nutrient uptake, and stimulating the biosynthesis of secondary metabolites. Additionally, optimized harvest timing and crop-specific adaptation further stabilize nutrient density and quality. These approaches redefine protected cultivation as an integrated, knowledge-based production system that combines productivity, sustainability, and nutritional security.

Coordinated innovation in agronomy and technology transforms protected cultivation from yield-oriented systems into nutrition-centered ones. By aligning physiological mechanisms with sustainable management practices, producers can achieve nutrient-dense crops without compromising yield or environmental efficiency. Future progress will depend on integrating digital monitoring, AI-assisted decision-making tools, and genotype-specific models to fine-tune cultivation strategies that enhance both nutritional value and resource-use efficiency.

Practical recommendation: Researchers, growers, and policymakers should strengthen interdisciplinary collaboration to advance nutrition-oriented protected cultivation. Promoting scalable solutions such as eustress management, biofortification, and sustainable agrotechnologies will support global efforts to combat hidden hunger and ensure resilient food systems.

Keywords: protected cultivation, nutritional quality, biofortification, eustress, sustainable innovation

Original source: Gruda, N.S., Gallegos-Cedillo, V.M., Nájera, C., Egea-Gilabert, C., Ochoa, J., & Fernández, J.A. (2025). *Advancing Protected Cultivation: A Pathway for Nutrient-Rich Vegetables*. *Critical Reviews in Plant Sciences*, 44(2), 88–116. <https://doi.org/10.1080/07352689.2025.2515801>

Research Regarding the Carbon Balance in Agricultural Farms

R. Neamt^{(1)*}, N. Dragomir⁽¹⁾, F. Neciu⁽¹⁾, Ghe. Saplacan⁽¹⁾, C. Mihali⁽¹⁾, A. Mizeranschi⁽¹⁾, A. Anton⁽¹⁾, L. Cziszter^(1,2)

¹*Animal Breeding Technologies Department, Research and Development Station for Bovine, Arad, Romania, Calea Bodrogului, no. 32, CP 310059*

²*Department of Animal Production Engineering, University of Life Sciences "King Mihai " from Timisoara, Romania, Calea Aradului, no. 119, CP 300645*

*Corresponding author: neamtr@yahoo.com

The aim of this study was to assess the carbon balance in an agricultural farm, with the aim of establishing the share of returned carbon to the atmosphere. Often accused of being responsible for pollution, agriculture was placed in second place with a weight of 24-30% of total carbon emissions. However, the agricultural activity by its specificity has the ability to capture a large part of the carbon produced (both directly and indirectly), compared to other domains such as transport, construction or the energy sector (based on fossil consumables) which do not have this capacity, the entire amount of carbon generated being eliminated in the atmosphere.

In this respect, 9 fodder crops were investigated, which constitute the fodder base for an average herd of 800 Simmental dairy cows. The amounts of raw carbon fixed by photosynthesis above and below ground, the amounts of raw carbon eliminated in the atmosphere by the physiological processes of plants, as well as the net amounts of carbon fixed by plants were evaluated.

The average proportion of net carbon fixed by plants was 75.6% (19460 kg CO₂ eq/ha), only 24.4% (6306 kg CO₂ eq/ha) of the total amount of carbon was removed as a carbon footprint. Of the total of 75.6% of net fixed carbon, 37% (7200 kg CO₂ eq/ha) was fixed underground, without a determining role in establishing the carbon footprint. The study highlighted that the straw plants release into the atmosphere between 13.7% (3455 kg CO₂ eq/ha) for the wheat crop and 21% (4531 kg CO₂ eq/ha) for the barley crop of the total fixed raw carbon. By comparison, the corn crop, according to its destination, release 19% (2236 kg CO₂ eq/ha) for the grain crop and 21.6% (2404 kg CO₂ eq/ha) for the silage crop. Alfalfa release 26% (13015 kg CO₂ eq/ha) of the total carbon, but it should be mentioned that due to the developed root system 65% (8459 kg CO₂ eq/ha) of the total carbon is fixed above ground and therefore immobilized. Perennial grasses remove the largest share of carbon, 28% (10464 kg CO₂ eq/ha), a fact for which the reduction of this percentage can be done through mixed cultivation with alfalfa. The studies highlighted a significant reduction ($p \leq 0.05$) in terms of the amount of carbon eliminated up to the threshold of 23% (9940 kg CO₂ eq/ha).

The amount of net sequestered C in the soil exerts a significant role on the efficiency of the farm's activity, given that each ton of sequestered carbon represents a carbon credit, at a current average price of around 65 euros/credit.

In conclusion, agriculture allows the release into the atmosphere of an average percentage of 24% of the total amount of associated carbon, a condition in which it cannot be considered a real threat compared to domains such as transport or construction or some branches of industry.

Keywords: agriculture, carbon, crops, farms, pollution

Source of the abstract: Research Regarding the Carbon Balance in Agricultural Farms.

Neamt Radu, Dragomir Neculai, Neciu Florin, Saplacan Gheorghe, Mihali Ciprian, Mizeranschi Alexandru, Anton Andreea, Cziszter Ludovic. 2nd Edition of Plant Science and Molecular Biology Conference PMBWC 2025, October 19 to 21, 2025, Paris, France

Smart Irrigation and Water Management Strategies in Eastern European Viticulture

A.C. Florea⁽¹⁾, D.I. Sumedrea^{(1)*}, S. Rodino^(2,3), M. Ion⁽⁴⁾, V. Dragomir⁽²⁾, A.-M. Dumitru⁽¹⁾, L. Pîrcalabu⁽⁴⁾ & D.G. Dinu⁽¹⁾

⁽¹⁾National Research and Development Institute for Biotechnology in Horticulture Stefanesti - Arges, 37 Bucharest - Pitesti Road, 117715 Stefanesti, Arges Co., Romania

⁽²⁾Research Institute for Agriculture Economy and Rural Development, 61 Marasti Boulevard, Sector 1, 011464 Bucharest, Romania

⁽³⁾National Institute of Research and Development for Biological Sciences, 296 Splaiul Independenței, sector 6, 060031 Bucharest, Romania

⁽⁴⁾Research and Development Institute for Viticulture and Enology, 2 Valea Mantei, 107620 Valea Calugareasca, Prahova Co., Romania

*Corresponding author: dsunedrea@yahoo.com

Keywords: climate change, viticulture, Eastern Europe, smart irrigation, water stress

Abstract

The objective of this study was to synthesize and analyze the impact of climate change on viticulture in Eastern Europe by assessing the phenological advance, grape quality and production, as well as the onset and intensification of water stress in the wine-growing regions of Romania, Bulgaria, Hungary, Poland and the Republic of Moldova. In parallel, based on scientific articles and regional reports published to date, the study aimed to update data on the evaluation of modern irrigation technologies and smart water management approaches, such as Research, Development and Innovation (RDI), real-time monitoring and automated systems, as well as integrating the relevant European and national legislative framework to highlight how current regulations support the adoption of these solutions. The article is based on a systematic review of scientific literature published mainly in the last decade, the selection being supported by a bibliometric analysis performed in the Web of Science database, to identify the main research trends and relevant contributions on the impact of climate change on viticulture and water management strategies in Eastern Europe. Regional data reported so far have shown a 1 to 3-week phenological shift in Romania (Iași, Ștefănești, Oltenia, Târnave), accompanied by increased sugar concentrations (+15–25g/L) and reduced total acidity. In Bulgaria and Hungary, similar patterns were associated with a shortened growing season and the need for intensified irrigation. In Poland, climate warming allowed the expansion of viticulture to higher altitudes and more northern latitudes, but generated a significant water deficit in the period June–August, necessitating additional irrigation. In the Republic of Moldova, the main wine-growing regions (Valul lui Traian, Codru) are strongly affected by drought and sugar-acid imbalances, leading to the adoption of computerized irrigation systems based on sensors and renewable energy sources. Modern irrigation in Eastern Europe is increasingly supported by sensor-based systems and renewable energy sources, providing the technological infrastructure necessary for the effective implementation of RDI. Regional data highlight the effective application of RDI in Romania (Dealul Mare, Valea Călugărească, Oltenia, Târnave), Hungary (Tata, Tokaj), Poland (vineyards affected by summer drought) and the Republic of Moldova (Valul lui Traian, Codru), where controlled water deficit contributed to improved grape quality and increased water use efficiency. In all five countries, RDI has been reported to have positive effects on sugar and phenolic content, berry quality and water use efficiency, without reducing yield when applied correctly. By updating the most relevant regional publications and integrating the results reported in recent studies, the article provides a comprehensive and up-to-date perspective on the main climate-related challenges facing Eastern European viticulture and on the irrigation technologies currently used, thus strengthening the knowledge base needed to develop sustainable climate change adaptation strategies.

Source of the abstract: Florea A.C., Sumedrea D.I., Rodino S., Ion M., Dragomir V., Dumitru A.-M., Pîrcalabu L., Dinu D.G. (2025). The Impact of Climate Change on Eastern European Viticulture: A Review of Smart Irrigation and Water Management Strategies. *Horticulturae*, 11(11), 1282. DOI: <https://doi.org/10.3390/horticulturae11111282>.

Supporting agroecological transition: pathway and tools for farmers' collectives

A, ALAPHILIPPE^{(1)*}, S. BATARD⁽¹⁾, C. RENAUD-GENTIÉ⁽²⁾ & S. DERNAT⁽³⁾

⁽¹⁾ INRAE UERI Gotheron, 460 chemin de Gotheron, 26320 Saint-Marcel-lès-Valence, France

⁽²⁾ USC INRAE GRAPPE, Ecole Supérieure d'Agricatures (ESA), 55 rue Rabelais, 49007 Angers, France

⁽³⁾ UMR Territoires, Université Clermont Auvergne, INRAE, AgroParisTech, VetAgro Sup, 63170 Aubière, France

* Corresponding author: aude.alaphilippe@inrae.fr

Keywords: Support pathway; toolbox; farmers' collective, agroecological transition; perennial crop

Fruit and grapevine productions historically rely on frequent pesticide applications, creating strong pressure to redesign cropping systems. The agroecological transition requires more than just replacing one input with another: it entails coordinated changes in farming techniques, learning dynamics and governance. Farmers' collectives play a crucial role in this transition by providing spaces for knowledge exchange, experimentation and mutual support. Yet advisors need specific methods and tools to support these groups plan ahead, evaluate trade-offs, and make informed choices.

The Vitarbae project addresses this challenge by developing a modular support pathway for farmers' collectives. This pathway includes a toolbox of serious games, multicriteria assessment tools and knowledge platforms to foster collective learning. The goal is to enable farmers to co-design farming systems combining agroecological practices that reduce pesticide use without shifting burdens to other environmental impacts or increasing costs. The project therefore aims to empower advisors to guide farmers in designing agroecological practices tailored to their local conditions and to integrate game-based learning with multicriteria assessments, helping farmers explore and compare different strategies before implementation. The project consists in three partially overlapping actions:

1. Inventory and needs analysis: survey of existing tools (serious games, environmental/economic assessment tools, knowledge platforms) and analysis of advisor practices to identify gaps and opportunities through a national online survey of advisors and qualitative interviews;
2. Toolbox development: assembly of a set of serious games and assessment tools, clarification of intended uses and interconnections, and provision of guidance;
3. Pathway co-development and testing: formalisation of its stages, feedback loops and decision points, and test of connections with the toolbox tools.

A centralised web platform will host all resources.

The needs analysis underlined requirements for accessibility, adaptability and clear sequencing of the pathway. We created a flexible six-step pathway, from the training of the farmers' collective and problem identification to system design and testing, with feedback loops for continuous improvement as understanding deepens. The resulting pathway allows advisors to tailor support to each group's specific needs, making it suitable for local transition initiatives and training programs. In parallel, co-development with partners has improved the operability of the tools, while linking the games to assessment tools allows farmers to evaluate strategies holistically, considering environmental, economic, and social impacts. Effective adoption, however, requires high-quality facilitation, advisor training and regular updates to maintain relevance.

The Vitarbae project provides a practical and scalable framework for supporting agroecological transitions in fruit and grapevine productions. It clarifies how serious games and assessment tools can be embedded within advisory sequences to couple social learning with multicriteria reasoning. It points to shifts in advisors' posture, from expert prescription to facilitation of peer-to-peer learning, fostering innovation within farmers' collectives. By equipping farmers and advisors with the appropriate tools and knowledge, it paves the way for more sustainable agriculture, while opening research avenues on how to adapt and transfer successful practices between different regions and production systems.

This project was supported by the French Office for Biodiversity, Ecophyto II+ plan.

<https://ueri.paca.hub.inrae.fr/thematiques-de-recherche/outils-et-accompagnement-a-l-agroecologie/projet-vitarbae>

Survey of several spoilage agents in Moldovan wines

I. Mitina⁽¹⁾, C. Grajdieru^{(1)*} & D. Zgardan⁽²⁾*(1) Department of Molecular Genetics, Institute of Genetics, Physiology and Plant Protection of Moldova State University, 20 Padurii street, Chisinau, Republic of Moldova**(2) Department of Oenology and Chemistry, Faculty of Food Technology, Technical University of Moldova, 168 Stefan cel Mare boulevard, Chisinau, Republic of Moldova***Corresponding author: cristina.grajdieru@sti.usm.md*

Keywords: wine, PCR, Brettanomyces, Acetobacter, sequencing

Certain bacterial and fungal species produce a wide range of secondary metabolites, which cause olfactory defects in wines and therefore are considered undesirable microbiota by winemakers. *Acetobacter aceti* and *A. pasteurianus* belong to the group bacteria that can convert ethanol into acetic acid, the latter contributing to wine's volatile acidity. These *Acetobacter* species are found at all stages of winemaking, being a part of the natural microbial consortia on grape berry surfaces together with other acetic acid bacteria (AAB). During the later stages of winemaking, *A. aceti* and *A. pasteurianus* dominate in mature wines since they are more tolerant to higher ethanol content compared to other related species. Other common spoilage agent in wines is *Brettanomyces bruxellensis* – ubiquitous yeast that is the most studied representative species found in almost every wine-producing area of the world with the highest spoilage potential among other *Brettanomyces* species. It causes wine spoilage by producing volatile phenols, which contribute to unpleasant aroma. For a long time, *Brettanomyces* was considered to be the issue of mature wines associated with poor sanitary practices in cellars. It was not until 2007 that the presence of *B. bruxellensis* on the grape berry surface was clearly demonstrated, thus this spoilage agent also being a natural part of grape microbiota. Assessing the propagation of *Acetobacter* and *Brettanomyces* via conventional methods is challenging since they are able to enter a viable but non-culturable state and not all media support their growth. One of the key steps in effective control strategies of these spoilage agents is their timely and precise detection starting with the initial stages of winemaking.

Molecular assays used in this study for detecting and monitoring wine spoilage agents demonstrated that *Brettanomyces* concentrations varied in different wine samples of the same vintage, highlighting the importance of the wine matrix and wine-making techniques in the suppression of *Brettanomyces* growth. For the first time, several *Brettanomyces* isolates from local Moldovan wines produced in a micro-winery were sequenced. The sequencing analysis revealed a polymorphism in the sequenced DNA fragment from *B. bruxellensis* isolates from different wines. This confirms the potential of sequencing analysis in tracing the contamination source. Regarding *Acetobacter* contaminants in wines, it was stated that the dynamics of *A. pasteurianus* showed a higher infection level in musts and wines, and more samples were infected with these bacteria. Contrary to expectations, in this study, *A. aceti* did not have a major effect on wine volatile acidity. Monitoring of AAB, especially *A. pasteurianus*, at different stages of wine production could help in forecasting the increase in the volatile acidity of mature wines. Apparently, the presence of solely *A. pasteurianus* in must and wine contributes significantly to wine volatile acidity. This species could be a potential predictor of increases in wine volatile acidity.

Detailed results can be consulted in the following paper:

Mitina, I.; Grajdieru, C.; Sturza, R.; Mitin, V.; Rubtov, S.; Balanuta, A.; Behta, E.; Deaghileva, A.; Inci, F.; Hacıosmanoğlu, N.; et al. Molecular Detection of *Acetobacter aceti* and *Acetobacter pasteurianus* at Different Stages of Wine Production. *Foods* 2025, 14, 132.

<https://doi.org/10.3390/foods14010132>

Tackling Weaning Stress in Dairy Calves Using Cannabidiol Oil Supplementation

M. Enculescu ⁽¹⁾, I. Nicolae ⁽¹⁾ & D. Gavojdian ^{(1)*}

⁽¹⁾ *Research and Development Institute for Bovine, 077015, Balotesti, Romania*

* *Corresponding author: gavojdian_dinu@animalsci-tm.ro*

Abstract

This study evaluated the effects of cannabidiol (CBD) oil supplementation on growth performance, stress biomarkers, and haematological profiles in dairy calves undergoing the weaning transition. Nineteen Holstein calves were divided into two paternal-sibling groups: a CBD-supplemented experimental group (n = 10) and a CON-control group (n = 9). The CBD group received 5 mL/head/day of CBD oil for the first two days (pre-weaning), followed by 10 mL/head/day for three consecutive days post-weaning. Body weight increased significantly over time in both groups (p = 0.000); nevertheless, no significant differences were observed between groups (p = 0.173) or for the group × time interaction (p = 0.929), indicating that CBD did not affect overall growth trajectory. However, a significant group × time interaction (p = 0.006) for average daily gains in the CBD group was observed. Serum cortisol concentrations were significantly lower in CBD-supplemented calves at Day 0 and +2 days, compared to the CON group, indicating a transient anti-stress effect (p = 0.043 for group effect). At +5 days, cortisol levels in the CBD group increased, surpassing control values, though this difference was not significant. A trend-level group × time interaction (p = 0.067) suggested a distinct temporal cortisol response in CBD-treated calves. Immune cell counts (LYM, MON, NEU) showed no significant differences, though monocyte levels trended lower in CBD calves at early time points. Platelet indices revealed a significant reduction in mean platelet volume (p = 0.047) and stable PDWc and plateletcrit values in the CBD group, suggesting modulation of inflammatory status. Alanine aminotransferase levels increased over time with a significant group effect (p = 0.014), indicating a mild hepatic response, while glucose and alkaline phosphatase remained within physiological ranges. These findings suggest that short-term CBD supplementation may transiently modulate stress and inflammatory responses during weaning, with potential benefits for physiological resilience. However, rebound endocrine effects and hepatic sensitivity highlight the need for further research to refine dosing strategies and assess long-term safety in dairy production systems.

Keywords

dairy calves; weaning stress; cannabidiol; serum cortisol; average daily gain

Source of the Abstracts

Enculescu, M.; Nicolae, I.; Gavojdian, D. Tackling Weaning Stress in Dairy Calves Using Cannabidiol Oil Supplementation. *Dairy* 2025, 6, 54. <https://doi.org/10.3390/dairy6050054>

The affinity of vascular plants and bryophytes to forest microclimate buffering

E. Gril^{(1)*}, Fabien Spicher⁽¹⁾, Alain Vanderpoorten⁽²⁾, Emilie Gallet-Moron⁽¹⁾, Boris Brasseur⁽¹⁾, Vincent Le Roux⁽¹⁾, Marianne Laslier⁽¹⁾, Guillaume Decocq⁽¹⁾, Ronan Marrec⁽¹⁾, Jonathan Lenoir⁽¹⁾

⁽¹⁾UMR CNRS 7058 "Ecologie et Dynamique des Systèmes Anthropisés" (EDYSAN), Université de Picardie Jules Verne, Amiens, France

⁽²⁾ Botany Institute, University of Liège, Liège, Belgium

*Corresponding author: evagril.science@gmail.com

Keywords:

managed forest; microclimate buffering; temperature extremes; species response curves; understory floristic communities

Abstract:

With recent advances in technology and modelling, ecologists are increasingly advised to use microclimate, not the usual coarse-scale macroclimate based on weather stations, to better reflect the proximal conditions that species experience. This is especially relevant in forest ecosystems, where natural disturbances and forest management create substantial heterogeneity in microclimates. Under dense canopies, species experience buffered (less extreme) microclimate temperatures relative to macroclimate, as well as increased relative humidity, reduced light and wind.

Focusing on understory plants, we investigated species response curves to the buffering capacity of the canopy layer, measured as the log-transformed slope parameter of the microclimate to macroclimate linear relationship. If lower or higher than zero, microclimate temperatures are buffered or amplified, respectively, relative to macroclimate.

During leaf-on conditions (July-September 2021), we measured hourly microclimate temperatures in 157 plots across three temperate deciduous forests with different macroclimates in France. We used paired hourly macroclimate measurements from nearby weather stations to derive the slope parameter, quantifying microclimate buffering.

We surveyed both vascular plant and bryophyte communities in 400 m² plots centred on our microclimate sensors. Species were classified into three groups of forest affinity: forest core specialists; edge specialists; and generalists. We fitted generalized linear mixed-effects models, by forest affinity group and then by species, to obtain logistic response curves of the probability of occurrence against microclimate buffering. The species' microclimate optimum was computed as the microclimate effect that maximizes its probability of presence.

We found contrasted microclimate preferences: most bryophytes as well as the vascular plants classified as forest core specialists had an optimum in microclimate buffering (less extreme temperature fluctuations relative to macroclimate), while forest edge specialists and generalists among vascular plants had an optimum in microclimate amplification. For bryophytes as well as vascular plants, the more thermally buffered the forest, the higher the proportion of core specialists.

Assessing plant responses and vulnerability to forest management and climate change is an objective shared by many ecologists and conservationists, and our results confirm that forest microclimates are key to that endeavour. As canopies undergo increased disturbance frequency and

intensity with climate change, more generalists and less forest core specialists might be expected within understory communities, especially for bryophytes. Augmenting forest cover and limiting canopy openings could counterbalance the negative impacts of climate change on these specialists. At the landscape scale, a mosaic of buffered and amplified microclimates may be the best option to promote forest biodiversity, by accommodating species across the whole microclimate gradient. Overall, we demonstrated that understory plants have a species-specific affinity to forest microclimate buffering, for which we provide the first quantitative index, that goes beyond an assignment to the discrete and expert-based classes of forest generalist or specialist. The investigation of species response curves to microclimate processes – buffering or amplification – can improve our understanding of the ecology of understory plants, and help us anticipate their redistribution under climate change.

Scientific Publication:

Gril, E., Spicher, F., Vanderpoorten, A., Gallet-Moron, E., Brasseur, B., Le Roux, V., Laslier, M., Decocq, G., Marrec, R., Lenoir, J., 2025. The affinity of vascular plants and bryophytes to forest microclimate buffering. *Journal of Ecology* 113, 22–38. <https://doi.org/10.1111/1365-2745.14425>

The Hidden Burden Limiting Europe's Agricultural Performance

Daniel Petrov^{1*}

¹ *Institute of Agricultural Economics – Sofia,*

Department of Economics and Management of Agricultural and Rural Organizations,

125 Tsarigradsko shosse Blvd., Sofia, Bulgaria

*Corresponding author: dpetrov.iae@gmail.com

Across Europe, farmers consistently report the same struggle: it is not only the weather, markets or technology that challenge them, but the growing number of tasks they must juggle every single day. Managing several crops with different biological needs, coordinating machinery, handling paperwork, meeting environmental requirements, organizing rented land and implementing new technologies - these tasks accumulate and compete for time and attention. Yet this combined functional burden has never been measured or examined as a structural factor shaping agricultural performance. This study addresses this gap by analyzing how the accumulation of these tasks affects the capacity of European agriculture to remain productive, competitive and sustainable. The purpose of this research is to quantify functional fragmentation—the extent to which farmers must perform multiple biological, technological, managerial and administrative functions simultaneously, and to assess how it influences agricultural outcomes across the European Union. Using harmonized data for all Member States over a twenty-year period, the study develops a new metric that captures how these diverse functions interact and how their combined weight affects productivity, yields and incomes. The findings are clear and consistent across countries. Agricultural sectors where farmers face heavier and more complex sets of tasks systematically achieve lower yields, lower productivity and lower competitiveness. This holds even in technologically advanced and well-governed systems. In other words, when everyday farming becomes too fragmented and operationally demanding, structural pressures inside the system can quietly erode performance. This suggests that internal functional overload may be an overlooked but critical determinant of agricultural outcomes in Europe. The applied implications are substantial. Reducing functional overload - through simpler administrative procedures, clearer regulations, better-coordinated policies and improved farm organization, may be one of the most effective and cost-efficient ways to enhance the competitiveness of European agriculture. Unlike capital-intensive interventions, reducing unnecessary complexity requires limited investment while immediately strengthening farmers' ability to adopt sustainable practices, manage risks and respond to changing market and climatic conditions. The environmental and food-system benefits are equally notable. When farmers face fewer conflicting tasks, they gain time and flexibility to invest in soil health, biodiversity protection, precision agriculture and long-term resource stewardship. Easing structural pressures therefore contributes not only to stronger economic performance but also to more resilient and environmentally responsible farming systems. By revealing a structural factor that has remained largely invisible in policy discussions, this research offers a new perspective on agricultural performance in Europe. It provides a practical framework for policymakers seeking farmer-centred and efficient system-level solutions aligned with the broader strategic direction of the Common Agricultural Policy. Addressing functional fragmentation can reinforce the foundations of agricultural competitiveness and strengthen the sector's ability to deliver economic, social and environmental outcomes. In doing so, it sheds light on the hidden forces that shape the future resilience of European agriculture.

Key words: Functional fragmentation, Agricultural competitiveness, Structural determinants, Farm-level complexity, Common Agricultural Policy

Reference: JURNAL EKONOMI MALAYSIA, published by Penerbit UKM, Universiti Kebangsaan

The potential of biochar to reduce carbon emissions from organic fertilizers

L. Verdi ^{(1)*}, A. Dalla Marta ⁽¹⁾, S. Orlandini ⁽¹⁾, A. Maienza ⁽²⁾, S. Baronti ⁽²⁾, F. P. Vaccari ⁽²⁾

⁽¹⁾ Department of Agriculture, Food, Environment and Forestry (DAGRI), University of Florence, Piazzale delle Cascine 18, 50144 Florence, Italy

⁽²⁾ Institute of BioEconomy (IBE), National Research Council (CNR), Via Madonna del Piano 10, Sesto Fiorentino, 50019 Florence, Italy

* Corresponding author: leonardo.verdi@unifi.it

The agricultural sector faces increasing awareness regarding its environmental footprint, particularly concerning the contribution of animal waste storage and management to global greenhouse gas (GHG) emissions. These emissions, primarily carbon dioxide (CO₂) and methane (CH₄), directly challenge the sustainability of livestock production systems. Traditional storage practices for animal wastes create ideal conditions for microbial activity that releases GHGs into the atmosphere. Developing innovative and scalable mitigation strategies is paramount for transitioning toward low-carbon agriculture. This study investigated the effectiveness of biochar addition as a practical and effective strategy to minimize CO₂ and CH₄ emissions arising from different common animal waste substrates. Three distinct types of animal waste were selected for evaluation: liquid digestate (post-anaerobic digestion), conventional slurry, and solid manure. The experiment was designed to compare the GHG fluxes from each substrate in its original, untreated form versus its form amended with biochar. Emissions were rigorously monitored over a 21-day incubation period utilizing the static chamber methodology coupled with a high-precision portable gas analyzer. The biochar was incorporated into the substrates at a specific ratio of 2:1 (substrate to biochar, on a mass basis), aiming to maximize the surface area contact and adsorption potential of the amendment. The results demonstrated a clear effect of biochar that substantially reduced the emissions of both CO₂ and CH₄ across all three substrates compared to their untreated counterparts. The highest overall emissions were observed in the slurry treatment, confirming its high potential for gas release. In slurry, biochar addition achieved notable reductions since CO₂ and CH₄ emissions decreased by 26% and 21%, respectively. However, the most pronounced effect of the biochar was seen in the digestate treatment. Here, the addition of biochar led to a remarkable decrease in gaseous fluxes, resulting in a 45% reduction for CO₂ and a 78% reduction in CH₄. This higher performance suggests a strong synergistic interaction between biochar and the complex composition of the digestate. Even for solid manure, which inherently exhibited a lower tendency to emit carbon-based gases, biochar proved highly effective. The amendment caused relevant decreases in CO₂ emissions (40%) and an impressive reduction in CH₄ emissions (81%). This highlights biochar's versatility as an effective amendment across different waste consistencies. To quantify the overall environmental benefit, the emission reductions were translated into a decrease in Global Warming Potential (GWP), a standardized measure integrating the radiative forcing of CO₂ and CH₄. Biochar successfully reduced the environmental impacts of the treatments, achieving a GWP reduction of 55% for digestate, 22% for slurry, and 44% for manure. The findings demonstrate that incorporating biochar into animal waste management practices is a powerful and viable strategy for mitigating agricultural GHG emissions. Given the significant reductions in CH₄, the use of biochar represents a critical step toward creating climate-smart organic fertilizers. Future research should focus on optimizing the biochar inclusion rate and exploring the long-term effects on nutrient retention and soil health when these amended wastes are applied to agricultural land.

Keywords

Digestate; Slurry; Manure; Methane; Global Warming Potential

Reference: Verdi, L., Dalla Marta, A., Orlandini, S., Maienza, A., Baronti, S., & Vaccari, F. P. (2024). Evaluation of biochar addition to digestate, slurry, and manure for mitigating carbon emissions. *Agriculture*, 14(1), 162.

Two decades of Field trials of ‘HoneySweet’ transgenic plum resistant to plum pox

I. Zagrai^{(1)*}, L.A. Zagrai⁽¹⁾, M. Ravelonandro⁽²⁾, R. Scorza⁽³⁾, C. Dardick⁽⁴⁾, N. Minoiu⁽¹⁾, P. van der Meer⁽⁵⁾

⁽¹⁾Fruit Research & Development Station Bistrita, 3, Drumul Dumitrei Nou, 420127, Bistrita, Romania

⁽²⁾Institut National de la Recherche Agronomique et Environnement Bordeaux, France,

⁽³⁾Ralph Scorza LLC, Shepherdstown, WV USA (formerly USDA-ARS-AFRS), USA;

⁽⁴⁾USDA-ARS Appalachian Fruit Research Station, Kearneysville, West Virginia, USA;

⁽⁵⁾Department of Biotechnology, Faculty of Bioscience Engineering, Ghent University, Belgium

*Corresponding author: izagrai@yahoo.com

Abstract

‘HoneySweet’ is the first transgenic plum resistant to *Potyvirus plumipoxi* (plum pox virus – PPV) via an RNA interference (RNAi) mechanism. Initiated with testing under confined greenhouse conditions, challenge assays were then moved to the field. Long term field trials (1996-2018) were conducted to test virus resistance in a PPV endemic area in Bistrita, Romania. Overall results revealed a high level of resistance to PPV infection as well as good agronomic performance that make ‘HoneySweet’ efficacious to PPV endemic areas and environmental conditions in Romania. In addition, field trials clearly demonstrated no effect of transgenic plums carrying the PPV-CP gene on the diversity of PPV variants and non-target organisms (aphids, bees). Benefits from the use for the environment and the agronomic performance demonstrated the potential for ‘HoneySweet’ to be an integral part of Integrated Pest Management programs to reduce the impacts of pesticide use on environment and health. Presently, the next challenge to practical application of utilizing the resistance mechanism of ‘HoneySweet’ is obtaining approvals for cultivation and consumption in the European Union countries, and in particular those highly affected by PPV. In the meantime, a new approach is developed to use the RNAi mechanism to obtain and test male sterile plum hybrids resistant to PPV.

Keywords: agronomic performance, genetic modification, PPV, resistance, safety assessment

Acta Horticulturae, <https://doi.org/10.17660/ActaHortic.2025.1439.43>

GRAPHICAL ABSTRACTS

Comparison Between Some Plant Fluids and the Human Blood

A. Sotirov⁽¹⁾ & S. Yordanov⁽²⁾

⁽¹⁾*Institute of Agriculture-Kyustendil, Agricultural Academy, Sofa, Bulgaria*

⁽²⁾*National Center of Infectious and Parasitic Diseases (NCIPD), Sofa, Bulgaria*

Corresponding author: a_sotir@iz-kyustendil.org

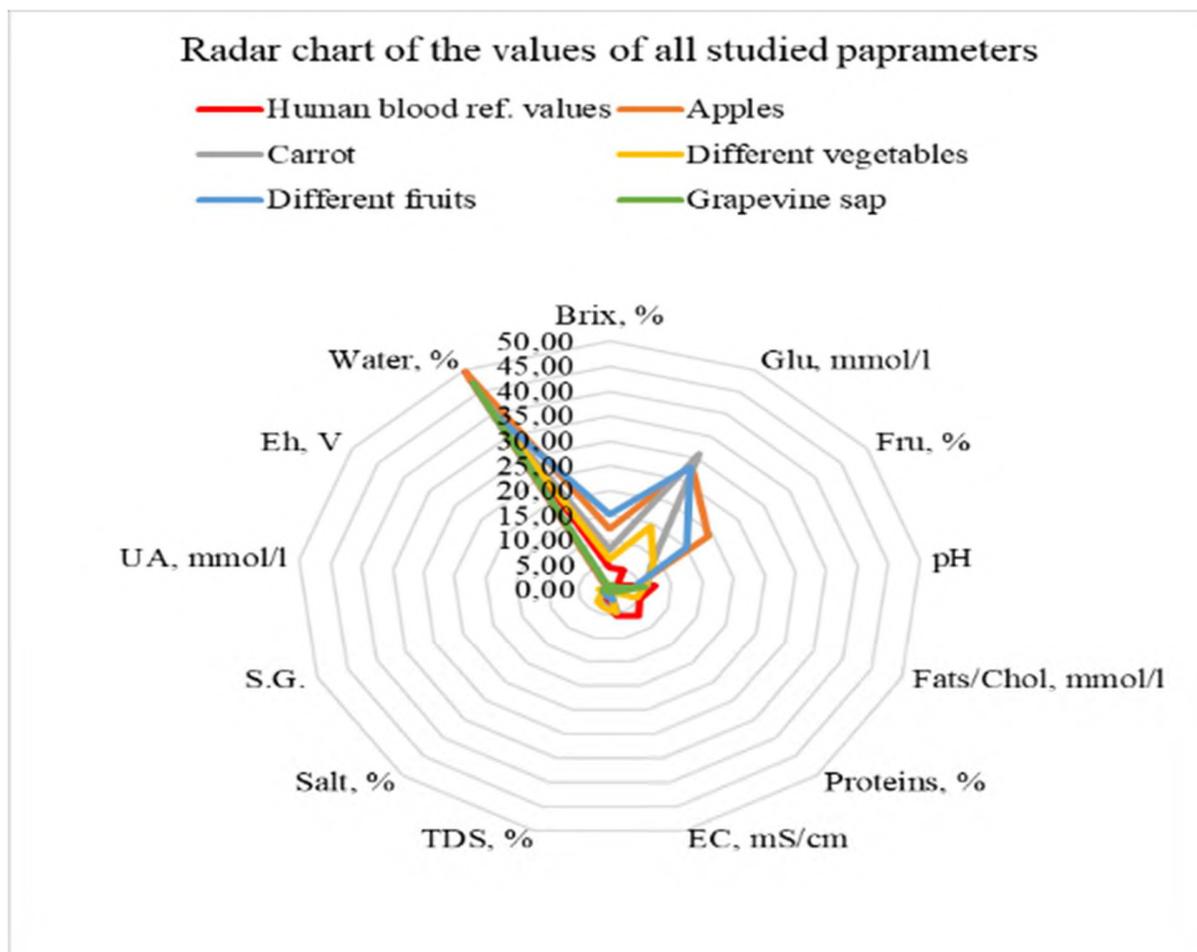


Figure: Radar diagram of the biochemical parameters of the human blood and plant fluids. Glu-glucose, fru-fructose, EC-electroconductivity, TDS-Total Dissolved Solids, S.G.-Special Gravity, UA-Uric acid, Eh – redox potential, Brix- total dissolved sugars

Key words: *biochemistry, plant fluids, juices, grapevine sap, human blood*

Source of information:

Sotirov, A., Yordanov, S. (2025). Comparative biochemistry between plant fluids and the human blood. *Trakia Journal of Sciences*, No 3, pp 173-185, 2025 Available online at: <https://trakia-uni.bg> ISSN 1313-3551

(online) doi:10.15547/tjs.2025.03.001. <https://tjs.trakia-uni.bg/index.php/tjs/article/view/126/142>

Application of the juxtaposition effect for enhancing crossover frequency in targeted chromosomal regions

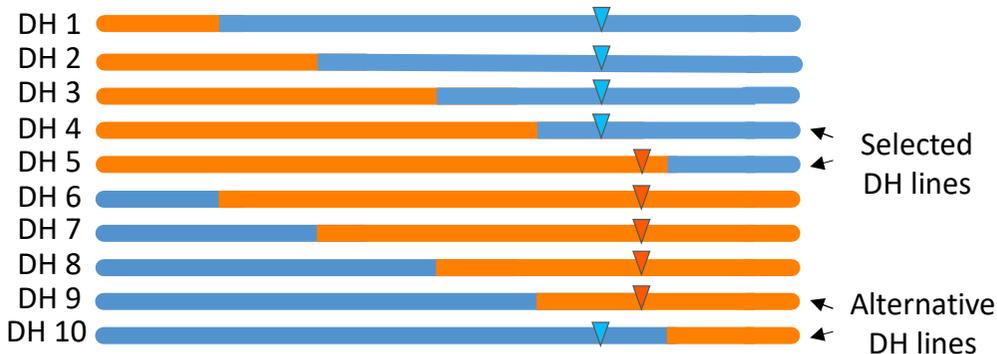
Goal: Combine two linked QTLs



Challenge: Few recombinants (tight linkage)

Strategy: Use the juxtaposition effect.

Step 1: Generate DH from F1 (P1 × P2).



Note: DH genomes are parental mosaics.

Step 2: Select two DHs differing at target.



Step 3: Cross selected DH lines and look for QTL1–QTL2 recombinants.



Outcome: 3× more recombination in target interval.

Mechanism: Crossovers shift from adjacent homozygosity.

Result: Desired recombinant—goal achieved.



Genome Editing and Cultivar Choice for Nutrient-Dense Vegetables

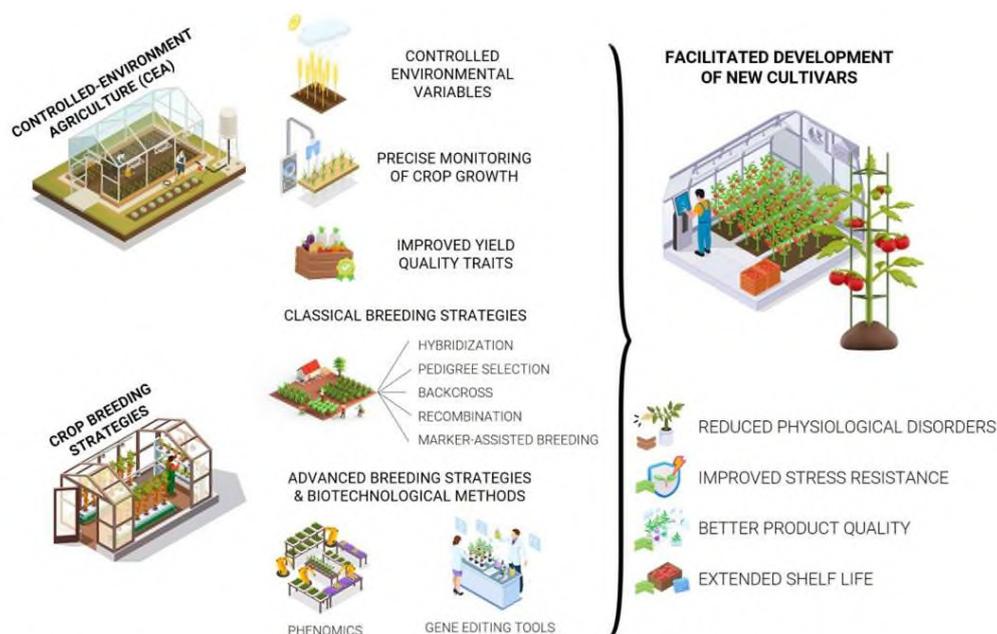
Julia Weiss^{1*}, Nazim S. Gruda^{1,2,3}

¹ Technical University of Cartagena, Cartagena, Spain

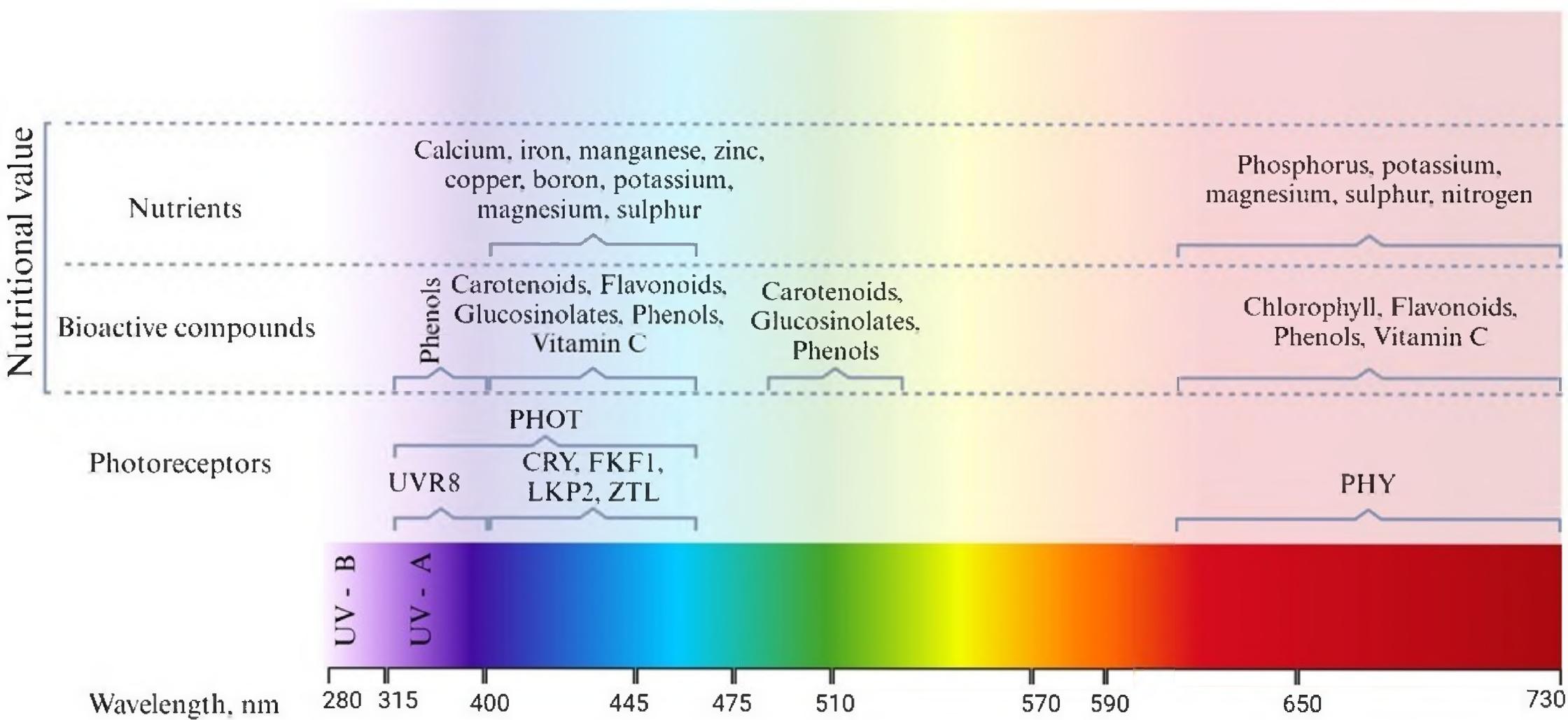
² University of Bonn, Bonn, Germany, and ³ Academy of Science of Albania

*Corresponding author: julia.weiss@upct.es

Graphical Abstract: Strategies to shorten breeding cycles, make quality improvements more predictable, and better align vegetables with market and public health goals.



Weiss J, Gruda NS. Novel Breeding Techniques and Strategies for Enhancing Greenhouse Vegetable Product Quality. *Agronomy*. 2025; 15(1):207. <https://doi.org/10.3390/agronomy15010207>

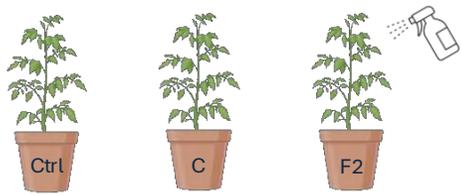


Light spectra affect the vegetable’s nutritional and bioactive properties through specific photoreceptors. Gruda et al. (2025) <https://doi.org/10.1111/1541-4337.70139>

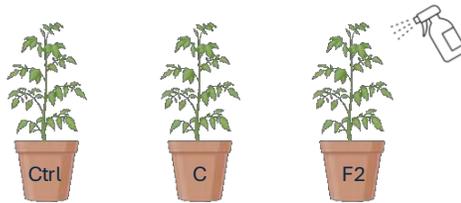
Natural Biostimulants Strengthen Tomato Response to Nitrogen Shortage

Monterisi S., Alzate Zuluaga M.Y., Senizza B., Cardarelli M., Rouphael Y., Colla G., Lucini L., Cesco S., Pii Y.

Optimal N (NO_3^- 14 mM)



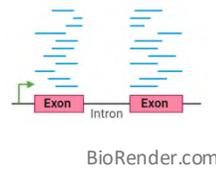
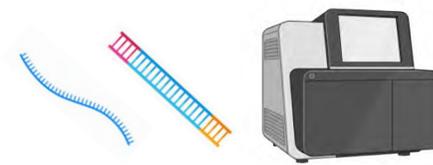
Low N (NO_3^- 2 mM)



BioRender.com

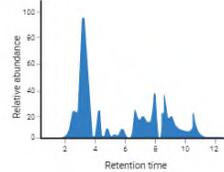
Ctrl: water
C: *Malvaceae*-derived
F2: C medium fraction (1–10 kDa)

RNA-seq



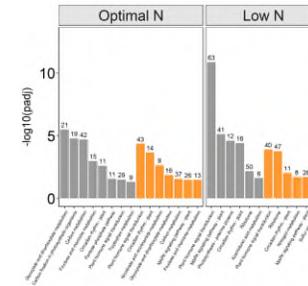
BioRender.com

UHPLC-QTOF-MS

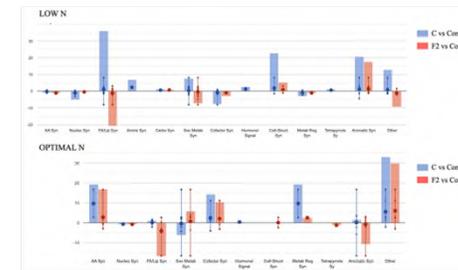


BioRender.com

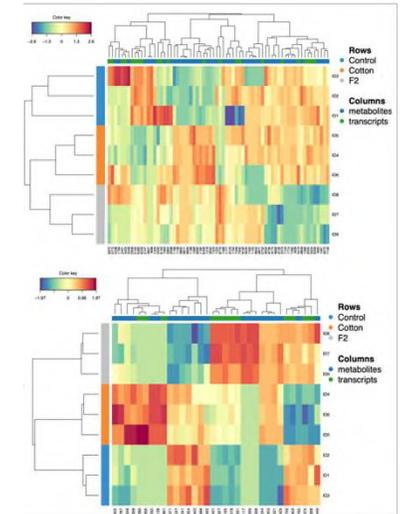
Transcriptomic



Metabolomic



Multomics data integration



Graphical Abstract. Experimental approach for the multi-omic integrated study of tomato plants subjected to different N availability and treated with *Malvaceae*-derived biostimulants.

Original Article: Monterisi, S., Alzate Zuluaga, M.Y.A., Senizza, B., Cardarelli, M., Rouphael, Y., Giuseppe, G., Lucini, L., Cesco, S., Pii, Y. (2025). The integrated multi-omics analysis unravels distinct roles of *Malvaceae*-derived protein hydrolysate and its molecular fraction in modulating tomato resilience under limited nitrogen availability. *Plant Stress*, 15, art. no. 100771. DOI: 10.1016/j.stress.2025.100771

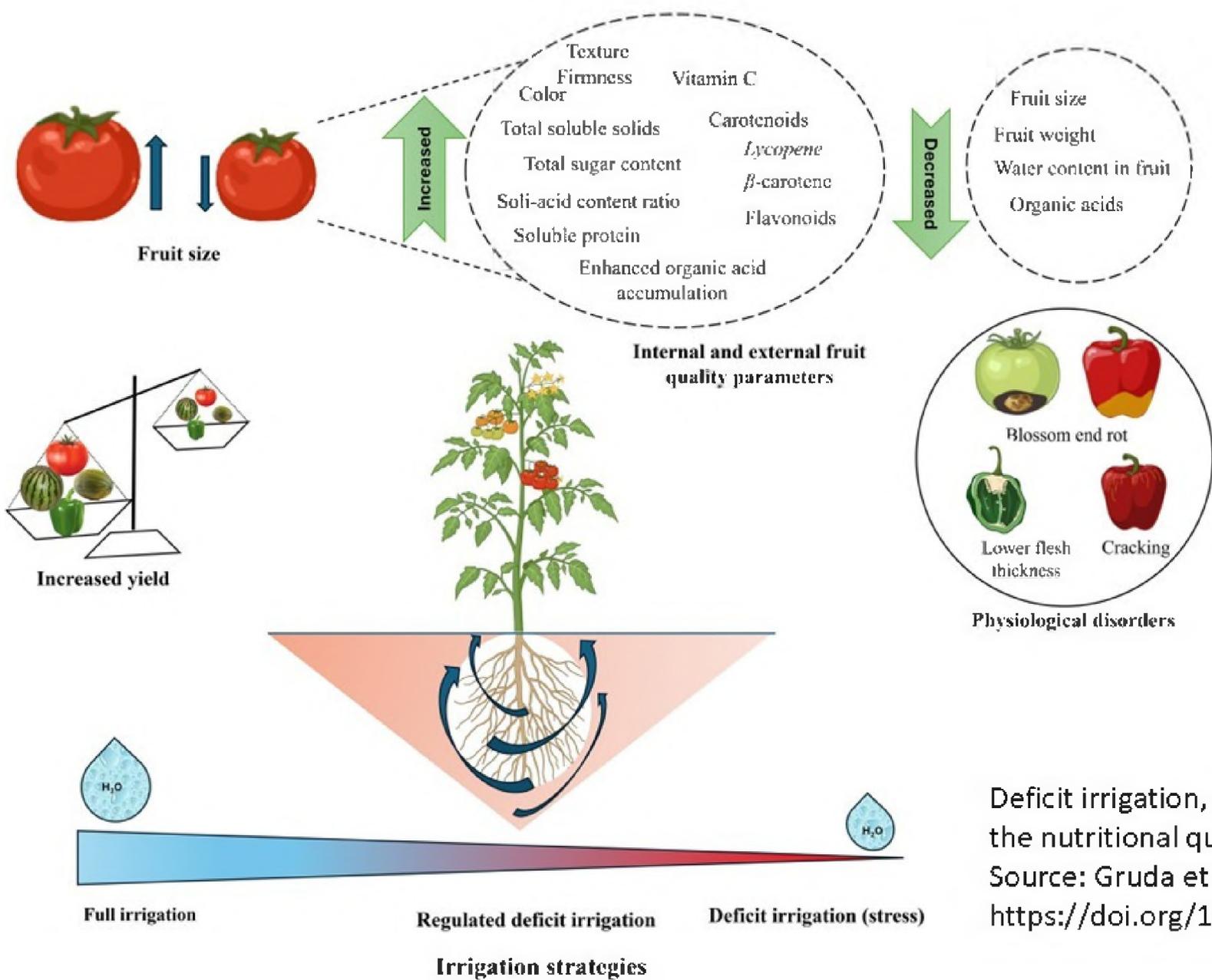
One Health and agriculture: bridging data gaps to tackle environmental chemical loads

J. Vos, M. Alessandrini, M. Trevisan, Y. Pii, F. Mazzetto, G. Orzes, S. Cesco

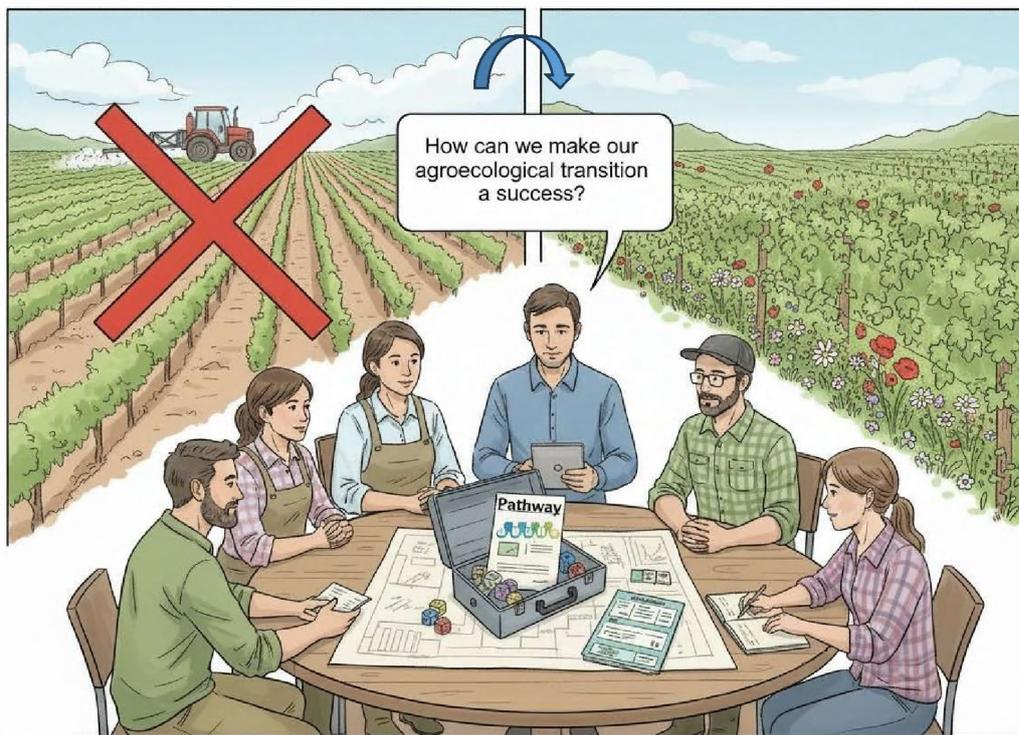


Graphical Abstract. Comparison of chemical inputs across One Health domains in the EU (2010–2020) and identification of major data gaps to support more effective and sustainable regulation aligned with One Health and the EU Green Deal.

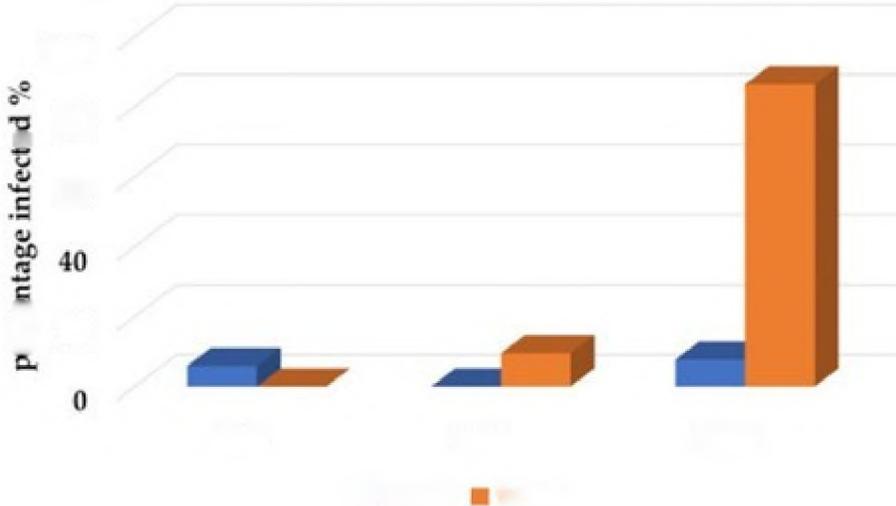
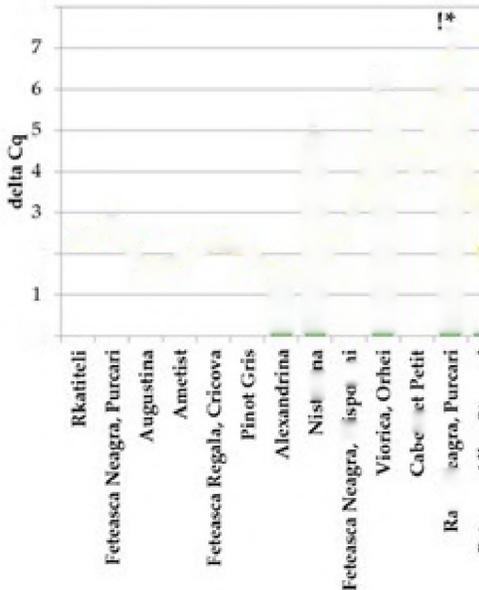
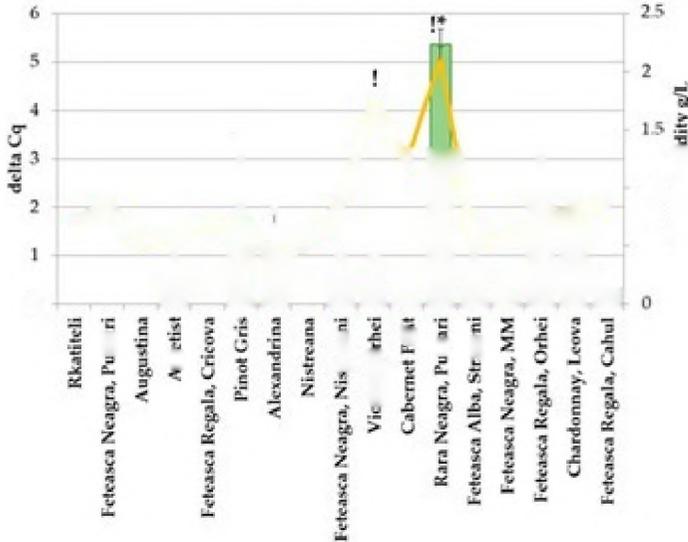
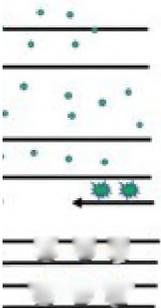
Original article: Vos, J., Alessandrini, M., Trevisan, M., Pii, Y., Mazzetto, F., Orzes, G., Cesco, S. (2025). One Health approach: Addressing data challenges and unresolved questions in agriculture. *Science of the Total Environment*, 977, art. no. 179312. DOI: 10.1016/j.scitotenv.2025.179312



Deficit irrigation, as an example factor, influences the nutritional quality of vegetables.
 Source: Gruda et al. (2025).
<https://doi.org/10.1080/07352689.2025.2515801>



Supporting agroecological transition: pathway and tools for farmers' collectives



Under dense canopies, species experience buffered (less extreme) microclimate temperatures, reduced light and wind, increased relative humidity

Understory plants have a **species-specific affinity to the forest microclimate**, which we quantify for the first time using presence ●/○ absence data

