VI_EUCARPIA CONFERENCE

Scientific Conference on Breeding to meet environmental and societal challenges

Abstract e-Book

26-28 May 2025
Coimbra Portugal

Co–organised by

EUCARPIA LiveSeeding Polytechnic University of Coimbra

LiveSeeding project co- funded by

Schweizerische Eidgenossenschaft
Confédération suisse
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UK Research and Innovation

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by

EUCARPIA- Section Organic and Low-Input Agriculture in cooperation with LiveSeeding, the Polytechnic University of Coimbra, and supporting organisations and projects

Coimbra, Portugal

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08.45 – 09.00	**S01 Words of welcome from the organisers** **Prof. Dr. Daniela Santos**, Vice Dean of Faculty, Instituto Politécnico de Coimbra **(PUC – ESAC, PT)** **Prof. Dr. Pedro Mendes-Moreira**, Instituto Politécnico de Coimbra **(PUC – ESAC, PT)** and Chair of the Eucarpia section organic and low-input agriculture **Dr. sc. agr. Monika Messmer**, Co-Lead Organic Plant Breeding, Research Institute of Organic Agriculture **(FiBL, CH),** LiveSeeding project Scientific Coordinator
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	Dr. Agata Gulisano, Plant Breeding and Genetic Resources Policy Officer, DG AGRI, European Commission
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	Prof. Dr. Pedro Mendes Moreira, Dr. sc. agr. Monika Messmer, Mariano Iossa
15:50 – 16:00	**S21 Concluding remarks and outlook** **Prof. Dr. Pedro Mendes-Moreira**, Instituto Politécnico de Coimbra **(PUC – ESAC, Portugal)** and Chair of the Eucarpia section organic and low-input agriculture

PREFACE

Dear participants of the conference "Breeding to address environmental and societal challenges",

It is a great pleasure for me to welcome you to this meeting organized by the Organic and Low Input Section of EUCARPIA.

I hope that from 26 to 28 May 2025 you will have a pleasant time discussing the most appropriate breeding strategies to respond in the most sustainable way to environmental issues and societal needs. The main objective of the Eucarpia association is to promote collaboration in plant breeding research. The meetings of our Sections act as intermediaries between different points of view. They are always a great opportunity for researchers, breeders and stakeholders interested in plant breeding to meet, share ideas, create networks and promote new collaborations. The program looks very promising. I therefore wish you a successful conference, characterized by a constructive dialogue for the application of breeding methodologies in the context of agroecological principles. I hope this meeting offers you a moment of inspiration for your work.

Maria Raffaella Ercolano, EUCARPIA President

Dear EUCARPIA Section Organic and Low Input Agriculture members and participants of the 6th conference of the Organic and Low Input Section on"Breeding to meet environmental and societal challenges", it is our great pleasure to welcome you to Coimbra, Portugal.

The conference will place special emphasis on three main sections: Breeding to meet environmental challenges (Breeding for abiotic stress tolerance and resource efficiency, Breeding for biotic stress tolerance), Breeding for Diversity (Breeding for Agrobiodiversity and Ecosystem Services, Breeding for healthy food), Breeding to meet societal challenges (Participatory breeding and decentralized on-farm cultivar testing, Innovative financial and governance models, Impact of EU regulations on Plant Reproductive Material (PRM) and New Genomic Techniques (NGT) on the organic sector).

Our section started in 2007 and targets Plant Breeding on Organic and other Agroecological Farming Systems. The Eucarpia section conference is organized in a 3 to 4-year interval. The last meeting was organized in 2021 by Dr. Linda Legzdina in Latvia. Since 2021, several activities took place, including: the EUCARPIA General congress online from 23rd to 26th August 2021, the Organic World Congress 6th -

10th September 2021 in Rennes (France), which included the Seed Ambassadors preconference on 6th and 7th September 2021. In addition, during this period the 3rd and 4rd Eucarpia Workshop on Implementing Plant-Microbe Interactions in Plant Breeding were organized in 2022 and 2024 respectively, and ECOBREED Organic Breeding Conference on 7th to 19th January 2024 in Ljubljana (Slovenia).

The present conference would not be possible without the contributions of EUCARPIA, LiveSeeding, and the Agricultural School of the Polytechnic University of Coimbra. We also have counted on the international support of ECO-PB, InnoBreed, DivinFood, Cousin, CropDiva, Prowild, Root2Res, Grapebreed4IPM, Legume Generation, IPMorama, radiant, Belis, Barley MicroBreed and Increase. The national support with CERTRA, AGROVILA, FARM4Future projects and sponsorship from Casa Mendes Gonçalves and Vivid Farms, were also vital for the organization of this event.

We wish you a pleasant stay and a fruitful discussion on plant breeding and related disciplines to share novel research findings addressing environmental and societal challenges, to network and to discuss during the 3-day conference, followed by an Organic Seed Policy and Stakeholder workshop on 29th May 2025.

On behalf of the organizing committee.

Pedro Mendes-Moreira

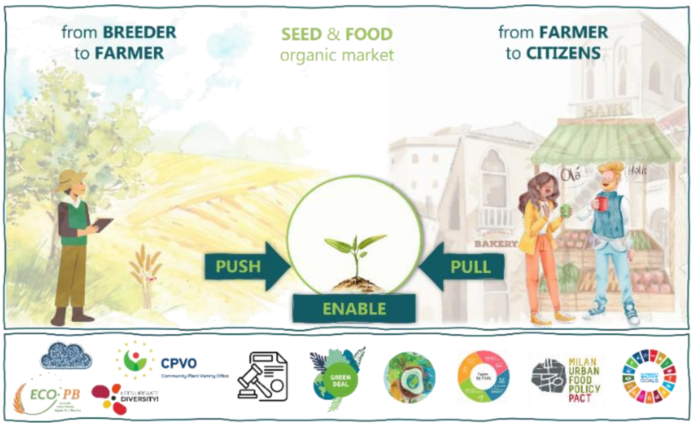
Chair of EUCARPIA Section Organic and Low-Input Agriculture

Projects and Organisations involved

LiveSeeding -Organic seed and plant breeding to accelerate sustainable and diverse food systems in Europe

LiveSeeding is a 4-year Innovation Action funded by the European Union, the Swiss State Secretariat for Education, Research and Innovation (SERI) and UK Research and Innovation (UKRI). The project started in October 2022 and brings together 37 organisations operating in 16 European countries. LiveSeeding provides science-based evidence and best practice solutions to help achieve 100 % organic seed. LiveSeeding contributes to the transition towards environmentally-friendly, climate-neutral, healthy and fair food systems through a PUSH-PULL-ENABLE strategy to

- enhance the availability and adequacy of organic seeds of cultivars appropriate to organic farming (PUSH),
- increase and stabilise the market demand for organic seeds of cultivars appropriate to organic farming (PULL),
- foster an enabling policy and regulatory environment where both demand and supply can harmoniously and productively negotiate without irrelevant constraints due to legal restrictions and/or regulatory fragmentation



LiveSeeding addresses the topics in a holistic multi-actor, multi-stakeholder, participatory approach involving stakeholders along the value chain in 17 local Living Labs (LLs) and 3 established networks of organic breeders (ECO-PB), seed savers (ECLLD) and Milan Urban Food Policy Pact (MUFPP). 15 European countries cover the different pedoclimatic zones and socio-economic contexts, including countries with a low level of development in organic seed and breeding in East and South Europe.

Legume Generation – Boosting innovation in breeding for the next generation of legume crops for Europe

The Legume Generation consortium invests in innovation that boosts the breeding of legumes in Europe by combining the entrepreneurial focus of breeders with the broad inventiveness of the supporting research base.

Six species-oriented breeder-led innovation communities link practical breeding with the research-base in a transdisciplinary framework. They lead the innovation work and each is focused on the breeding of a single species or species type: soya bean (Glycine max); lupins (Lupinus spp); pea (Pisum sativum); lentil (Lens culinaris); phaseolus bean (Phaseolus spp. e.g. 'common' bean); and white and red clover (Trifolium repens and T. pratense). These are supported by the cross-project collection of intelligence on ideotype concepts, beneficial traits, a catalogue of legume species and cultivars, and breeding methods assembled in the Legume Generation Knowledge Centre; the production and validation of novel resources (genotypes, methods, and tools); screening, demonstration and testing of germplasm and new cultivars in different regions; training to support breeding gains in our innovation communities; governance and financial models, and business plans for inclusive plant breeding. All this will be supported by consortium internal and external dissemination and communications, including the extension of the European Legume Hub as a platform for sharing of knowledge. We currently run 75 breeding and pre-breeding programmes. We will give these a decisive boost through access to resources that accelerates the production of novel germplasm, innovating up to the point where newly bred germplasm and cultivars are proven on farm. Breeders will use the results to support expansion of legume production. Our innovation communities are open to all relevant actors and provide a direct route for the dissemination of results to other users and interested stakeholders. Their sustainability beyond the life of the project will be supported by business plans.

The total project budget is €7.0 million, including a €5.5 million contribution from the European Union along with contributions from the United Kingdom, Switzerland and New Zealand. The consortium is led by Dr Lars-Gernot Otto at the IPK and by Dr Donal Murphy-Bokern from Lohne in Germany, who is the science coordinator.

Legume Generation (Boosting innovation in breeding for the next generation of legume crops for Europe) has received funding from the European Union's Horizon Europe research and innovation programme under grant agreement No.101081329. It also receives support from the governments of the United Kingdom, Switzerland and New Zealand.

BELIS - Breeding European Legumes for Increased Sustainability

The European Union has identified the expansion of legume cultivation and yield improvement as key to increasing protein sovereignty and sustainability of agriculture. Legume production is hampered by low genetic progress, which is linked to low profitability of the seed business and low adoption of improved varieties. The BELIS project (Breeding European Legumes for Increased Sustainability http://www.belisproject.eu/), coordinated by INRAE, consisting of 34 partners from 18 different countries, aims at improving breeding methods and governance structures in the seed sector to increase its competitiveness.

BELIS focus on seven forage crops and seven grain crops that are currently grown to produce feed (for ruminants – cattle, sheep, goat and monogastric animals – pig, poultry), food (as is or after processing), or to deliver ecosystem services. BELIS specific objectives are:

1. To develop tools and methodologies for cost-effective breeding programmes and deliver proofs of concept, with and for breeders.
2. To facilitate the economic regulatory environment, variety registration, variety recommendation and business models.
3. To implement an efficient, ambitious and durable transfer of innovation through the BELIS platform that includes a network of breeders and actors from scientific research, extension services and seed, food and feed industries, as well as a training portfolio.

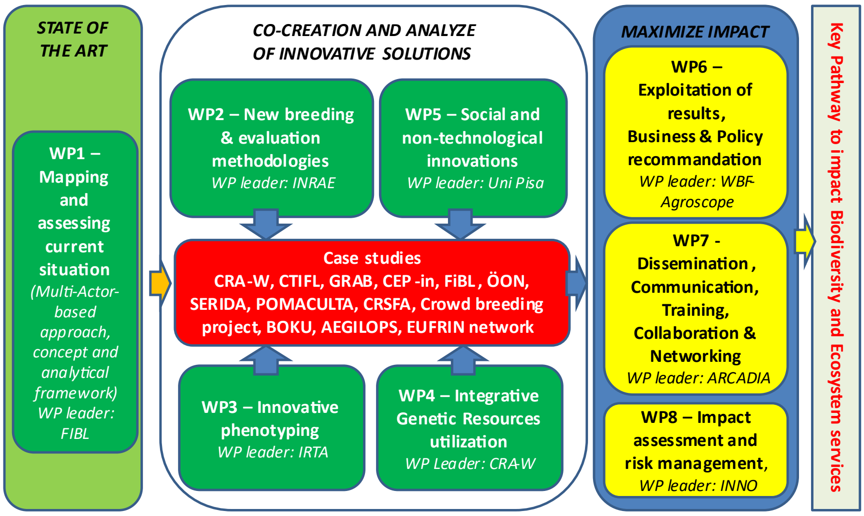
By enabling the creation of improved varieties in many species, adapted to different areas and uses in Europe, this project is relevant for the destinations towards «Biodiversity and Ecosystem Services», mainly contributing to «Access to a wider range of crops and breeds with a broadened genetic base is improved in line with global biodiversity commitments». It also supports the «Practices in agriculture and forestry support biodiversity and the provision of other ecosystems services». In addition, BELIS will have a positive input on natural biodiversity, reduction of air and water pollutions and farming system sustainability. For all the species under study, the BELIS platform, which includes a network of breeders, scientific researchers, development services and the seed, food and feed industries, as well as a portfolio of training courses, is being set up. Anyone wishing to join the BELIS network can send their details to info@belisproject.eu, indicating their areas of interest.

BELIS is supported by the European Union for the period 2023-2028 (European Union's Horizon Europe research and innovation programme under grant agreement No. 101081878).

InnOBreed - Innovative Organic fruit Breeding and uses

InnOBreed - Innovative Organic fruit Breeding and uses is a 4-year Innovation Action funded by the European Union, and Swiss State Secretariat for Education, Research and Innovation (SERI). The project started in July 2022 and brings together 21 organisations operating in 10 European countries (from EU and CH). InnOBreed provides science-based innovations and best practice solutions to amplifiy fruit organic production through a targeted approach based on the maximisation of the impacts of Technological, Environmental and Social Innovations. Project budget is 6.4 million Euro. InnOBreed contributes to the transition of the Fruit sector towards a focus on Fruit Genetic resources to address a fair agrifood system suitable for organic farming, based on agroecology with pesticide use reduction, adaptation to climate change, and enhanced fruit quality and production. A three phase strategy has been implemented to

- Identify innovative solutions (IS) in traits and methodologies suitable for organic farming through a multi-actor approach.
- Assess the feasibility, transferability, and efficiency of biotechnical, social, and economic innovations at breeding and evaluation stages through case studies.
- Implement the identified technical-socio-economic innovations in case studies, assess risks, and transfer successful innovations to the fruit industry via established expertise-sharing platforms.



InnOBreed addresses its objectives in a holistic multi-actor, multi-stakeholder participatory approach involving stakeholders along the value chain with 13 case studies and a strong anchorage onto established relevant networks (ECPGR, EUFRIN, …).

Website: www.innobreed.eu
Linkedin: https://www.linkedin.com/company/innobreed

AGROVila - Organising family farming through digital processes for the development of short food supply chains

AgroVila is a three-year Next Generation EU project designed to connect farmers and consumers by establishing production and consumption communities, supported by a nationally accessible digital platform for all local producers and consumers. The project budget amounts to €996,030.79.

The activities to be undertaken and the anticipated outcomes are as follows:

- Engagement and participation of local farmers, their organisations, and consumers.
- Implementation of the AgroVila Marketplace.
- Installation and oversight of technology supporting local initiatives (pilot projects).
- Creation of installation manuals and support guides for the Marketplace to enhance AgroVila initiatives.
- Training programs for farmers participating in pilot projects and capacity-building initiatives for technicians from Producers' Organisations.
- Dissemination and communication.

Website: https://agrovila.org/

Facebook: https://www.facebook.com/profile.php?id=61565971684455

Instagram: https://www.instagram.com/agrovila_pt/

PRR Plano de Recuperação e Resiliência
REPÚBLICA PORTUGUESA
Financiado pela União Europeia NextGenerationEU

Casa Mendes Gonçalves – Innovation with a Sustainable Flavour

Casa Mendes Gonçalves, founded in 1982 and based in Golegã, seamlessly blends deep family tradition with cutting-edge food innovation. Renowned for producing high-quality vinegars, sauces, and condiments, the company celebrates regional flavours, such as fig vinegar, while implementing eco-friendly solutions across its value chain. On a five-hectare estate, it has adopted Ernst Götsch's syntropic agroforestry system, regenerating soil through layered biomass and fostering rich biodiversity. In parallel, it applies rotational grazing inspired by Gabe Brown's methods, enhancing natural pasture fertility and ensuring animal welfare. Casa MG is also committed to preserving autochthonous breeds of cattle, sheep, and chickens—many at risk of extinction—thereby strengthening Portugal's genetic heritage. At its Golegã facility, the use of solar energy and the valorisation of 91.8 % of production waste underscore its circular-economy ethos. By offering 100 % natural, fully traceable products without unnecessary additives, it meets the rising demand for healthier foods from consumers and retailers alike. Collaborations with local farmers, universities, and startups foster a collaborative ecosystem that drives research, innovation, and sustainable practices. Membership in the UN Global Compact and cooperation with research centres reflect its ambition to shape public policies and environmental certifications. This journey shows that tradition, profitability, and environmental responsibility can go hand in hand, inspiring the food sector towards a more balanced future.

PUSH–PULL–ENABLE Strategy

PUSH – Continuous innovation in low-impact products and processes, upcycling agro-industrial by-products and integrating renewable energy into manufacturing.

PULL – Encouraging conscious consumption through natural, healthy, and fully traceable goods, aligned with consumer and retailer expectations.

ENABLE – Forging strategic partnerships with farmers, universities, and startups to build a resilient, collaborative food ecosystem that champions sustainable best practices.

Website: https://www.mendesgoncalves.pt
Linkedin: https://www.linkedin.com/company/casamendesgoncalves/

CERTRA – Traditional Cereal Value Chains for Sustainable Nutrition in Portugal

CERTRA is a 32-month, multi-actor project (Jan 2023 – Sep 2025) funded by the Portuguese Recovery and Resilience Plan (PRR, Measure 12 – Sustainable Food) and co-financed by NextGenerationEU. The **€751 945** consortium, coordinated by the Polytechnic Institute of Bragança, joins nine Portuguese organizations covering genetic resources conservation, primary production, milling, food processing, retail, research, consulting, sustainability food systems and circular economy strategies: ADER-SOUSA - Associação de Desenvolvimento Rural das Terras do Sousa, CNA - Confederação Nacional da Agricultura, EMAC – Cascais Ambiente, INIAV - Instituto Nacional de Investigação Agrária e Veterinária, IPB - Instituto Politécnico de Bragança, IPC - Instituto Politécnico de Coimbra, IPL - Instituto Politécnico de Leiria, Moagem Duarte & Amélia, NOP - New Organic Planet

CERTRA operating framework – Produce · Promote · Align:

Produce – Map of existing farmers who do conservation genetic resources; perform characterization and agronomic and quality trials, and genetic diversity analyses; do breeding and selection, select and multiply seed lots suited to organic and low-input systems; quantify adaptation for climate changes.

Promote – Adapted populations to farmers fields, formulate and pilot value-added flours, breads, pastas, snacks and other food products based on Mediterranic dieta; determine nutritional profiles and sensory acceptance; design evidence-based outreach materials underscoring health and heritage benefits.

Align – Establish a multi-actor knowledge-exchange platform linking farmers, seed banks, millers, bakers, retailers, chefs and consumers; draft voluntary codes of practice and traceability protocols; issue recommendations for public procurement and regional labelling that reward authenticity and short supply chains.

Expected Outcomes:

- Consolidation of a **nation-wide value chain** dedicated to heritage cereals.
- Expanded possible evidence base on the **nutritional, organoleptic and safety attributes** of local germplasm.
- **Increase farmers' access** to varieties that are regionally adapted and climate resilient.
- **New market opportunities** and greater consumer visibility for products derived from traditional cereals.
- An **active, multi-actor knowledge-exchange network** spanning the entire agri-food chain.

Website: https://esa.ipb.pt/certra/

Desenvolvimento de Cadeias de Valor de Cereais Tradicionais para uma Alimentação Sustentável em Portugal
Projeto PRR -C05-i03-i-000181
MEDIDA 12 – ALIMENTAÇÃO SUSTENTÁVEL
PRR Plano de Recuperação e Resiliência
REPÚBLICA PORTUGUESA
Financiado pela União Europeia NextGenerationEU
DIETA MEDITERRANICA

VIVID Farms – Regenerative Agriculture

VIVID FOODS was born in the food industry with a strong commitment to quality, innovation, and promoting active, healthy lives. However, we soon realised that we could do more and better by going to the root of true impact: the soil. This led to the creation of **VIVID FARMS**, a natural extension of our mission, where we put into practice principles of food production that are more conscious, more respectful of nature, and aligned with the life cycles of ecosystems.

We see our farm and regenerative agriculture as an opportunity not only to cultivate better food but to inspire people to become better human beings. Guided by "Seeding the Future", our farm is designed to be a model, a beacon of hope for others. It's a space for other farmers to learn that it's possible to produce better food at lower costs. For them to understand that they have a greater impact on people's health than the medical community. For doctors to realise that not all food is equal—that its quality and health benefits are directly tied to farming practices.

We aim to remind everyone that "we are what our food "ate" and how it was produced determines its impact on us, and there's no escaping this truth.

VIVID FARMS is a living example for decision-makers, educators, farmers, and consumers, showing that it is possible to produce high-quality food without chemicals, improve soils, and live happily while contributing to a healthier, fairer, and more prosperous planet. By producing food without chemicals, rich in nutritional density and integrity, we can replace future medical interventions with healthy food today. We want society to understand this profound connection.

Our farm creates models and practices that can serve many, combining cutting-edge science with agriculture. Our greatest pride lies in transforming degraded soil into productive land within two years, convincing sceptics that it is possible. We've inspired hundreds of people, farmers, decision-makers, educators, students, and consumers through farm visits, workshops, and training sessions. Our team radiates contagious energy for change.

We've become a reference for good agricultural practices, knowledge sharing, and community building. Our events bring together a cross-section of the food system, chefs, doctors, agronomists, nutritionists, producers, animal farmers, industry players, retailers, end consumers, ... creating powerful synergies and shared understanding.

We see agriculture not just as a means of production, but as a profound tool for climate action, health resilience, and economic revitalisation.

Every choice we make transforms the planet. We aim to lead, inspire, and create a regenerative, prosperous future. What we learn and know must serve many.

This is our vision. This is our mission. #SeedingTheFuture

Website: https://www.vivid-farms.com/; https://www.vivid-foods.com/
Linkedin: https://www.linkedin.com/company/vivid-farms
https://www.linkedin.com/company/vividfoods/
Instagram: https://www.instagram.com/vividfarmsofficial/; https://www.instagram.com/vividfoodsofficial/

GrapeBreed4IPM - Developing sustainable solutions for viticulture through multi-actor innovation targeting breeding for integrated pest management

GrapeBreed4IPM is a four-year Horizon Europe Research and Innovation Action launched in April 2024 to help reshape European viticulture through innovation in breeding and integrated pest management. Coordinated by INRAE, the project gathers 19 partners and 2 associated partners from France, Germany, Italy, Spain, Austria, Switzerland, and Serbia. It operates with a total budget of €5.6 million (€5M from the European Commission and €600k from the Swiss SERI).

Viticulture holds major economic and cultural importance in the EU, yet remains one of the most pesticide-dependent agricultural sectors. This dependency, combined with growing climate-related challenges, has intensified the need for more sustainable practices. GrapeBreed4IPM addresses this pressing issue by developing disease-resistant grapevine varieties that preserve wine quality while aligning with the expectations of producers, consumers, and regulatory bodies. The project takes a multi-actor and co-design approach to ensure the new varieties and management solutions are adopted across diverse European regions. It combines conventional and new genomic techniques with field-level experimentation and social research to assess and improve the acceptance of disease-resistant cultivars and their wines.

GrapeBreed4IPM is structured around five key objectives: co-designing a shared vision with stakeholders across European wine regions; advancing knowledge on grapevine resistance mechanisms and environmental interactions; developing locally adapted resistant varieties through participatory breeding; creating emblematic cultivars that combine resistance with traditional wine profiles; and providing end-users with decision-support tools and IPM guidelines for sustainable vineyard management.

Website: https://grapebreed4ipm.com
Linkedin: https://www.linkedin.com/company/grapebreed4ipm-eu-project/
Contact: Komlan Avia – komlan.avia@inrae.fr
Grant Agreement: No. 101132223 (Horizon Europe) and Nr. 24.00152 (SERI)

Root2Resilience - Root phenotyping and genetic improvement for rotational crops resilient to environmental change

Root2Res project (2022–2027) aims to enhance the resilience of rotational cropping systems across Europe in response to climate change. With 22 partners from Europe, Morocco, and South Africa, the project brings together a wide range of expertise to develop crops that can better tolerate environmental stresses—such as drought, waterlogging, and reduced nutrient availability.

Root2Res focuses on root traits and their plasticity, demonstrating their key role in supporting crop stability and environmental benefits. By improving root systems, the project seeks to increase water use efficiency, reduce dependence on synthetic fertilizers, lower greenhouse gas emissions, and boost soil carbon sequestration. The studied species are cereals (barley, wheat), tubers (potatoes, sweet potatoes and legumes (faba beans, lentils, peas).

In particular, the project aims to:

- Define, identify and test root/rhizosphere ideotypes for a changing environment in crops common to rotational systems in Europe.
- Define and provide a complete set of tools to consider root traits.
- Identify, develop and multiply germplasm and populations for phenotyping activities at different scales and use materials to identify new candidate genes and markers connected to root traits and their plasticity and enable novel pre-breeding germplasm.
- Quantify plasticity of extended root phenotype for germplasm under a range of environmental conditions, including the identification of the relevant root traits, trade-offs with other characteristics and impact on carbon sequestration.

Agricultural stakeholders—especially breeders and farmers— are strongly connected to the project, ensuring that solutions are practical, scalable, and aligned with their needs. In this sense, key practical deliverables of the project being developed include:

- Phenotyping tools to assess root traits in field and controlled environments;
- Genetic tools and markers to support breeding of resilient crop varieties;
- Modelling tools to predict performance across diverse agroclimatic zones.

For more information: www.root2res.eu

INCREASE - Intelligent Collections of Food-Legume Genetic Resources for European Agrofood Systems

INCREASE is a project funded from the European Union Horizon 2020 Research and Innovation programme under grant agreement No 862862 (Project budget 7 million Euro, Coordinator Prof Roberto Papa, UNIVPM, Italy). The project started in May 2020 involving 28 partners from 14 different countries across the world, with the goal to valorise agrobiodiversity and promote food legumes consumption and cultivation in Europe. Implementing cutting-edge approaches INCREASE aims to secure the conservation, management and characteriszation of plant genetic resources (PGR), helping food systems to develop towards sustainable practices and to support food production and consumption to protect the environment, mitigate the effect of climate change and promote human health.

Guided by the European Commission principles "open science, open innovation and open to the world", INCREASE takes advantage of digital technologies to make science and innovation more collaborative and global, involving Stakeholders in a Participatory Approach. Moreover, with the purpose to enhance agrobiodiversity conservation and food legumes cultivation/consumption, the project runs the INCREASE Citizen Science Experiment (CSE, Figure 1), engaging citizens across Europe in the evaluation and conservation activities of legumes PGR.

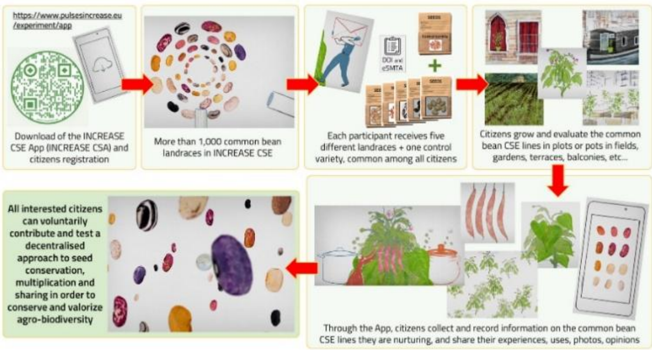


Fig.1 – INCREASE Citizen Science Experiment, from Bellucci E. et al, 2021, TPJ, 108:646-660. DOI: https://doi.org/10.1111/tpj.15472

Over five growing seasons, the INCREASE CSE has involved more than 25,000 participants and collected, using advanced digital tools and AI, extensive citizen-generated data to evaluate the potential of Decentralised PGR conservation strategies and citizen science as effective approaches for assessing the value of plant genetic resources.

pulsesincrease.eu
Instagram: https://www.instagram.com/pulsesincrease/
YouTube: https://www.youtube.com/channel/UCpv279DcqgKRJpMWufbDWMg
https://www.youtube.com/channel/UC9u7UJeJqvWis38o3gnzLLA
BlueSky: https://bsky.app/profile/pulsesincrease.bsky.social
Facebook: https://www.facebook.com/pulses.increase

ECO-PB – European Consortium for Organic Plant Breeding s

The European Consortium for Organic Plant Breeding (ECO-PB) was founded on 20th April 2001 in Driebergen (NL) in order to

- provide a platform for discussion and exchange of knowledge and experiences among organic breeders, seed producers and researchers
- initiate and support organic plant breeding programs and strengthen networks among partners
- develop of scientific concepts of organic plant breeding
- provide independent, competent expertise to develop standard setting with respect to organic plant breeding
- represent the organic plant breeding and organic seed sector at a European level

ECO-PB is committed to the principles of organic agriculture as laid down in the IFOAM Basic Standards and EU Regulation (EEC) 2092/91 and is a member of IFOAM Organics International, IFOAM Organics Europe, TPOrganic and founder of the international IFOAM Seed Platform. ECO-PB has observer status in the technical meetings of CPVO and is an acknowledged organisation of the EU transparency register.

ECO-PB offers membership to all organisations that are actively and predominantly engaged in the development and promotion of organic plant breeding or organic seed and supporting membership to individual persons predominantly engaged in organic seed and plant breeding and complying with the objectives of the association. Presently, ECO-PB consists of 15 full member associations and 30 associated members spread across Europe (www.eco-pb.org).

The main activities of ECO-PB are to

- carry out and support meetings and workshops on legal, political, technical, socioeconomic aspects related to organic seed and plant breeding
- work out a sound concept based on principles of organic agriculture and systems-based breeding as a basis for organic plant breeding strategies
- promote research topics on organic breeding and set up and participate in research projects and networks on organic plant breeding
- provide discussion paper on plant breeding issues to support the decision making process in European and international level
- find alliance with other organizations and represent our members in political and stakeholder dialogs
- participate in consultations, workshops, stakeholder and policy meetings in order to promote the interests of our members
- provide a platform for young breeders supported by experienced mentors
- collect training material on organic seed and plant breeding
- support the preconferences on plant breeding of the Organic World Congress

ORAL PRESENTATIONS

SECTION I | Environmental Challenges

BREEDING FOR MULTI-STRESS RESILIENCE IN CEREALS: INTEGRATING ENVIRONMENTAL ADAPTABILITY AND UAV-ASSISTED SELECTION

Marta da Silva Lopes [1]; Adrian Gracia-Romero [1]; David Gomez [2]; [1];

1 – IRTA, Spain; 2 – CSIC, Spain

Abstract Text:

Breeding for multi-stress resilience in cereals is crucial for maintaining agricultural productivity amid increasing environmental variability. The simultaneous occurrence of drought, heat, salinity, and nutrient deficiencies necessitates breeding strategies that enhance both adaptability and yield stability across diverse conditions. This study integrates long-term historical field data with replicated multi-location trials from our breeding program to identify high-plasticity genotypes—those capable of adjusting physiological and developmental responses to environmental fluctuations. To enhance stress tolerance, we focus on selecting genotypes with deep root systems for improved water access, stay-green phenotypes to sustain photosynthesis under prolonged stress, and flexible flowering and maturity times to enable crops to avoid peak stress periods. Unlike conventional breeding approaches that emphasize maximizing yields under optimal conditions, our strategy prioritizes yield stability across diverse and unpredictable environments. This is achieved through multi-location trials and stress-gradient assessments, ensuring that selected genotypes perform consistently across variable climates.

Field trials were screened using both classical phenotyping methods and low-cost RGB cameras mounted on drones, allowing for efficient and scalable data collection. Classical phenotyping involved manual measurements of key agronomic traits, while UAV-based imaging provided high-throughput, non-invasive assessments of plant responses to abiotic stress. The use of RGB cameras for predictive phenotyping enhances breeding efficiency by enabling rapid and cost-effective monitoring of essential parameters, such as water-use efficiency, plant height, flowering time, and maturity time. Integrating unmanned aerial vehicles (UAVs) for high-throughput phenotyping significantly accelerates the breeding process. UAV-based monitoring enables real-time assessment of plant performance under multiple stress conditions, facilitating early selection of resilient genotypes. The incorporation of automated phenotyping pipelines and machine learning algorithms allows for precise trait prediction, reducing reliance on labor-intensive field measurements while improving selection accuracy. This study presents recent advancements in UAV-driven phenotyping and explores its role in modernizing breeding programs to enhance climate resilience. By combining environmental plasticity selection with UAV-assisted high-throughput phenotyping, we can develop cereals that not only tolerate multiple stressors but also maintain stable yields under fluctuating environmental conditions. This integrative approach bridges the gap between traditional field-based evaluation and cutting-edge digital phenotyping, leading to greater efficiency, shorter breeding cycles, and improved genetic gains. Ultimately, by leveraging both conventional and UAV-driven methods, breeding

programs can contribute to more sustainable and climate-resilient agriculture, ensuring global food security in the face of escalating climate challenges.

Reference:

Gómez-Candón, D.; Bellvert, J.; Pelechá, A.; Lopes, M.S. A Remote Sensing Approach for Assessing Daily Cumulative Evapotranspiration Integral in Wheat Genotype Screening for Drought Adaptation. Plants 2023, 12, 3871. https://doi.org/10.3390/plants12223871

Gracia-Romero, A., & Lopes, M. S. (2024). Heading and maturity date prediction using vegetation indices: A case study using bread wheat, barley, and oat crops. European Journal of Agronomy, 160, 127330. https://doi.org/10.1016/j.eja.2024.127330

PROMISING TOMATO ROOTSTOCK IDEOTYPES FOR SUSTAINABLE FERTILIZER USE EFFICIENCY

Purificación A. Martínez-Melgarejo[1]; Cristina Martínez-Andujar[1]; José Ángel Martín-Rodríguez[1]; Maialen Ormazabal Oria[1]; Juan José Guerrero Franco[1]; Juan Antonio López García[1]; Francisco Sandoval[1]; Angela Sánchez Prudencio[1]; Fracisco Pérez Alfocea[1];

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Abstract Text:

Inefficient use of fertilizers and water in agriculture leads to environmental degradation and increased economic costs. This study aimed to identify tomato genotypes with root ideotypes that enhance nutrient uptake and can be used as rootstocks to reduce water and fertilizer usage. A greenhouse trial with 96 tomato lines was conducted under low fertilization (-NPK) conditions to evaluate nutrient use efficiency and yield stability. The most efficient lines were hybridized with both cultivated and wild tomato accessions. Female parent lines included L66, L76, L77, L96, TL0, and K, while male parent lines were M82, TA209, and Pimpi. The resulting F1 hybrids, along with the cultivated M82 accession and wild species *S. pennellii* (Pen) and *S. pimpinellifolium* (Pimpi), were evaluated as rootstocks, with Maxifort F1 as a reference due to its high vigor and stress tolerance. The aerial part of the plants was represented by the high-value cherry-type hybrid Unidarkwin F1, with non-grafted (NG) and self-grafted (SG) versions as controls. Grafting was done at the 2-3 leaf stage, and plants were transferred to a commercial greenhouse after 3-4 weeks. A complete Hoagland solution was provided for 25 days, followed by two fertigation treatments: one with reduced N, P, and K levels (3, 0.5, and 1.5 mM), and another with optimal levels (N 12 mM, P 2 mM, K 6 mM) for 78 days. After the reduced fertigation period, all hybrid rootstocks, except L66 xM82, showed increased total fresh biomass (TFW) compared to NG and SG controls. Hybrids with Pimpi as the pollen donor and TL0 as the recipient had the highest TFW, approximately 25% higher than Unidarkwin NG and SG controls. All hybrids, except L66 and L76 xM82, had higher shoot fresh weight (SFW) under restricted fertigation, with Pimpi and TL0 hybrids showing the highest SFW. Hybrids like TL0 x M82, TL0, L66, L96, and K x Pimpi achieved about 30% more SFW than the controls. Most hybrids exhibited greater root biomass compared to controls, with L76 hybrids (M82 and TA209) showing the highest root fresh weight (RFW), followed by L77 and TL0. Under nutrient-deficient conditions, all hybrids (except L66 xM82) produced higher fruit yields than Unidarkwin F1 NG and SG controls. Maxifort F1 was the most productive under these conditions. Among the hybrids, L76 and L77 xPimpi yielded 40-45% more than their parent lines (M82 and Pimpi) and the controls. Two root ideotypes were identified based on performance under nutrient deficit conditions: '**Deep, Light, and Thick**' (DLT), with long, thick, and scattered roots suited for water and nitrogen uptake, and '**Superficial, Dense, and Delicate**' (SDD), with fine, branched roots adapted to phosphorus-deficient soils. The best-performing hybrids (TL0 x Pimpi, TL0 x M82, 76 x Pimpi, L66 x Pimpi, and Maxifort) exhibited the DLT ideotype, associated with high leaf

nitrogen levels and efficient nutrient uptake. Lower-yielding hybrids showed the SDD ideotype, linked to higher leaf phosphorus and better performance in phosphorus-poor soils. Overall, hybrids demonstrated improved biomass and yield under low NPK conditions, suggesting a heterosis effect. Hybrids with Pimpi as a pollen donor and TL0 as the recipient showed the highest biomass and yield. These hybrids, particularly TL0 x Pimpi, TL0 x M82, and L66 x Pimpi, have potential as commercially viable rootstocks to improve nutrient and water efficiency, offering a sustainable solution for agriculture.

INTEGRATING SUSTAINABILITY CRITERIA INTO RAPESEED VARIETY PERFORMANCE TESTING - AN ON-FARM RESEARCH NETWORK TO ASSESS VARIETY PEST TOLERANCE

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Abstract Text:

It is now widely acknowledged that a shift toward more sustainable practices is essential. This is particularly true for rapeseed crops, which rely on multiple insecticide applications to control infestations by cabbage stem flea beetles (Psylliodes chrysocephala), rape stem weevils (Ceutorhynchus napi), and pollen beetles (Brassicogethes aeneus). Moreover, recent policy changes and rising insect resistance to phytosanitary products highlight the need for sustainable rapeseed protection. Varieties could be a potential lever, but further research is needed to evaluate their tolerance to pests. Moreover, organic farming in Switzerland only allows open pollinated varieties (OP), for which very few novelties are available.

In order to identify pest tolerant varieties, an on-farm organic network was set up to better understand the complex interactions between pest insects and rapeseed varieties. Data collection consistency was ensured across the trial network conducted throughout Switzerland. It included 10 strip trials with hybrids and OP compared over three years. Three of the hybrids were special varieties with different fatty acid composition. These varieties, grouped under the name “HOLL”, are widely grown in Switzerland for their ability to produce an oil suitable for cooking and frying. Pest attacks were evaluated (flea beetle bites and larvae, stem weevil oviposition punctures, number of pollen beetles per inflorescence) and linked to symptoms (bushiness, stem burst) as well as variety features (early vigour, biomass, spring vegetation recovery, collar diameter, stem elongation, yield).

These trials revealed differences in attractiveness to insects and associated symptoms between varieties. However, the lack of correlation between the two suggests a form of tolerance in some varieties The ranking of varieties based on yield reached in various locations subjected to various pest pressure provides insights into their pest tolerance. Variety ranking differed according to the insect considered, making it difficult to identify a general tolerance, even though the results regarding yield enabled us to identify varieties with better tolerance to each insect assessed individually. Yield was not correlated with infestation levels or symptoms observed, suggesting that vigour and compensatory capacity

were predominant in maintaining yield under extensive conditions. Overall, under moderate or low infestation rate, hybrid, open-pollinated and HOLL varieties do not show significant differences in yield while under a high infestation rate, hybrid varieties stand out with a higher yield.

MOLECULAR BREEDING APPROACHES TO SUPPORT ORGANIC WHITE LUPIN BREEDING IN SWITZERLAND

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Abstract Text:

White lupin (*Lupinus albus*, L.) is a very promising crop in organic farming. White lupins are extraordinarily efficient atmospheric nitrogen fixers through their symbiosis with *Bradyrhizobium lupini*. Under phosphorus deficiency, they form specialized root structures, cluster roots, that improve soil exploration and phosphorus use efficiency. Lupins are also biodiversity-friendly crops: their flowers are frequently visited by insects as they attract many pollinators to forage for their pollen. White lupin seed also has great potential as ingredient in plant-based protein foods because of the high protein content, ranging from 28 to 40% in materials (landraces, varieties and breeding lines) tested by FiBL. It has an excellent fibre content and it is gluten-free. Thanks to its desirable ratio of omega-3 to omega-6 fatty acids, non-starch carbohydrates, oligosaccharides and antioxidant content, white lupin seed can be an excellent component of a healthy diet.

FiBL is conducting a pre-breeding programme with the aim of developing material with (i) increased anthracnose resistance (the major fungal disease threat to this crop), (ii) low quinolizidine alkaloid content (these toxic and bitter compounds accumulating in white lupin seeds are a major obstacle to its use in food processing) and (iii) adapted maturation time for Central Europe (as it is used as a spring sown crop in this region). FiBL collaborates with gzpk (non-profit organic breeding organization) to jointly develop varieties for market-release.

In white lupin, anthracnose resistance is polygenically controlled, no complete resistance was observed and only few sources of resistance were identified. Quinolizidine alkaloids (QA) are water soluble and can be removed from the grain by water-based debittering, but this is water, energy and time consuming and difficult to apply where there is no wet step in the food production process. Hence, low QA content is a highly important breeding target. Alkaloid accumulation in the seeds has been described to be controlled by multiple loci, one major locus, *pauper*, with known causal mutation, and several other loci reported, but not genetically mapped.

The organic breeding programme started in 2014, with greenhouse crosses (from 2024 in the field) and all selection steps carried out in certified organic fields, supported by additional phenotyping of breeding lines for anthracnose resistance in climate chamber conditions. Since both anthracnose resistance and QA content are complex traits, the integration of molecular marker based diagnostic tools is envisaged to support the selection

process. We are therefore working to define strategies for combining phenotypic selection under organic conditions with molecular marker-based approaches that are affordable in our small-scale organic breeding programme. As with other minor crops, selection in white lupin lacks the molecular breeding tools (e.g. validated molecular markers) available for major crops, making our objective more challenging.

Therefore, as a first step, we have identified marker-trait assocations for anthracnose resistance and low-alkaloid content through GWAS, Genomic Prediction and Bulked Segregant Analysis. PCR-based markers were developed based on the identified associations from own studies and literature in order to apply marker assisted selection (MAS).

We present our current state of play in complementing phenotypic selection for anthracnose resistance and low alkaloid content with validated diagnostic PCR-based markers

IDENTIFICATION AND PHYSIOLOGICAL CHARACTERIZATION OF SOURCES OF RESISTANCE TO APHANOMYCES ROOT ROT IN PISUM

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Abstract Text:

The root rot caused by *Aphanomyces euteiches* (ARR) is one of the most devasting diseases that affect the production of peas (*Pisum*). Its destructive impact on the root system, combined with its ability to adopt long and high resistance structures that persist in the soil, makes this disease management challenging. Integrated control strategies, including crop rotation, biocontrol, and fungicides, have been employed; however, none of these approaches provides a complete solution. Breeding for resistant pea varieties has shown promising results, although only genotypes with tolerance or partial resistance have been identified to date (Lavaud et al. 2024; Wu et al. 2018).

To explore new sources of resistance, a diverse *Pisum* spp. collection of 322 accessions was evaluated. Six plants per accession were inoculated with 5 mL of a 1,000 zoospores/mL solution of two *Aphanomyces* isolates. Foliar symptoms were evaluated every 3 days using a 0-5 scale during 20 days after the inoculation (DAI). At the end of the experiment, accessions which present foliar symptoms index less or equal to 3, along with 10 highly susceptible accessions were selected for a second trial. In the second trial, the selected accessions were inoculated following the same procedure as in the first, but with an additional 10-fold higher inoculum concentration (1,000 and 10,000 zoospores/mL) for both isolates. The progression of the foliar symptoms was monitored as in the first trial. Additionally, at the conclusion of the experiment, root symptoms were evaluated on a 0-9 scale, and wet biomass weight was recorded. As a result, the foliar evaluation demonstrated a strong correlation with root symptomatology, providing a rapid, non-destructive alternative to the traditional root evaluation for identifying resistant genotypes. Despite most accessions displayed high susceptibility, a subset exhibited sustained health across all three measured parameters making them promising candidates for exploring new sources of resistance against this pathogen (Rodriguez-Mena et al. 2024).

With the objective to detect physiological differences in the response, 10 accessions with varying resistance levels were selected for a second experiment. Under controlled conditions, four plants per accession were inoculated with a 1,000 zoospores/mL solution of four *A. euteiches* isolates independently. As a control, four additional plants per accession were inoculated with water. Photosynthetic parameters were periodically monitored using the MultispeQ device (PhotosynQ, MI, USA) for up to 30 DAI. Additionally, foliar evaluations were conducted on the same days as the MultispeQ measurements, while root evaluations were performed at the end of the experiment. Differences between susceptible and resistant genotypes became apparent 26 DAI, with susceptible accessions showing an increase in the

PhiNPQ parameter and a decrease in PhiNO, Phi2, SPAD, LEF, and FvP/FmP compared to their respective controls. No significant differences were observed in resistant accessions. To simulate field conditions, 4 plants of the same accessions were inoculated with a 1,000 zoospore/mL solution of RB84, the most aggressive of the tested isolates, in 3 L pots in greenhouse. As in the controlled experiment, photosynthetic parameters were periodically measured for 90 DAI detecting the same pattern from 30 DAI onward. These findings confirm that photosynthetic differences among accessions correlate with their resistance levels to *A. euteiches*, validating the MultispeQ device as a reliable phenotyping tool for disease monitoring and early detection.

Reference:

Lavaud, C, Lesné, A, Leprévost, T and Pilet-Nayel ML (2024) Fine mapping of Ae-Ps4.5, a major locus for resistance to pathotype III of *Aphanomyces euteiches* in pea. Theoretical and Applied Genetics 137, [47]. https://doi.org/10.1007/s00122-024-04548-6

Wu L, Chang KF, Conner RL, Strelkov S, Fredua-Agyeman R, Hwang, SF and Feindel D (2018). *Aphanomyces euteiches*: A Threat to Canadian Field Pea Production. Engineering, 4, [542–551]. https://doi.org/10.1016/j.eng.2018.07.006

Rodríguez-Mena S, Rubiales D, González M (2024). Identification of Sources of Resistance to Aphanomyces Root Rot in *Pisum*. Plants, 13, [2454]. https://doi.org/10.3390/plants13172454

SECTION II | Breeding for Diversity

MARKER ASSISTED BREEDING OF ORGANIC HETEROGENEOUS WHEAT IN DENMARK

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Abstract Text:

Organic plant breeding started in Denmark 2006 with the attempt to develop Organic Heterogeneous Material (OHM) of wheat with baking quality, good weed competition and resistance to plant diseases, including common bunt. We conclude that OHM is preferable over pure line varieties as a strategy for organic farming, as both yield and baking quality is more stable than in pure line varieties. There seems to be a synergy of baking quality and taste between the components of a mixture. OHM can be composed by mixing of all offspring from crosses (original composite cross populations), but the mixture will be similar or slightly better than the average of the parents. It is therefore crucial to use only well adapted parents. If suboptimal parents are included, pure lines needs to be selected, and the OHM be composed only by selected offspring (complex variety mixture). Some traits are difficult but not impossible to improve further after the OHM have been composed. Baking quality can be improved by Single seed NIR sorting (eg. BoMill Insight® technology), colour sorting or by gravity sorting. However, at this point this can only increase gross grain protein content and seed hardiness but will not improve gluten index. To compose mixtures with optimal gluten index above the average of the parents, we have developed SNP markers for gluten subunits to be used for MAS in order to compose mixtures with a diversity of HMWG subunits within the mixture. Weed competition is best improved by visual assessment and selection for early vigour, and plant height before heading stage with due respect of the risk of lodging. Cereal Cyst Nematodes (CCN, Heterodera avenae) is in Denmark mainly a problem in spring wheat and no varieties on the EU Catalogue are resistant. The market for special varieties with this trait is limited as farmers tend to use non susceptible crops in case of nematode infestation of a field. Therefore CCN resistance should be included in all spring wheat as a preventive rather than a curative measure. Marker Assisted Selection (MAS) is the best way for selection, as field phenotyping is difficult and expensive. We have therefore developed SNP markers the Cre1 resistance gene for this selection. Common bunt needs special attention in organic breeding programs, as most varieties are susceptible. Only a few susceptible plants in an OHM is enough to maintain an infection, and close to all plants must therefore have resistance to the virulence in the region. Virulence are present in Europe against most of the known resistance genes, and pyramiding genes are therefore the only safe way for durable resistance to common bunt. We have identified 59 resistance genes and developed SNP markers to 20 of them for MAS. Leaf diseases such as mildew and in particular rust diseases can be devastating in organic farming. These diseases can be selected in the field based on leaf symptoms, but the experience indicates that if resistance is based on one or few vertical resistance genes, the varieties or OHM can turn susceptible within 1-3 years. Therefore, horizontal (adult plant) resistance genes or multiple vertical

resistance genes must be included to maintain durability of the resistance. We therefore develop SNP markers for the most important rust resistance genes for MAS. Funding organic plant breeding is difficult as the market is too small to fund the breeding. The OHM developed from this breeding program is therefore distributed via the member organisation Landsorten, based on home saved seed production to reduce cost for the seed production. Two OHMs have been officially registered, 'Mariagertoba®' and 'Popkorn', whereas other OHMs are produced in smaller amount without registration. By not selling seed, the activities of Landsorten is legal, and small seed lots can be distributed under the Article 3 exemption or research, trial and breeding purposes as a base for multiplication of home saved seed. Landsorten supports in this way a production of 1500ha of organic bred varieties in Denmark, England, Belgium and The Netherlands.

TAPPING COWPEA AGROBIODIVERSITY FROM MOZAMBIQUE WITH GENOMICS AND PARTICIPATORY APPROACHES TO ENHANCE LOCAL ADAPTATION

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Abstract Text:

Cowpea (Vigna unguiculata [L.] Walp) is an understudied and underappreciated crop that exhibits resilience to climatic extremes, is nutrient-rich, and is a staple in numerous sub-Saharan low-input agricultural systems. Cowpea is a source of proteins, helps improve soil fertility, and contributes to food security in marginal lands. To fully realise its potential, cowpea needs breeding programs aligned with local agroecological contexts and farmer preferences, improving the adoption of improved varieties by farmers and reducing genetic erosion from the vast allele pools maintained by local farmers.

This research focuses on the genetic and phenotypic analysis of a comprehensive collection of previously unexplored cowpea landraces from Mozambique and neighbouring countries. These cowpea genotypes have been selected and maintained by farmers in different agroecologies through repeated cultivation cycles and may have accumulated adaptation traits to local growing conditions and farmers' use and taste. We sampled 351 such accessions, including the entire collection maintained at the Mozambique gene bank. The accessions were genotyped using double digest restriction site associated with DNA genotyping (ddRAD), producing 202,946 high-quality SNP markers distributed on the entire genome. We further filtered our data to gain reliability and retained 49,727 SNP markers with higher minor allele frequency (MAF > 0.05). These markers were used to study genetic diversity in the collection, unveiling unique genetic diversity found from the cowpea accessions from Mozambique. Discriminant Analysis of Principal Components (DAPC) was used to assess the population structure by clusters, unveiling three genetic clusters best describing the allelic frequencies. We found that there were samples from Mozambique in all three clusters, suggesting that other factors besides geographical origin account for genetic diversity in this cowpea allele pool.

The collection was also characterised by its phenotypic diversity with two approaches. On one hand, a subset of cowpea accessions was phenotyped with an imaging approach for seed-related traits, such as seed shape, seed coat colour, seed coat pattern, seed area, and seed circularity. On the other hand, a participatory variety selection (PVS) approach was carried out on 351 accessions in open fields to identify the best genetic combinations from a

breeding perspective. Our study reveals that gender differences exist in cowpea trait preferences such as seed coat colour, grain size, and growth habit. However, traits such as drought tolerance, short cycle, pod size, and pest and disease tolerance are among the most preferred traits from both men and women. We argue that breeding for features that women and men want may receive the same consideration as programmes that aim to increase genetic improvements for yield improvement and abiotic challenges. Integrating farmers' needs and preferences into breeding programs that align with the genetic diversity found in Mozambique cowpea landraces may lead to resilient cropping systems and food security.

PEA EVOLUTIONARY POPULATIONS DISPLAY SPECIFIC ADAPTATION TO PURE STAND OR INTERCROPPING AND PERFORM COMPARABLY OR BETTER THAN THEIR BEST PARENT CULTIVAR

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Abstract Text:

Modern agriculture caused a substantial genetic erosion of cultivated inbred crops by replacing landrace populations with a small number of genetically homogeneous cultivars grown across vast areas. Reintroducing genetically heterogeneous cultivars may counterbalance this trend and stabilize the crop yields across environments characterized by increasing climate unpredictability. Evolutionary populations (EPs) are heterogeneous cultivars with lower selection cost than pure lines or mixtures of lines. The agronomic value of these populations has scarcely been explored for grain legumes despite the crucial importance of these crops for the sustainability of low-input farming systems. Adopting pea (Pisum sativum L.) as a model grain legume, this study aimed to: (a) assess the specific adaptation to pure stand (PS) or mixed stand with cereals (MS) of EPs derived from the same genetic base that had evolved under PS or MS conditions, and compare the yielding ability, competitive ability, and farmers' acceptability of these populations with those of their six parent cultivars; (b) compare one EP selected for Central Italy with its three parent cultivars for yielding ability, acceptability by farmers, and yield stability. All the EPs originated from crosses among a small number of elite semi-dwarf, semi-leafless parent cultivars with high yielding ability and yield stability across Italian environments in previous studies. The EPs underwent several generations of natural selection (from pooled F2 seed) in their target growing conditions. The adaptation to PS or MS cropping of the EPs that evolved under either condition and their parent cultivars was assessed in Lodi (Northern Italy), one year under conventional crop management and another year in an organic system. The EP selected for Central Italy and its parent cultivars were evaluated (a) for yielding ability and farmers' acceptability over two years in Perugia (Central Italy) under an organic management, and (b) for yield stability as Environmental variance and yield reliability as lowest yield expected in 80% of cases across seven environments (two years each in Central Italy, coastal Algeria, and inland Morocco; and one environment with managed drought in Northern Italy). Farmers' acceptability was evaluated by organic farmers by a nine-level visual score attributed a few weeks before crop harvest. Additional agronomic traits were evaluated in PS experiments.

Pea in intercropping was at competitive disadvantage, with an average pea proportion of 24% on total crop dry grain yield. The EPs displayed definite specific adaptation to the condition of MS or PS under which they had evolved, showing a grain yield advantage (P <

0.05) in that condition relative to the other population. The EP that evolved in MS showed grain yield and competitive ability in this condition that were higher than the average value of its parent cultivars and very similar to those of the best-performing parent cultivar. Likewise, the EP that evolved in PS showed grain yield in PS very similar to that of the top-yielding parent cultivar, along with top-ranking total biomass, and higher values of farmers' acceptability, resistance to Ascochyta blight and plant height than the mean of its parent cultivars. The EP selected for Central Italy out-yielded any parent cultivar (P < 0.10) and showed top-ranking values of farmers' acceptability and plant height in this region. In addition, this EP exhibited top-ranking yield reliability across the seven environments due to high mean yield and/or yield stability compared with its parent cultivars. In conclusion, the EP material could display high adaptation to environments under which it evolved, as well as high yield stability and adaptability conferred by its genetic heterogeneity. These results confirm previous findings for EP material of pea assessed in eight environments of Northern and Central Italy featuring organic or conventional management and PS or MS cropping (Annicchiarico et al., 2023). The current EPs selected for PS cropping in Northern or Central Italy have been registered as organic heterogeneous material under the names of Ellen and Alice, respectively.

Reference:

Annicchiarico P, Russi L, Romani M, Notario T, and Pecetti L (2023). Value of heterogeneous material and bulk breeding for inbred crops: a pea case study. Field Crops Research 293, 108831. https://doi.org/10.1016/j.fcr.2023.108831

EXPLORING PLANT-PLANT INTERACTIONS BETWEEN BRASSICA OLERACEA AND ALLIUM FISTULOSUM TO PROVIDE NEW INSIGHTS FOR BREEDING FOR INTERCROPPING

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Abstract Text:

Intercropping, the agricultural practice of cultivating two or more crop species or genotypes on the same field is gaining increased attention in developed countries due to its potential to increase yield and yield stability, enhance aboveground biodiversity (Juventia & van Apeldoorn. 2024) and promote soil health (Cong et al. 2015). With the rising focus on implementing intercropping, there is a need for plant breeders to explore genetic diversity and select for cultivars better suited to intercropping systems. Brassica–Allium intercropping has shown promising results in terms of both crop productivity and pest suppression across multiple field trials (Asare-Bediako et al. 2010, Carrillo-Reche et al. 2023). As a model intercropping system, it also provides a contrasting context for how different crops interact with soil life. Alliums are considered 'outsourcing' plants, forming beneficial associations with arbuscular mycorrhizal fungi (AMF), whereas Brassicas are 'do-it-yourself' plants that do not form such associations (Lambers & Teste. 2013). Interestingly, contrary to the outcomes from field trials, there is ample literature suggesting that Brassicas are not the best companions for AMF host plants. Some studies suggest that the glucosinolate compounds present in the Brassicaceae species can adversely affect the growth and root colonization of AMF host plants which result in a growth reduction. Furthermore, there is evidence to suggest that AMF can also negatively impact the growth of AMF non-host plants by infecting their root tissue (Veiga et al. 2013).

The objective of this project was to investigate plant-plant interactions between *Brassica oleracea* and *Allium fistulosum*, providing breeders with new insights to optimize breeding strategies for intercropping systems. In a two-year field experiment, we assessed this crop species combination by evaluating 11 Brassica genotypes representing different morphotypes (Broccoli, Brussel sprouts, Cabbage and Kale) when intercropped with a single Allium genotype. In addition to the intercropping system, we included corresponding monocropping of each genotype to assess their effects on overall system performance. We collected data on yield, AMF colonization of Allium roots, and both above and belowground plant functional traits of Brassica and Allium plants to better understand the impact of phenotypic and genotypic variation on intercropping performance. We observed significant variation in the plasticity of functional traits between and within Brassica morphotypes when

intercropped with Allium, compared to when they were grown as a monoculture. This variation highlights the diverse responses of Brassica genotypes under intercropping conditions. Notably, most of the Brassica genotypes did not reduce AMF colonization on Allium roots. Based on the performance of both crops, we identified specific Brassica genotypes that show strong potential as effective companions in intercropping systems. We conclude that investigating plant-plant interactions with a wide range of contrasting genotypes is a valuable tool that can provide breeders with new insights for developing crop varieties optimized for intercropping systems, and that despite variations in their interactions with AMF and differences in competitive dynamics, the Brassica-Allium combination is a promising species combination that can increase crop performance and merits further investigation to unravel the mechanisms behind these interactions.

Reference:

Juventia, S. D., & van Apeldoorn, D. F. (2024). Strip cropping increases yield and revenue: multi-year analysis of an organic system in the Netherlands. Frontiers in Sustainable Food Systems, 8. https://doi.org/10.3389/fsufs.2024.1452779

Lambers, H., & Teste, F. P. (2013). Interactions between arbuscular mycorrhizal and non-mycorrhizal plants: do non-mycorrhizal species at both extremes of nutrient availability play the same game? Plant, Cell & Environment, 36(11), 1911–1915. https://doi.org/https://doi.org/10.1111/pce.12117

BREEDING FOR CROP MIXTURES: ROOT PHENOTYPING FOR TRAIT MATCHING IN LUPIN-WHEAT INTERCROPPING

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Abstract Text:

Agricultural intensification has progressively reduced the agro-ecosystem biodiversity through monoculture and large use of crop inputs, thereby disrupting the complex interplay and functional complementarity between species on which the system self-sustainability and resilience depend. Intercropping can help mitigate this trend by increasing agricultural biodiversity and ecosystem services in a more sustainable agro-ecological vision. Breeding has mostly focused on monoculture and novel programs specific for intercropping are envisaged (Annicchiarico et al. 2019). A large part of plant-to-plant interactions occurs in the underground. Breeding for intercropping should, therefore, necessarily involve selecting for root traits that maximize facilitative interactions. Phenotyping roots in crop mixtures is especially challenging and time-consuming. This work, to the best of knowledge, is the first root phenotypic screening of white lupin (Lupinus albus L.) for intercropping breeding, with a focus on affordable, high-throughput phenotyping. An indoor (in rhizoboxes) and a field experiment were carried out to study the effect of spring wheat (Triticum aestivum L.) intercropping on lupin root architecture. In the rhizobox experiment, we compared two contrasting lupin genotypes for plant height, namely the tall 5/23 and the intermediate-size 17/124, under the hypothesis that shoot traits were positively correlated with root traits and competitive ability. We used fast and simple indexes of root interaction based on a novel graphical measures of root zone overlap: the root merge index (Rossi et al., 2024) and root 2D projected area. In the field experiment, we applied the 'shovelomics' (Trachsel et al., 2013) at flowering stage. We screened five genotypes (cv. Arsenio, 1/46, 5/65, 17/124 and 5/23) in pure stand or intercropped with the spring wheat cv. Nefertari. In both trials we found significant differences between lupin genotypes, as well as different responses to intercropping. In the rhizobox experiment, 5/23 produced more biomass than 17/124. The difference was enhanced by intercropping, where 5/23 produced +45% biomass than 17/124, compared to +29% in pure stand. Lupin root area increased in intercropping compared to pure stand (+17.8%) and was consistently larger in 5/23 than in 17/124 (+15% on average). Both genotypes exhibited root avoidance between plants in pure stand and a large root overlap with the neighbour wheat plant in intercropping (47% and 87% average root area overlap between neighbouring plants in the two conditions, respectively). In intercropping, extensive root intermingling is generally associated to facilitative interactions. Genotype 5/23 showed a higher shoot and root vigour than 17/124, as well as more rhizobial nodules (+42%), all traits being suggestive of a greater competitive ability in intercropping. In the field experiment, intercropping reduced lupin biomass by 40% (average across

genotypes). Consistent with the rhizobox experiment, genotype 5/23 produced more biomass than 17/124 and about twice the biomass of least vigorous genotype 1/46, and had the least biomass reduction in intercropping (-27%). GxE interaction was found for lateral root number. Intercropped 17/124 increased the number of lateral roots in the topsoil (+22%) while 1/46 showed the largest reduction (-25%) compared to the pure stand. The root gravitropic angle (RGA) increased by 8% in intercropping compared to the pure stand, with two genotypes, 1/46 and cv. Arsenio, displaying the greatest plasticity (46% and 20% wider angles in intercropping, respectively). RGA is generally interpreted in terms of root foraging strategy; in intercropping it can be an indicator of crop tendency to avoid or interact with the companion. In our case, there did not seem to be a relationship between RGA and plant performance in intercropping. Further work is needed to assess if wider RGA was associated to root confinement in shallow layers due to competition. Genotype 5/23 confirmed also in the field experiment its great nodulation ability. Taproot diameter (a conservative trait associated to resource storage, hydraulic conductivity and penetration ability) was reduced by intercropping. Interestingly, the most promising genotype 5/65 also showed the least decrease of taproot diameter in intercropping. In conclusion, our study indicated that lupin genotypes can respond differently to wheat intercropping for root traits such as root area, area of root overlap between neighbouring plants, and taproot diameter, and suggested that this variation can be correlated to competitive ability. These responsive yet relatively high-throughput traits should therefore be included in phenotyping for intercropping.

Reference:

Annicchiarico P, Collins RP, De Ron AM, Firmat C, Litrico I and Hauggaard-Nielsen H. (2019). Do we need specific breeding for legume-based mixtures? Advances in Agronomy, 157, 141-215.

Rossi R, Cavalli D, Notario T, Passerini A, Morone G, Pecetti L (2024). A low-cost simple and rapid phenotyping platform to study early belowground interactions in intercropping. Proceedings of the 53rd Conference of the Italian Society of Agronomy (Bindi M., Di Miceli G., Maggio A., Eds.) Matera, Italy, 11th-13th September 2024, pag. 236-237.

Trachsel S, Kaeppler SM, Brown KM & Lynch JP (2011). Shovelomics: high throughput phenotyping of maize (Zea mays L.) root architecture in the field. Plant and soil, 341, 75-87.

EVALUATION OF THE ASSOCIATION OF A PGPB RCA25 WITH INTROGRESSION LINES (ILS) OF ORYZA RUFIPOGON X ORYZA SATIVA CV VIALONE NANO

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Abstract Text:

Rice (Oryza sativa) is a monocotyledonous plant and is one of the most important crops in the world as it is a staple food for more than half of world population. Rice domestication and varietal selection in Europe (ssp. japonica) and in Asia (ssp. indica) improved desirable agronomic traits but also lead to lose different genetic traits, while the wild relative O. rufipogon possesses greater allelic variation and it is a donor of genetic variability. Besides that, rice cultivation is facing different problems worldwide. Even the soil itself presents a decrease in microbial biodiversity due to the use of fertilizers and paddy soil promotes waste of water, greenhouse gas emissions (CH4) and the increase of bioavailability of some heavy metal, such as Arsenic, whose accumulation in the pericarp of whole seeds can have implications on human health. There are different possible solutions to achieve sustainable rice cultivation. One of these is the exploitation of the genetic variability lost during domestication. Analysis of various crops and their wild relatives highlighted differences in the composition of the root/rhizosphere microbiome (such as AMF and PGPB) and genetic loci involved in establishing these traits in tomato and barley. The microbiota associated with wild relatives evolved under marginal soil conditions, thus representing an untapped resource for low-input agriculture. In particular, the wild rice Oryza rufipogon accession 602-131-2 showed an aptitude to associate with RCA25-Kosakonia sacchari, an endophytic strain recently reclassified (Enterobacteriaceae), at least sixty times more than Vialone Nano (O. sativa ssp. Japonica), variety currently renowned and cultivated in Italy (unpublished data). K.sacchari presents nitrogenase activity, thus increasing nitrogen fixation in plants and productivity in some rice varieties. Our research project aims to identify genomic regions of Oryza rufipogon involved in the association between roots and the selected PGPB by using introgression lines (ILs) obtained from the crossing between Vialone Nano and O. rufipogon 602-131-2. The ILs are being screened to detect their capability to associate with K.sacchari, by applying a specific protocol for seedlings inoculation. Phenotyping for the association aptitude with the tested strain is being conducted by counting the colony forming units (CFU) obtained from roots homogenate. Preliminary data are showing an outstanding variability in the association with RCA25, thus reflecting a genetic variability and suggesting the presence of genetic loci that promote bacterial colonization, putatively host genes

involved in immune response or microbe recognition mechanisms, which enhance the ability to interact with endophytes such as RCA25-Kosakonia sacchari. Analysis of these phenotypic data with respect to SNPs generated by low pass sequencing of the ILs is currently underway for the identification of rice loci possibly affecting the root colonization by this PGPB.

MAIZE BREEDING FOR INCREASING CAROTENOID CONTENT IN THE GRAIN

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Abstract Text:

Maize is a major food source especially in developing countries, and a major component of livestock feed. But the amounts of some essential nutrients in maize kernels may be deficient for these consumers. Carotenoids can be found in several organs in maize, including the grain (Revilla et al. 2022), although the most common white maize varieties are deficient in carotenoids. We have carried out a full-sib intrapopulation recurrent selection for increasing the grain carotenoid content of the maize population Fino, a Plata-type maize with flint orange grains. Five cycles were carried out by sib-pollinating more than 200 plants and selecting the 20 ears with the darkest orange color in the grain. The objectives of this study were (1) to evaluate the response of total carotenoid content to selection, and (2) having carotenoids a strong antioxidant activity, to explore the effects of an increased carotenoid content on the response of maize plants to drought and cold as stresses associated with oxidative damage.

The response to carotene selection was significant and positive for most individual and total carotenes in the grain; accordingly, effective selection was also reported for other pigments (Rodríguez et al. 2013). In addition, there were high correlations between some individual carotenes and total carotene content in grains and leaves.

Some individual carotenes can have significant effects on physiological and agronomic traits, such as beta-carotene, which has a significant negative effect on stomatal conductance and basic fluorescence (Fo); esters have a negative effect on photosynthesis, efficiency of the photosystem II, early vigor and plant height. Total carotene content in the grain has a positive effect on stomatal conductance; zeaxanthin in the grain has a significant negative effect on photosystem efficiency; finally, the ratio of adamantine/lutein affects the ear length and the number of grains per row. Under drought conditions, yield was lower in all cycles compared with control conditions, and the selection response of carotenoid content under drought conditions was not significant for agronomic or physiological traits. In contrast, β-carotene significantly increased germination rate under cold conditions.

Therefore, carotenoid content in maize grains can be improved though phenotypic selection for grain color in order to increase the value of maize as a healthy food, and the tolerance to oxidative stresses.

Reference:

Revilla P, Alves ML, Andelković V, Balconi C, Dinis I, Mendes-Moreira P, Redaelli R, Ruiz de Galarreta JI, Vaz Patto MC, Žilić S, and Malvar RA (2022) Traditional foods from maize (Zea

mays L.) in Europe. Frontiers in Nutrition 8 :1235.
https://www.frontiersin.org/article/10.3389/fnut.2021.683399.
DOI=10.3389/fnut.2021.683399

Rodríguez VM, Soengas P, Landa A, Ordás A, and Revilla P (2013) Effects of selection for color intensity on antioxidant capacity in maize (Zea mays L.). Euphytica 193:339-345, DOI 10.1007/s10681-013-0924-0

EVALUATION OF TOMATO TRADITIONAL VARIETIES (SOLANUM LYCOPERSICUM) FOR DROUGHT TOLERANCE UNDER ORGANIC FARMING CONDITIONS

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Abstract Text:

The production of tomato (Solanum lycopersium L.) is severely affected by abiotic stresses, causing up to a 75% of yield loss, depending on the type of stress, developmental stage, genotype, and duration (Dariva et al., 2021). From these stresses, drought is the most common, given that only 15% of the agricultural land worldwide is well-irrigated (FAO, 2022). This is particularly relevant in the Mediterranean areas, where the edaphoclimatic conditions might promote low water availability and salination of soils. Tomato is sensitive to drought, due to its lack of novel tolerance genes to this stress, causing severe damage and, even, plant death. Mainly, drought disturbs tomato plant physiology and alters the osmotic balance in the cells, producing reactive oxygen species (ROS) (Kirshna et al., 2022). Moreover, the quality of fresh fruits can be affected because of the alteration of sugars, acids and antioxidant compounds, the main quality components in tomato (Bai et al., 2023). Tomato traditional varieties have been grown by farmers during centuries, constantly adapting to changes in the environment, and avoiding the severe selection which caused loss of tolerance genes and flavor. This work aims to show the importance of landraces as breeding materials for improving drought tolerance and promoting a more sustainable and efficient use of water resources. Moreover, we want to present traditional varieties as a good alternative to revert lack of flavor in commercial tomatoes.

For this purpose, ten traditional cultivars of the western Mediterranean coast, representing different typologies, were grown in organic farming under two different irrigation levels: a 100% irrigation or control treatment and a 40%-reduced irrigation treatment. The experimental design included five plants per bulk and three bulks in a randomized design. After harvesting the fruits, yield was calculated as kg m-2 and ripen tomatoes were used to analyze antioxidant content (carotenoids and flavonoids), sugars (glucose, sucrose, and fructose) and organic acids (citric, malic and oxalic acid) by High Performance Liquid Chromatography (HPLC) as described by Guijarro-Real et al. (2023). In average, our results showed a reduction in yield for most of the studied varieties. However, some landraces were more stable in terms of production, suggesting that many landraces are quite tolerant to drought. In terms of fruit quality, we observed that sugars and acids depend on the treatment and the genotype, while antioxidants like carotenoids and flavonoids were more dependent on the genotype and less altered with the treatment. Moreover, some genotypes accumulated more sugars when drought was applied. In agreement with our findings,

previous reports indicate an increase of these compounds under drought stress in commercial tomato varieties, due to the 'accumulation effect', enhancing tomato overall flavor (Medyouni et al., 2021; Bai et al., 2023). These results could set the basis for new breeding strategies involving traditional varieties, improving drought tolerance but, also, maintain yield, and improve sensory fruit quality under organic culture.

Reference:

Bai, C., Zuo, J., Watkins, C.B., Wang, Q., Liang, H., Zheng, Y., Liu, M., Ji, Y. (2022). Sugar accumulation and fruit quality of tomatoes under water deficit irrigation. Portharvest Biology and Technology 195(2023), [112112]. https://doi.org/10.1016/j.postharvbio.2022.112112

Dariva, F.D., Pessoa, H.P., Ferreira Copati, M.G., Queiroz de Almeida, G., Filho, M.N., Picoli, E.A., França da Cunha, F., Nick, C. (2021). Yield and fruit quality attributes of selected tomato introgression lines subjected to long-term deficit irrigation. Scientia Horticulturae 289(2021), [110426]. https://doi.org/10.1016/j.scienta.2021.110426

Food and Agriculture Organisation of the United Nations (FAO). (2022). Available at: https://www.fao.org/home/es (Accessed: January 2025).

Guijarro-Real, C., Adalid-Martínez, A.M., Pires, C.K., Ribes-Moya, A.M., Fita, A., Rodríguez-Burruezo, A. (2023). The Effect of the Varietal Type. Ripening Stage, and Growing Conditions on the Content and Profile of Sugars and Capsaicinoids in Capsicum peppers. Plants, 12(2), [321]. https://doi.org/10.3390/plants12020231

Kirshna, R., Ansari, W.A., Soumia, P.S., Yadav, A., Jaiswal, D.K., Kumar, S., Singh, A.K., Singh, M., Verma, J.P. (2022). Biotechnological Interventions in Tomato (Solanum lycopercosum) for Drought Stress Tolerance: Achievements and Future Prospects. BioTech 11(4), [48]. https://doi.org/10.3390/biotech11040048

Medyouni, I., Zouaoui, R., Rubio, E., Serino, E., Ahmed, H.B., Bertin, N. (2021). Effects of wáter déficit on leaves and fruit quality during the development period in tomato plant. Food Science & Nutrition, 9(4), [1949-1960]. https://doi.org/10.1002/fsn3.2160

SECTION III | Breeding to meet societal challenges

SUITABILITY OF A NETWORK MODEL TO FACILITATE TESTING AND INCREASE ADOPTION OF ORGANIC SEED: REFLECTIONS FROM 12 YEARS OF THE NORTHERN ORGANIC VEGETABLE IMPROVEMENT COLLABORATIVE (NOVIC)

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Abstract Text:

Access to seed of adapted varieties that meets agronomic, and market needs of organic farms is essential to the optimization of organic agriculture. Organic farms in the Global North are often smaller scale, decentralized and highly diversified in crop type and markets and thus centralized research station trials may not represent the range of on-farm environments and desired crop ideotypes. For plant breeders and seed companies this presents challenges to efficiently and effectively test the agronomic and market suitability of organically available varieties. Despite the challenges researchers broadly recognize that advancing organic seed systems necessitates testing under organic conditions and soliciting input from organic farmers familiar with their production environment and market demands. For these reasons farmer-participatory network approaches are proposed to improve representation of trial results across the range of farm environments (Lyon et al. 2019, Rivière et al. 2021). The Northern Organic Vegetable Improvement Collaborative (NOVIC) in the USA sustained a participatory plant breeding and variety testing network, across four geographic regions, over the span of 12 years with the aim of achieving these goals (https://eorganic.info/novic).

The NOVIC project employed a mother-daughter variety trial design as first described by Snapp (1999). Researchers evaluated crops in replicated trials with three replications at each research station and single plots of the full set of varieties on at least three farms per crop per region with each farm environment representing blocks as a replicated complete block design (RCBD). All four regions evaluated all crops involved in breeding activities (5-7 crops

per 4-year project period) each year and the farmers within each region identified additional crops for trials based on regional farmer priorities. The current study analyzes reflections from NOVIC researcher and participant experience collected through surveys and interviews. It presents outcomes, lessons learned and recommendations for future trial networks. The collective experience of the farmers and researchers over the course of the three phases of the project serves as a prime opportunity to assess the outcomes and lessons learned to inform future projects. It also serves as an opportunity to assess the suitability of a network-model for making suitable seeds of adapted varieties available for organic farmers, involving the participatory research methodologies employed.

Plant breeding efforts of NOVIC researchers resulted in development of 43 new varieties of 10 different species. The trial network supported testing and commercialization of an additional 6 new varieties released by project farmer breeders or other researchers. The network facilitated farmer adoption of these varieties and additionally, identified organic seed of suitable varieties available from organic seed companies, thus expanding market access. Researchers and farmers alike however struggled with time limitations, narrow evaluation windows of vegetable crops and evaluator consistency impacting quality of on-farm data. Eighty-six percent of farmers responding to the survey (n=31), and all nine farmers interviewed, reported that they purchased and planted seed of new varieties as a direct result of participation in the trials; 90% indicated that at least some of the new varieties were of certified organic seed. While NOVIC achieved many positive outcomes, at times the researchers and farmers alike experienced limitations in capacity, leaving gaps in communication and farmers wishing for greater engagement of researchers on their farm and at times resulting in turnover in participating farmers. Participants highlighted the importance of the role of trial coordinator in network facilitation. The experience of NOVIC underscores the importance of recognizing the cost, time, and skills necessary to maintain and foster relationships in a participatory network and the potential return on investment in project impacts.

Knowledge exchange, relationship building, expanded awareness of crop qualities, market access, and insights into seed system dynamics emerged as project highlights among network participants. Decision making dynamics shifted across the 12-year span toward expanded farmer consultation in trial objectives and regional autonomy in choice of crops and trial goals reflecting the dynamic regional nature of organic farms. Positive impacts and sustained engagement for over a decade are attributed to adaptability in management informed by iterative participant reflections during the project.

Reference:

Lyon A, Tracy WF, Colley M, Culbert P, Mazourek, M, Myers, J, Zystro J and Silva EM (2019) Adaptability analysis in a participatory variety trial of organic vegetable crops. Renewable Agriculture and Food Systems 35: 296-312. https://doi.org/10.1017/S1742170518000583

Rivière P, Goldringer I, Rey F (2021) Selecting the appropriate methodology for organic on-farm variety trials. Rey F and Flipon E (eds.) LiveSeed. https://www.liveseed.eu/wp-content/uploads/2021/07/PUBLICATIONITAB_LIVESEED.final_.pdf

Snapp S (1999) Mother and baby trials: a novel trial design being tried out in Malawi. Target – Newsletter of the Soil Fertility Research Network for Maize-based Cropping Systems in Malawi and Zimbabwe. 17 (8).

PARTICIPATORY AGRONOMIC DIAGNOSIS, A NEW APPROACH TO COMBINE FARMERS' EXPERTISE AND AGRONOMIC SCIENCES

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Abstract Text:

A good agronomic diagnosis is critical to understand and analyse on-farm trials. They can be classified into three types. Oral agronomic diagnosis, based on farmers' expertise, is rapid and inexpensive, but subjective (Banerjee, 2015). Conventional diagnosis is based on field measurements and agronomic interpretation, with back-and-forth comparisons between plot and network scales (Doré et al., 1997), but it is cumbersome and neglects farmers' expertise. Automatic diagnosis uses field measurements and processes numerous indicators to explain yield at the network scale (Gouache et al., 2015), but it is also complex, leave little room for practitioner knowledge and neglect plot-specificities. For a more comprehensive approach, we proposed a participatory agronomic diagnosis (PAD) that combines farmers' internal diagnosis with a conventional diagnosis. We applied it to a participatory on farm experiment to test farmers' varieties of wheat (Triticum aestivum L.). The study had two objectives: (i) to promote the farmers' expertise in interpreting the results, while enabling the farmers to gradually take on board the agronomists' expertise, in order to question and supplement their own diagnosis; (ii) to test hypotheses on the adaptation of farmers' varieties to environmental factors. In 2021-22 and 2022-23, 77 wheat varieties have been evaluated in organic conditions through a network of 32 trials (farm x year x practice), of which 20 varieties were replicated in more than four environments. The DAP consisted of five steps: -1 The research team proposed a conceptual model based on literature and experience, identifying the environmental factors impacting wheat yield. -2 Farmers formulated hypotheses on the causes affecting yield in their trials. -3 A structured discussion between farmers and the research team enabled farmers' hypotheses to be verified or new ones to be formulated, leading to a hybrid diagnosis. -4 Reasons why certain varieties seemed better adapted to certain environments, were identified based on the expertise of farmers and the research team. -5 The research team proposed a synthesis of knowledge from hybrid diagnostics at the network- scale to validate varietal adaptation hypotheses. The data collected included information on the trial context, environmental and agroclimatic indicators, stand condition and yield components. Measurements were recorded at different stages of wheat development by the research team and farmers. Statistical models (Rivière et al 2015; Turbet-Delof et al 2024) were used to compare varieties within trials, between trials, and to assess the adaptation of varieties to stresses. Hybrid diagnostics were conducted during interviews lasting 1h30 to 2h. A high variability in yield components was observed between trials, with yields ranging from 4.8 to 43.1 qx/ha. The hybrid diagnoses allowed to confirm 74 hypotheses formulated by the farmers while 43 unformulated hypotheses

emerged during the discussions. In some cases, the proposed indicators were questioned and led to constructive criticisms from the farmers. Of the 24 yield-limiting factors identified in the hybrid diagnostics, six were widespread in the trials: lack of nitrogen, weed competition, water deficit, high temperatures and stand establishment problems. Although the limiting factors were identified at trial level, the comparison of yield and yield components between stressed and unstressed situations were very consistent for the six main stresses. For example, trials that experienced water stress between 1cm ear stage and flowering led to a lower number of plants per m2, with partial catch-up through the number of grains per ear. Finally, it was more challenging to test the varietal adaptation hypotheses as only a few of them could be confirmed or rejected. The study demonstrated that participatory agronomic diagnosis enabled farmers' expertise to be integrated into the analysis of results, and promotes a detailed understanding of the specific features of each production situation. It made it possible to objectify farmers' internal diagnoses, identify factors not initially considered, and criticize methods for estimating environmental indicators. The results were consistent across trials, enabling global analysis. Yet, there is still a need to improve methods for validating hypotheses on the adaptation of varieties to specific stresses. Although the method is complex and requires rapid analysis of many heterogeneous data, it responds to issues of democratization of science by creating an analysis community and valuing farmers' interpretation.

Reference:

Banerjee, R.R., 2015. Farmers’ perception of climate change, impact and adaptation strategies: a case study of four villages in the semi-arid regions of India. Natural Hazards 75, 2829–2845. https://doi.org/10.1007/s11069-014-1466-z Doré, T., Sebillotte, M., Meynard, J.-M., 1997. A diagnostic method for assessing regional variations in crop yield. Agricultural Systems 54, 169–188. https://doi.org/10.1016/S0308-521X(96)00084-4 Gouache, D., Bouchon, A.-S., Jouanneau, E., Le Bris, X., 2015. Agrometeorological analysis and prediction of wheat yield at the departmental level in France. Agricultural and Forest Meteorology 209, 1–10. Rivière P, Dawson JC, Goldringer I, David O. (2015) Hierarchical Bayesian modeling for flexible experiments in decentralized participatory plant Breeding. Crop Science 55(3): 1053-1067. DOI: 10.2135/cropsci2014.07.0497 Turbet-Delof M, Rivière P, Dawson JC, Gauffreteau A, Goldringer I, van Frank G, David O. (2024) Bayesian joint-regression analysis of unbalanced series of on-farm trials. HAL, ver.2, peer-reviewed and recommended by PCI Math Comp Biol https://hal.science/hal-04380787

SCALING UP PARTICIPATORY PLANT BREEDING FOR DIVERSIFIED AGRICULTURAL SYSTEMS

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Abstract Text:

As weather patterns become increasingly erratic, breeding and commercialization frameworks must evolve to support greater cultivar diversity while maintaining cost-effective development and adoption strategies. Participatory plant breeding (PPB) provides a powerful, decentralized approach to developing and testing regionally adapted varieties that meet the needs of organic and diversified agricultural systems. By directly engaging farmers in the breeding process, PPB fosters rapid adoption, reduces the cost of field testing, and improves the resilience of local food systems (Ceccarelli, 2015; Dawson et al., 2017). However, scaling participatory research requires new tools and methodologies to coordinate widespread testing while maintaining scientific rigor. Advances in digital technology and statistical modeling now facilitate decentralized trialing, enabling collaborative networks to generate large, high-quality datasets at a fraction of the cost of traditional breeding methods (Van Etten et al., 2019). Through the integration of genotype-by-environment (GxE) interaction modeling, AI-driven analytics, and participatory evaluation, we can enhance breeding precision while simultaneously engaging a broader spectrum of stakeholders in the breeding process (Steinke et al., 2017). This presentation will highlight how SeedLinked's digital platform has scaled up PPB by leveraging crowdsourced data, real-time analytics, and machine learning algorithms to streamline variety testing and selection. In the past six years, over 13,000 growers have participated in trials spanning 55 crops and multiple production systems, contributing more than 400,000 data points. These efforts have led to a 70% increase in adoption rates, demonstrating the impact of integrating digital technology with community-driven breeding initiatives (Enjalbert et al., 2025). Key case studies will be presented, including a multi-environment sprouting broccoli breeding initiative aimed at improving resistance to Alternaria and black rot while optimizing flavor and regrowth traits for organic systems in the U.S. Midwest (Dawson et al., 2025). This project, conducted in collaboration with independent breeders and small seed companies, exemplifies how decentralized trial networks can accelerate selection in outcrossing crops with complex trait requirements. Additionally, we will discuss a tomato breeding project focused on enhancing Septoria leaf spot resistance through multi-location participatory trials, showcasing the integration of molecular markers with farmer-led evaluations (McCaslin et al., 2025). Looking forward, the future of participatory breeding will rely on enhancing predictive modeling through GxE analysis, expanding interoperability with global breeding databases, and refining AI-assisted variety recommendations. Our goal is to develop robust, data-driven decision-making tools that empower independent breeders, farmers, and seed companies to identify and commercialize high-performing, regionally adapted cultivars efficiently (Hellin et al., 2008; Morris & Bellon, 2004). By demonstrating the scalability of participatory plant

breeding through digital collaboration, this work contributes to a paradigm shift in variety development—one that balances genetic diversity, farmer autonomy, and agronomic resilience in the face of climate change.

Reference:

Ceccarelli, S. (2015). Efficiency of Participatory and Conventional Breeding in Rainfed Environments of the Developing World. Annual Review of Plant Biology, 66, 541-563. Dawson, J., et al. (2017). Organic Seed Alliance Variety Trials: Assessing Adoption Barriers and Performance Metrics. Journal of Organic Agriculture Research, 12, 55-67. Enjalbert, N., et al. (2025). Digital Tools for Scaling Up Participatory Breeding. Proceedings of EUCARPIA 2025. Hellin, J., et al. (2008). The Evolution of Participatory Plant Breeding. Agricultural Systems, 96(1), 139-150. McCaslin, M., et al. (2025). Breeding for Disease Resistance in Organic Tomato Production. Midwest Organic Seed Network Report. Morris, M.L., & Bellon, M.R. (2004). Participatory Plant Breeding Research: Opportunities and Challenges. Euphytica, 136(1), 21-35. Steinke, J., Van Etten, J., & Zelan, P. (2017). Crowdsourcing for Smallholder Farmers: A New Approach to Variety Evaluation. Field Crops Research, 202, 33-44. Van Etten, J., et al. (2019). The Power of Participatory Data for Crop Improvement. Nature Plants, 5, 706-716.

BREEDING AND MULTIPLYING CULTIVARS FOR THE ORGANIC FARMING SECTOR IN EUROPE – AN EXPLORATIVE FACTOR ANALYSIS ON SEED SUPPLIERS` AND BREEDERS` PERSPECTIVES

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Abstract Text:

To foster the transition towards sustainable food systems the European Union targeted the Green Deal and Farm-to-Fork strategy to increase the organic area from 10 to 25% by 2030 (European Commission 2020). To achieve this goal the production of organic seed and planting material of cultivars suited for organic production must be increased dramatically. It is important to understand the seed market dynamics and bottlenecks in Europe. This study focused on breeders' and seed suppliers' perspectives towards the market opportunities and challenges of organic seed and planting material of cultivars that are especially suited for the European organic farming sector. Through a principal factor analysis, two sets of statements from an online survey with 210 responses were examined for possible factors underlining perspectives of responding suppliers and breeders on the European organic seed and breeding market. The analysis revealed five most influential factors concerning organic seed production: Factor A-I refers to "demanding more information and support to perform organic seed production". A significant barrier to market development is the lack of sufficient and comparable data on organic seed production and usage. Additionally, this factor is associated with lower company turnover, suggesting that the size of the company may affect its training needs. Factor A-II refers to "technical and marketing aspects". This factor correlates with high company turnover but a low relevance of the organic seed business. It indicates that larger companies, which are either new to the organic seed market or produce organic seed to a limited extent, face difficulties in scaling up their organic seed production. Factor A-III refers to "regulatory barriers in organic seed production". Companies involved in trading organic seeds encounter significant challenges due to regulatory barriers. The availability of derogations for non-organic seeds reduces the pressure on farmers to use organic seeds, which subsequently diminishes the demand for and investment in organic seed production and breeding. Factor A-IV refers to "trust in the development of the organic seed market". This factor correlates with medium company turnover and a moderate relevance of the organic seed business. It suggests that actors trading both organic and conventional seeds, typically small to medium-sized companies, may benefit from this dual approach. By offering both types of seeds, these companies can reduce their dependency on

fluctuating organic seed demand, allowing farmers access to a broader selection of suitable varieties with specific traits Factor A-V refers to “seed health and technical production aspects”. This factor is associated with a low relevance of the organic seed business. Companies just beginning in organic seed production encounter several technical challenges, such as seed-borne pests and diseases, as well as issues related to storage and seed treatments. In the context of breeding for the organic farming sector, five key factors have been identified: Factor B-I refers to “strong focus on organic and participatory breeding for diversity”. This factor shows a strong negative correlation with companies’ turnover, suggesting that companies engaged in this type of breeding typically have a low yearly turnover. However, it shows a strong positive correlation with the relevance of the organic seed business. This indicates that primarily small companies and non-profit breeding initiatives focus on organic breeding, which may imply that organic breeding is currently a niche business model. Factor B-II refers to “encountering knowledge gaps to breed under organic conditions”. Like Factor B-I, this factor also negatively correlates with companies’ turnover. It is assumed that the actors are mostly from small companies or non-profit breeding initiatives that do not breed under organic conditions due to a lack of familiarity with the principles of organic breeding. Factor B-III refers to “breeding for traits needed in organic farming”. This factor likely refers to companies that aim to breed for organic conditions but do not carry out all breeding steps under those conditions. Factor B-IV refers to “targeting conventional breeding goals”. Companies that fall under this category show minimal involvement in the organic seed business. Factor B-V refers to “financial barrier to conduct breeding under organic conditions”. This factor highlights the perception among actors that financial obstacles hinder organic breeding. Seed suppliers and breeders face several challenges in providing organic seeds and suitable varieties. Addressing both technical and regulatory challenges will be crucial for developing a organic seed market that supports sustainable agriculture.

Reference:

European Commission (2020). A Farm to Fork Strategy for a fair, healthy and environmentally-friendly food system. https://eur-lex.europa.eu/resource.html?uri=cellar:ea0f9f73-9ab2-11ea-9d2d-01aa75ed71a1.0001.02/DOC_1&format=PDF

POSTER PRESENTATIONS

INTEGRATING GEO-POSITIONING AND PHENOTYPING FOR POLLINATOR-ASSISTED BREEDING TO ADDRESS ABIOTIC STRESS IN TOMATOES

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Abstract Text:

Abiotic stresses like drought and heat challenge Southern Europe agriculture and are expected to increase in scope due to climate change (Pastor et al., 2019). Breeding for tolerance against these stresses is essential, especially for organic and low-input agriculture. The DARkWIN project, funded by the Horizon Europe, aims to develop Tomato cultivars that withstand multiple abiotic stresses. We combine plant physiology, root morphology, microbiome interactions, molecular genetics, and advanced phenotyping. Our approach also incorporates pollinator-assisted natural selection.

Central to DARkWIN's methodology is the development of a geo-positioning platform specifically designed for bumblebees (Bombus terrestris) to detect and quantify the sequential spatial-temporal interactions between a high number of plants and the pollinating insects that feed on them. By tracking and ranking pollinators' preferences for flowers in a tomato mapping population exposed to heat and drought, the project assesses functional source-to-sink relationships, providing insights into plant well-being and resilience (Pérez-Alfocea, 2024).

The project is structured into four technical work packages (WPs) over 42 months: 1) Insect Geo-positioning Device Development (WP1): CSIC, DORIANE, and NOVAGRIC will develop the core component that will be integrated with other plant-growth and data capture-related elements to build the phenotyping platform. 2) Phenotyping Platform Construction (WP2): Design, construction, and compartmentation of a phenotyping platform with a capacity to grow up to 1,000 tomato plants for the complete cycle at optimal planting density to secure individual and automated phenotyping by the pollinator. The platform will integrate a versatile environmental and irrigation control system and the insect geo-positioning device connected to a data acquisition, notation, and management system integrated into pollinator-assisted breeding software. 3) Scientific Basis Establishment (WP3): CSIC, MAX PLANCK, DORIANE, and NOVAGRIC will use the platform to phenotype a tomato mapping population, generating multi-omic datasets for breeding purposes based on insect decisions. This includes the identification of morphological, nutritional, metabolic, transcriptomic, and hormonal traits influencing pollinator's choices; the identification of QTLs and candidate genes of flower's traits influencing resilience and pollinator's foraging decisions; and the integration of all data into a pollinator-assisted breeding software. 4) Proof of Concept and Pre-commercial F1 Hybrids Production (WP4): Breeding lines provided by UNIGENIA and selected in WP3 will be used in WP4 to produce pre-commercial F1 hybrids. These hybrids will undergo phenotyping for pollinator preference under climate

change scenarios. Future new F1 varieties based on natural selection of pollinators will be protected.

The phenotyping platform developed for the DARkWIN project integrates geo-positioning, multi-omic traits, and multi-environmental variables, combined with genomic data. DORIANE, the IT partner of this project, develops a specific digital phenotyping platform, and configures their standard plant breeding software. In WP1-2 we develop software for annotation of spatial - temporal plant x pollinator information. And in WP3-4 we integrate all datasets into pollinator-assisted breeding software.

The platform will enable the team to analyze the varieties preferred by pollinators under climate change scenarios. DORIANE and SCIS have been identified as ‘key innovator’ by the European Commission's Innovation Radar for this pollinator-assisted breeding platform.

By integrating these interdisciplinary approaches, DARkWIN aims to establish a new paradigm in plant breeding, utilizing ecological interactions to inform selection processes. The project's outcomes are expected to enhance crop resilience to drought and heat stress in Tomato varieties, contributing to sustain yield and quality in organic and low-input agriculture.

Reference:

Pastor, A.V., Palazzo, A., Havlik, P., Biemans, H., Wada, Y., & Kabat, P. (2019). The global nexus of food–trade–water sustaining environmental flows by 2050. Nature Sustainability, 2, 499-507. https://doi.org/10.1038/s41893-019-0287-1

Pérez-Alfocea, F.; Borghi, M.; Guerrero, J.J.; Jiménez, A.R.; Jiménez-Gómez, J.M.; Fernie, A.R.; Bartomeus, I. Pollinator-assisted plant phenotyping, selection, and breeding for crop resilience to abiotic stresses. Plant J. 2024, 119. https://doi.org/10.1111/tpj.16748

HIGH-THROUGHPUT FIELD PHENOTYPING OF VICIA SATIVA L. USING HYPERSPECTRAL REFLECTANCE INDICES

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Abstract Text:

Common vetch (*Vicia sativa* L.) is a high-protein legume crop, widely cultivated for forage and grain as animal feed (Ballesta et al. 2004). Known for its strong nitrogen-fixing capacity, it plays a crucial role in sustainable agriculture (Ramírez-Parra et al. 2023). As a cover crop, common vetch enriches the soil with nitrogen, suppresses weeds, and reduces the need for herbicides (Pan et al. 2011). With the rising demand for plant-based protein in animal feed and the European Union's emphasis on sustainable crop production, common vetch represents a valuable agricultural option, with significant economic potential.

Nevertheless, like many crops, common vetch yields are primarily limited by drought. To address this challenge, genetic resource collections offer a valuable means to introduce variability into breeding programs. This study aimed to screen a Mediterranean collection of 284 common vetch accessions to identify higher performance accessions under Mediterranean field conditions, which can be further targeted in breeding programs.

We used a high-resolution spectroradiometer (ASD FieldSpec 4) to assess non-invasively key plant functional traits in mature leaves of this Mediterranean vetch collection, under an alpha lattice design, with three plot repetitions, in a rainfed field experiment at IAS-CSIC (Córdoba, Spain). Several spectral vegetation indices were calculated related to physiological traits such as chlorophyll, anthocyanin, carotenoid, water and nitrogen content, senescence, plant stress, and photosynthetic light-use efficiency. This study represents the first year of a three-year field trial.

For data analysis, we employed linear mixed models (Trait = Accession × Block + Replicate) to identify differences among the accessions. We also performed a correlation analysis between the selected indices and a principal component analysis (PCA). Significant accessions effects were detected for most of the indices based on a Wald test ($P < 0.01$). Strong correlations were observed, particularly between the RARS index, which expresses carotenoid content, with the chlorophyll a ($R=0.90$) and chlorophyll b ($R=0.98$) indices and with Cl, a plant stress indicator ($R=0.95$). The Cl index also showed a strong correlation with RENDVI – chlorophyll content ($R=0.96$), and PSSRb ($R=0.91$), an index related to chlorophyll b. This shows a high correlation between plant stress and pigment content.

From the PCA analysis, the first two principal components explained 79.8% of the total variance. K-means clustering identified two main groups, with Cluster 1 showing higher levels of the selected indices. While the PCA did not reveal a strong separation among accessions, heatmap analysis highlighted distinct profiles of spectral indices across different accessions. Interestingly, when PCA was plotted based on accession origin, no significant separation was observed, suggesting a well-established plant material. Several accessions with high pigment content were identified, indicating potential resilience to drought stress. However, further years of data are needed to draw definitive conclusions.

Although preliminary, these findings highlight the potential of reflectance-based data for high-throughput phenotyping. This approach provides valuable insights into plant performance and could serve as an effective tool for screening better performing accessions under Mediterranean conditions in common vetch breeding programs.

Reference:

Ballesta A, Lioveras J, Santiveri P, Torrent D, and Vendrell A (2004). Varieties of vetch (*Vicia sativa* L.) for forage and grain production in Mediterranean areas. Cahiers Options Méditerranéennes, 62, [103–106]. http://om.ciheam.org/article.php?IDPDF=4600139

Ramírez-Parra E, and de la Rosa L (2023). Designing novel strategies for improving old legumes: An overview from common vetch. Plants, 12, [1275]. https://doi.org/10.3390/plants12061275.

Pan F, Lu J, Liu W, Geng M, Li X, and Cao W (2011). Effect of different green manure application on soil fertility. Journal of Plant Nutrition and Fertilizers, 17, [1359–1364]. https://doi.org/10.11674/zwyf.2011.1115.

POTENTIAL OF ROOT TRAITS IN WILD VITIS SPECIES TO IMPROVE DROUGHT ADAPTATION OF GRAPEVINE ROOTSTOCKS

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Abstract Text:

Global warming will increase the impact of abiotic stresses on viticulture. This is particularly true for drought, which will reduce yields and compromise crop survival in certain regions [1]. The rootstock plays an important role in water uptake and transpiration regulation. However, most of the commercial rootstocks currently in use are the result of an ancient selection and have low genetic diversity [2]. The selection of new rootstocks resilient to drought represents a lever for adaptation of viticulture to future environmental conditions. For this purpose, it is essential to characterize the genetic variability of root traits in grapevine and how they influence the responses to drought. We hypothesized that there is scope for innovation on new rootstocks adapted to drought in grapevine using wild Vitis spp. and that the genetic variability of constitutive root traits can be linked to whole plant drought responses. To test this, we explored the genetic variability of Wild Vitis spp for their root syndromes and its relationship to drought responses. In 2022, a drought experiment was conducted on a panel of 12 wild Vitis species, with several accessions per species, available in European germplasm collections. Six-month-old-cuttings were subjected to two treatments during 3 weeks: water-deficit (40% soil water content) versus a well-watered treatment. Genetic variability of morphological and functional root traits was measured under well-watered treatment. Drought responses were evaluated through aerial transpiration and growth, measured in the water-deficit treatment. The plasticity of root molecular (i.e. untargeted metabolomics) and functional traits (i.e. osmotic adjustment) in response to drought was estimated between both treatments. Quantitative genetic methods were used to estimate heritability, and variance partitioning at interspecific and intraspecific level. A multivariate approach, including hierarchical clustering, allowed to group accessions according to the overall behavior of genetically controlled constitutive root traits. A similar approach was applied to classify accessions based on aerial drought responses and root plasticity in metabolic and functional traits. The relationship between root traits syndromes and aerial drought responses was established using dendrogram comparison, via cophenetic correlation. Root syndromes and aerial drought responses showed a correlation coefficient of 0.38. This shed new light on the understanding of into root strategies contributing to drought resilience in grapevine that could be used in breeding programs. Additionally, they improve the characterization of genetic resources within European germplasm collections for their rooting and drought response strategy. This could therefore help in the choice of these

genetic resources in pre-breeding programs for the selection of rootstocks better adapted to drought.

Reference:

[1] van Leeuwen, C., Sgubin, G., Bois, B., Ollat, N., Swingedouw, D., Zito, S., and Gambetta, G. A. (2024). Climate change impacts and adaptations of wine production. Nat Rev Earth Environ 5:258–275. [2] Riaz, S., De Lorenzis, G., Velasco, D., Koehmstedt, A., Maghradze, D., Bobokashvili, Z., Musayev, M., Zdunic, G., Laucou, V., Andrew Walker, M., et al. (2018). Genetic diversity analysis of cultivated and wild grapevine (Vitis vinifera L.) accessions around the Mediterranean basin and Central Asia. BMC Plant Biol 18:137.

TOLERANCE OF COMMON BEAN (PHASEOLUS VULGARIS L.) TO BEAN WEEVIL (ACANTHOSCELIDES OBTECTUS SAY) AND RELATION OF QUANTITATIVE SEED TRAITS TO CROP RESISTANCE

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Abstract Text:

Common bean (Phaseolus vulgaris L.) is considered as one of the most valuable legume for human consumption. Worldwide distribution of common bean is justified with its good adaptation to diverse ecological conditions and production systems, followed by great morphological and genetic variability. Also, common bean is well known as rich source of proteins, fibers and minerals that are becoming increasingly deficient in human diet. Unfortunately, bean production is hampered and limited by insect pests, where bean weevil (Acanthoscelides obtectus (Say)) causes major losses. Even though bean weevil infests common bean in both field and storage, its population is mainly observed postharvest. It is estimated that qualitative and quantitative seed losses made by bean weevil are often higher than 30%. Therefore, the aim of this research was to assess the tolerance of different common bean genotypes to bean weevil by insect biotest. Additional efforts were made to explore and identify seed traits responsible for bean tolerance to this pest. This research is part of larger initiative, where the final goal is to develop new and improve existing pest management tools for bean seed storing, with emphasize on biorational solutions, such as selection of pest-tolerant seed ideotype. In the long run, this should result in reduced use of pesticides in storages. Tolerance of 37 different common bean accessions to bean weevil was studied in "no-choice" biotest under laboratory conditions, in three replications. The adults of laboratory reared population of A. obtectus were placed on different common bean accessions (in petri dishes, on pre-measured seed amount) and were allowed to develop for six months (180 days). The number of newly emerged weevils was counted each month, and they were left for further development. After six months, seed damage was estimated based on the amount of consumed seeds (%), but also the final weevil population density was estimated. Data on total number of emerged insects, together with percentage of damaged seeds for each bean accession, were subjected to an analysis of variance, while corresponding means were compared by Duncan's homogeneity of variance test (0.05 significance level) using SPSS software. Analysis of quantitative seeds traits included measurement of 1000 seed weight (g), seed length (mm), seed width (mm), seed thickness (mm) and seed hardness. In order to identify seed characteristics that could potentially be sources of common bean tolerance to bean weevil, Pearson correlation coefficients were analyzed between aforementioned seed traits and percentage of seed damage, together with A. obtectus population density. Significant differences between bean accessions were

observed for the percentage of seed damage and number of emerged weevils. The percentage of damaged seeds varied from 1.03% (KP40) to 100% (KP114 and KP236), while number of imagoes ranged from 25 (KP149) to 935 (KP95). Usually, accessions with larger observed number of imagoes had the largest percentage of damaged seeds (KP70, KP327, KP305, KP51, for example) and vice versa (KP149, KP170, KP161), with some deviations. It was noted that accessions that suffered severe seed damage also had larger and longer seeds, which was confirmed with Pearson correlation coefficient in this paper. Namely, there was strong correlation between percentage of damaged seeds and seed weight ($P<0.01$) and percentage of damaged seeds and seed length ($P<0.005$). On the other hand, significant correlation between number of imagoes and studied seed traits was not found. In addition, studied accessions showed overall diversity regarding number of imagoes and percentage of damaged seeds, CV = 48.3% and CV = 37.1%, respectively. It can be concluded that studied common bean collection can be good source of variation towards breeding for tolerance to bean weevil, while detected correlations imply which quantitative seed traits should be used in the selection process. It must be stressed out that these are preliminary results, while more comprehensive research will include assessment of qualitative seeds traits, comprising both nutritive and antinutritive parameters and other biochemical properties, in order to identify most responsible traits associated with bean tolerance to bean weevil.

FROM FIELD TO GENOME: UNRAVELLING AGRONOMIC TRAIT GENETIC ARCHITECTURE IN LATHYRUS SATIVUS THROUGH QTL LINKAGE MAPPING

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Abstract Text:

Lathyrus sativus (grass pea) is an annual cool-season grain legume that is easily cultivated and offers significant dietary benefits, providing high protein content for both human consumption and animal feed (Lambein et al. 2019). It is recognized for its exceptional agronomic properties, including tolerance to drought, cold, flooding, and poor soils, which make it a promising crop for sustainable agriculture (Vaz Patto et al. 2006; Lambein et al. 2019; Gonçalves et al. 2022). Moreover, *L. sativus* exhibits considerable resistance to pests and diseases (Martins et al. 2020).

This study aims to identify the genomic regions (QTLs – Quantitative Trait Loci) and candidate genes controlling important *L. sativus* agronomic traits. A recombinant inbred line (RIL) population, comprising 102 lines in F8 generation, derived from a cross between an Asian line ('Raipur-4') and a Canadian line ('LS87-124-4-1'), along with three commercial *L. sativus* varieties as controls, were field trialed using a randomized complete block design, with three plots replications. This evaluation was conducted across two different environments (Oeiras, Portugal, and Cordoba, Spain), over two growing seasons. Each location implemented three repetition plots, each containing 10 plants per line. Agronomic traits, including days to first flower and pod (earliness-related traits), flower colour, plant height, seed production, and pest susceptibility to weevils (*Bruchus* spp.) were measured. These measurements were carried out as part of the "Oeiras Experimenta" citizen science project.

Phenotypic evaluations revealed significant agronomic variability among the RIL, showing differences in germination rates, plant height, flower color, seed yield, and pest susceptibility. The observed variability indicates high genetic diversity within the RIL population, providing an opportunity to identify genomic regions associated with these traits. Additionally, this RIL population was genotyped and a high-density *L. sativus* genetic linkage map was previously developed (Santos et al. 2021). This map, consisting of 2,149 markers spanning 674.4 cM, offers a robust framework for QTL mapping. The QTLs controlling key agronomic traits in *L. sativus* will be identified by integrating phenotypic and genotypic data through a linkage mapping approach.

These results will support marker-assisted selection in breeding programs, ultimately contributing to the development of improved grass pea varieties with enhanced agronomic performance and adaptability.

Reference:

Gonçalves L, Rubiales D, Bronze MR, and Vaz Patto MC (2022). Grass Pea (*Lathyrus sativus* L.): A sustainable and resilient answer to climate challenges. Agronomy 12, 1–19. doi:10.3390/agronomy12061324.

Lambein F, Travella S, Kuo Y-H., Van Montagu M, and Heijde M (2019). Grass pea (*Lathyrus sativus* L.): orphan crop, nutraceutical or just plain food? Planta 250, 821–838. doi:10.1007/s00425-018-03084-0.

Martins D, Araújo, SS, Rubiales D, and Vaz Patto MC (2020). Legume crops and biotrophic pathogen interactions: a continuous cross-talk of a multilayered array of defense mechanisms. Plants 2020, Vol. 9, Page 1460 9, 1460. doi:10.3390/plants9111460.

Santos C, Polanco C, Rubiales D, and Vaz Patto MC (2021). The MLO1 powdery mildew susceptibility gene in *Lathyrus* species: The power of high-density linkage maps in comparative mapping and synteny analysis. Plant Genome 14, 1–14. doi:10.1002/tpg2.20090.

Vaz Patto MC, Skiba B, Pang ECK, Ochatt, SJ, Lambein F, and Rubiales, D. (2006). *Lathyrus* improvement for resistance against biotic and abiotic stresses: From classical breeding to marker assisted selection. Euphytica 147, 133–147. doi:10.1007/s10681-006-3607-2.

EMERGING SUPERIOR COMMON BEAN GENOTYPES THROUGH ORGANIC BREEDING FOR VIRAL RESISTANCE AND HIGH YIELD PERFORMANCE

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Abstract Text:

The common bean (*Phaseolus vulgaris L.*) is an important staple crop cultivated worldwide. As the leading grain legume in human diet, the common bean could have a crucial role in future food security, featuring high quality plant protein and contributing to the transition to organic agriculture, by reducing the environment footprint through nitrogen fixation. Concurrent exposure of this crop to multiple abiotic and biotic factors has a negative impact on plant homeostasis and causes devastating losses in yield production. Specifically, viral infections (e.g. CMV, BCMV, BYMV, BLRV, AMV) are a critical inhibiting factor for ensuring stable yields. Consequently, genetic resistance is the most successful and sustainable strategy to mitigate the adverse effects of virus infections. This effort highlights the significant role of plant breeding in exploring natural resistance and selecting tolerant genotypes. Moreover, the employment of a multifaceted approach, combining classical and molecular methods, is necessary to comprehensively assess the responses of genotypes to diverse viruses. The utilization of efficient screening methods is a crucial step in developing resistant varieties, by uncovering potential resistance mechanisms and markers that could be exploited in breeding programs. Of particular interest, is the fact that the integration of resistance to seed-borne virus diseases is inevitably linked to organic agriculture, as it enables the avoidance of chemical seed treatments. Therefore, through a systematic phenotypical exploration of genotype responses and the adoption of an applicable marker assisted sceme, the identification of genotypes that perform effectively in marginal stress environments under low inputs, is possible.

Particularly, in the context of climate change, the fundamental objective of common bean breeding is to promote the productive ideotype, thus the genotype characterized by its capacity for high yield potential and stability under organic farming systems, combined with

tolerance to biotic and abiotic stresses. Breeding for resistance to viruses incorporates the deciphering of the genetic background determining the genotype immune response. However, this is possible by achieving the maximum phenotypical expression and differentiation. In addition, it is imperative to acknowledge the pivotal role of the choice of the appropriate unit of plant phenotyping in the field, so that the efficiency of selection in plant breeding programs and the corresponding measurable genetic gain are maximized (Kargiotidou et al. 2014). Following such breeding approaches, the present study aimed to facilitate the emergence of superior common bean genotypes through phenotypical and molecular screening methods, as well as to evaluate the adaptability of the studied genetic materials to organic farming system.

Pedigree selection method, under honeycomb design R-7 was applied to evaluate and select superior single-plants, initiating from 4 commercial varieties (Pyrgetos, Cannellino, Lingot, Northern) and 3 bean local populations (Florina, Karatzova, Smyrni), as starting genetic material. Phenotypical selection was followed by retention of only high-yielding individual plants through analysis of production potential and predictive equations (Fasoula et al. 2019). The combined data of yield components revealed the superiority of local populations Florina and Smyrni in organic system, bearing as a control the commercial variety Pyrgetos. Florina demonstrated a great stability index (SI= 3.101) under low-inputs, reflecting stress resistance. This research has resulted in a protocol for the rapid detection of resistant genotypes in early generations. This protocol combines molecular markers (CAPS and SCAR) linked to viral resistance genes (BCMV, BCMNV- I locus & bc-3 gene) and digestion with restriction enzymes. Regarding viral disease resistance alleles, considerable variability was observed, with the desired alleles occurring in individual genotypes. The overall results confirm the intra-population selection of individual plants, for further evaluation as progeny lines. Finally, through comparative analysis of yield components in conventional and organic fields, it was proposed that the genotypes that demonstrate notable individual performance in a given farming system exhibit equivalent consistency across both systems. These early findings indicate the potential of these genotypes to be integrated into low-input systems, while carrying desirable resistance alleles. The increase of our knowledge about the biodiversity and population structure of beans and the selection of specific progeny lines will help in the conservation of this genetic potential and its proper utilization by Plant Breeding Programs, while safeguarding this crucial global food resource.

Reference:

Fasoula, V. A., Thompson, K. C., & Mauromoustakos, A. (2019). The prognostic breeding application JMP add-in program. Agronomy, 9(1). https://doi.org/10.3390/agronomy9010025

Kargiotidou, A., Chatzivassiliou, E., Tzantarmas, C., Sinapidou, E., Papageorgiou, A., Skaracis, G. N., & Tokatlidis, I. S. (2014). Selection at ultra-low density identifies plants escaping virus infection and leads towards high-performing lentil (Lens culinaris L.) varieties. Journal of Agricultural Science, 152(5), 749–758. https://doi.org/10.1017/S0021859613000403

EXPLORING GENETIC DIVERSITY AND SEED COAT COLOUR VARIATION IN COMPOSITE POPULATIONS OF COMMON BEAN USING WHOLE GENOME SEQUENCING

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Abstract Text:

Maintaining and enhancing agrobiodiversity is of crucial importance for the resilience of agricultural systems. Composite populations, consisting of phenotypically diverse individuals, represent a promising approach for increasing genetic variability, adaptation potential, and ecosystem services (Šajgalik et al. 2019). In common bean (Phaseolus vulgaris L.), seed coat colour is an important trait, influencing market preferences and being also linked to agronomic performance (García-Fernández et al. 2021). However, the genetic mechanisms underlying seed coat colour variation in composite populations remain poorly understood. The present study, therefore set out to explore the genetic diversity and structure of composite populations of common bean with a focus on seed coat colour variation using whole genome sequencing (WGS). A total of 50 composite populations were characterised in field trials in Slovenia across two consecutive growing seasons (2022 and 2023). Each composite population exhibited variation in seed coat colour, consisting of two to five different phenotypes. Four composite populations and two standard varieties (Golden_Gate and ETNA) were selected for detailed genetic analysis in 2023, based on their segregation patterns and colour diversity. Leaf tissue samples from a total of nineteen phenotypic variants were collected for DNA extraction and WGS. Sequencing was performed using the Illumina platform, generating high-quality short-read data. Following quality control and filtering, the reads were mapped to the common bean reference genome, achieving a 97.7% success rate and an average depth of 30× per individual. This analysis identified more than 8.6 million single nucleotide polymorphisms (SNPs). A significant proportion of these SNPs (98%) were identified in non-coding regions of the genome, indicating a potential correlation between seed coat colour and gene expression regulation. Furthermore genetic diversity analysis revealed substantial variation among populations and was consistent with phenotypic diversity, with the composite population exhibiting the highest number of diverse phenotypes also demonstrating the highest genetic diversity (pi = 0.21) and the highest number of private alleles (129,138). Conversely, the composite population comprising seeds that differed solely in the proportion of background seed coat colour exhibited the lowest genetic diversity (pi = 0.08) and the smallest number of private alleles. Nevertheless, the results from principal component analysis (PCA) and the unweighted arithmetic mean algorithm (UPGMA) demonstrate that composite populations generally cluster together, with the exception of one composite population, where one of the phenotypes deviates significantly from the others. In order to identify genomic regions associated with seed coat colour variation, composite populations were classified into two groups. The first group comprised populations that remained stable in colour across

generations (both standard varieties and one composite population), while the second group included populations exhibiting segregation in seed coat colour (remaining three composite populations), which showed 15% less genetic diversity, suggesting the presence of a selective signature. Two complementary tests (XP-CLR, XP-EHH) were performed to identify genomic regions, and the top 1% of significant regions (118) identified by both tests were used as candidate regions. Pathway analysis revealed that phosphatidylinositol signalling pathways were the most prevalent. Phosphatidylinositols, as membrane lipids, have been demonstrated to participate in the regulation of pigment transport, as evidenced by the present study. The identified regions highlight the involvement of both regulatory elements and structural components in the emergence of phenotypic variability, thus offering valuable insights for breeding programs aiming to select for diverse and resilient populations.

Reference:

Šajgalík M, Ondreičková K, Hauptvogel P, Mihálik D, Glasa M, Kraic J (2019). Higher Effectiveness of New Common Bean (Phaseolus vulgaris L.) Germplasm Acquisition by Collecting Expeditions Associated with Molecular Analyses. Sustainability, 11 (5270), https://doi.org/10.3390/su11195270

García-Fernández C, Campa A, Ferreira JJ (2021). Dissecting the Genetic Control of Seed Coat Color in a RIL Population of Common Bean (Phaseolus vulgaris L.). Theoretical and Applied Genetics, 134, [3687–3698]. https://doi.org/10.1007/s00122-021-03922-y

ADVANCING OAT BREEDING IN THE MEDITERRANEAN CLIMATES THROUGH DISSECTION OF GENETIC DIVERSITY AND STRUCTURAL VARIANTS.

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Abstract Text:

Oat (*Avena sativa* L.) is a globally important cereal crop with considerable economic and nutritional value. In the Mediterranean region, oat is a crucial component of agricultural systems, providing feed for livestock and contributing to sustainable cropping rotations. However, Mediterranean oat production faces multiple biotic and abiotic stresses, including several diseases, drought, and extreme temperature fluctuations. These challenges need the development of improved oat varieties with enhanced adaptability to regional environmental conditions. Understanding the genetic diversity and structural complexity of oat germplasm is critical to achieving this goal.

Our research has focused on characterizing a comprehensive oat collection comprising 709 accessions, primarily landraces, from across the Mediterranean rim. This collection has been extensively characterized phenotypically and genotypically. After stringent curation, 17,288 polymorphic SNP markers were identified, confirming the high genetic diversity present and the suitability of the collection for association and genomic studies aimed at oat improvement. Further studies in the frame of the Panoat consortium identified several oat accessions from the Mediterranean collection carrying structural variants compared with more than 9,000 accessions worldwide characterized by GBS.

Structural variants (SVs) play a critical role in plant genetic diversity, impacting gene function and phenotypic traits through mechanisms such as gene loss, gene duplication, and the emergence of novel genes. Unlike SNPs, which are typically short sequence variations, SVs are larger (>50 bp) and often have more profound effects on gene expression and protein functionality. Despite their significance, early genetic technologies had limited resolution for detecting SVs, thereby constraining their exploration in plant genomes. Recent advancements in long-read sequencing and whole-genome mapping now offer unprecedented opportunities to construct high-resolution pan-genomes and explore a broader spectrum of SVs. These approaches are expected to improve our understanding of the genetic basis of important agronomic traits and facilitate the development of superior oat varieties with enhanced adaptability and resilience.

To further elucidate the role of SVs in oat, we aim to perform whole-genome sequencing on two oat accessions identified as carrying significant structural variants. By leveraging long-read sequencing technologies, we seek to accurately characterize these SVs and assess their

potential functional impacts on key agronomic traits. Understanding the role of SVs will allow us to identify genes or genomic regions associated with stress resistance/tolerance to biotic and abiotic stresses, yield, and adaptation. Moreover, insights from SV analysis could contribute to marker-assisted selection and genomic-assisted breeding strategies, accelerating the development of superior oat varieties. This work will also facilitate the construction of a more comprehensive oat pan-genome, offering a valuable reference for future genetic and breeding studies. Ultimately, our research underscores the importance of integrating structural variant analysis into oat breeding programs to accelerate genetic gains and enhance crop performance under Mediterranean environmental conditions.

INTEGRATING HIGH-THROUGHPUT PHENOTYPING (HTP) INTO THE FORAGE LEGUME BREEDING PROCESS

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Abstract Text:

Forage legumes, such as red clover (*Trifolium pratense* L.), as well as less known minor species like zigzag clover (*Trifolium medium* L.) and bird's-foot trefoil (*Lotus corniculatus* L.), play a key role in agroecological and low-input farming systems by enhancing soil fertility, supporting biodiversity, and providing high-quality forage. However, conventional breeding methods are labor-intensive, time-consuming, and influenced by environmental variability, limiting genetic gains. The integration of high-throughput phenotyping (HTP) offers an automated, non-destructive approach to improving selection efficiency, particularly for underutilized species (Panjvani et al. 2019).

This study aimed to integrate HTP-derived phenotypic traits with traditional field evaluations to assess biomass production, canopy structure, and persistence across breeding lines of *T. pratense*, *T. medium*, and *L. corniculatus*. The PlantEye F600 system (Phenospex, Netherlands) was used to generate plant height, digital biomass estimation, 3D leaf area, and multispectral data. These parameters were compared with conventional morphological measurements collected from field trials to evaluate their reliability and potential for breeding applications. The results revealed a strong correlation between PlantEye F600 biomass estimations and manual yield assessments, confirming the potential of digital phenotyping for rapid and objective trait evaluation. Species-specific growth differences were also observed, highlighting the need for tailored breeding strategies.

Although we did not find specific data on the precision phenotyping of red clover or other minor forage legume species using 3D multispectral scanning, we identified studies that successfully simulated environmental conditions. For instance, wild rocket (*Diplotaxis tenuifolia* L.) was analysed under drought stress in a controlled environment. In this study, researchers effectively minimized unwanted sources of variability, and over an extended period of drought stress, they discovered that irrigation could be reduced by 30% while still maintaining adequate performance of *D. tenuifolia* (Tripodi et al. 2024). This demonstrates that the PlantEye F600 is sufficiently powerful to dissect both the morphological and physiological mechanisms involved.

Despite the advantages of early selection using HTP, field variability remains a key challenge, underscoring the need for multi-environment validation. The integration of HTP with genomic selection and AI-driven data analysis provides further opportunities to enhance breeding efficiency by accelerating cultivar development, optimizing resource use, and improving resilience to environmental stressors.

This study highlights the value of digital phenotyping in forage legume breeding, supporting increased productivity and sustainability in agroecological farming systems. Continued advancements in phenotyping technologies are essential to fully exploit genetic potential and drive innovation in legume breeding programs.

Reference:

Panjvani K, Dinh AV, Wahid KA (2019). LiDARPheno - A Low-Cost LiDAR-Based 3D Scanning System for Leaf Morphological Trait Extraction. Frontiers in Plant Science, 10, 147. https://doi.org/10.3389/fpls.2019.00147

Tripodi P, Vincenzo C, Venezia A, Cocozza A, Pane C (2024). Precision Phenotyping of Wild Rocket (Diplotaxis tenuifolia) to Determine Morpho-Physiological Responses under Increasing Drought Stress Levels Using the PlantEye Multispectral 3D System. Horticulturae, 10(5), 496. https://doi.org/10.3390/horticulturae10050496

AGRONOMIC PERFORMANCE OF WINTER WHEAT COMPOSITE CROSS POPULATIONS IN ORGANIC FARMING SYSTEMS IN POLAND.

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Abstract Text:

There are various methods to increase genetic diversity in cereals that can stabilize the crop performance and buffer against environmental fluctuations, especially in organic or low input cropping systems. One way to increase genetic diversity of the crop is to use segregating composite cross populations (CCPs). To do so, in the mid-nineties last century, nine winter wheat commercial cultivars were crossed together in a complete half-diallel. As a result nine CCPs were produced, by bulking F2 seeds from the individual crosses and multiplied them for 5-6 consecutive years in diverse sites. In the years 2016, 2017, 2018 and 2019, all CCPs and their parental cultivars were multiplied and observed in few sites all over the country. In each year, CCP seed that had been harvested in the preceding cropping year, was used to set-up next multiplications, thereby allowing for potential evolutionary adaptation of the genetically heterogeneous materials to site-specific cropping conditions. In the growing seasons 2021/2022 and 2022/2023, all developed CCPs and their parents were tested under organic growing conditions, using RCBD block design at Plant Breeding and Accclimatization Institute, Radzików. Plot size used was 15 - 16 m2. Assessments of main morphological and agronomic parameters and grain quality parameters were carried out on a plot basis on each (CCPs and their parental cultivars). In addition to grain yield level (t*ha−1, at 15% moisture content), other agronomic characters and yield components were assed. Winter wheat CCPs, and their parental cultivars were compared for various attributes such as grain yield together with important agronomic and quality parameters. Different statistical indices were used for experimental data processing. Where winter wheat disease pressure was high, the disease infestation of the parental lines was generally greater than that in the populations. Especially, under organic conditions, when no fungicides were applied, the winter wheat CCPs were always considerably healthier, presumably due to their inherited diversity in disease resistance. We can therefore conclude, that introducing higher diversity of crops in the form of CCP is an appropriate way to improve overall adaptation and stability of winter wheat in organic and low-input systems in diverse environmental conditions. Summarizing, crop diversification by growing mixtures or CCPs may be considered as an alternative or supplementary way to achieve higher and more stable crop productivity, especially in the face of climate change.

DIVERSIFICATION THROUGH ORGANIC HETEROGENOUS MATERIAL: HOW TO ADAPT BREEDING PROGRAMS FOR ITS DEVELOPMENT?

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Abstract Text:

The resilience of the agricultural and food system is threatened by numerous challenges such as climate change, loss of biodiversity and soil degradation. Plant breeding can contribute to the resilience of agro-eco-systems by developing high-yielding and high-quality cultivars that are adapted to biotic and abiotic stresses. Modern plant breeding has primarily focused on combining desired traits in genetically homogeneous genotypes as the basis for varieties. With the category organic heterogeneous material (OHM) created in the EU regulation on organic farming, breeders are legally allowed to develop, notify and market heterogeneous cultivars for organic farming. OHM creates opportunities to release cultivars with a higher level of genetic and phenotypic diversity, having the potential to dynamically adapt to different production environments and provide increased stability in yield and quality over time (Annicchiarico et al. 2023, Ceccarelli et al. 2020). gzpk is a plant breeding organization based in Switzerland that develops arable crops for organic and low-input agriculture. gzpk aims to start the development of OHM of wheat (Triticum aestivum L.) and pea (Pisum sativum L.) to provide cultivars with increased diversity for farming. This requires an expansion of its current breeding program, which has so far been focused on breeding homogeneous varieties of self-pollinated species. In those programs, a large number of breeding lines is produced and tested, of which only a tiny fraction can be selected for variety registration. In OHM development, understanding und using beneficial trait combinations of different genotypes and their interaction with the environment becomes increasingly relevant. In practice, OHM enables the combination of evolutionary breeding and human selection. Evolutionary breeding uses the plasticity potential of various diverse populations to adapt to different target environments. Human selection refers to the targeted composition of populations and genotypes generated in the breeding process. The combination of these approaches enables a variety of strategies for the development of OHM, which can be combined depending on the breeding goal and available resources. When selecting breeding strategies for OHM, the desired level of homogeneity of key agronomic and qualitative traits such as plant height or protein content must be considered. In principle, the degree of control over the desired traits increases when components for OHM are selected and combined at higher breeding levels, using pre-tested breeding lines. Plant breeders of gzpk consider three approaches to adjust the variety development approach towards OHM by using the following breeding material as basis for OHM-compositions: a. diverse populations in different environments b. Pre-tested material of the F5 generation (selected single plants) c. Pre-tested material of the F6 or higher generations (single plants descendants) In the presentation, potential advantages and disadvantages of

the three approaches will be introduced and discussed. The internal discussion at gzpk revealed that OHM breeding requires a new perspective on cultivars and plant breeding as well as increased consideration of scientific disciplines such as ecology and population genetics in the breeding process. The integration of OHM development into plant breeding has the potential to take greater account of interactions in the plant-environment system.

Reference:

Annicchiarico, P., Russi, L., Romani, M., Notario, T., & Pecetti, L. (2023). Value of heterogeneous material and bulk breeding for inbred crops: A pea case study. Field Crops Research, 293(108831), https://doi.org/10.1016/j.fcr.2023.108831 Ceccarelli, S., & Grando, S. (2020). Evolutionary plant breeding as a response to the complexity of climate change. Iscience, 23(12), https://doi.org/10.1016/j.isci.2020.101815

PARTICIPATORY TOMATO BREEDING FOR ORGANIC CULTIVATION IN AUSTRIA

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Abstract Text:

In 2010, the working group “Bauernparadeiser”, an Austrian participatory tomato breeding network, was founded on the initiative of farmers due to a lack of open-pollinating tomato varieties which suit the needs of direct-marketing organic producers. Many conventionally bred tomato varieties are hybrids and are not adapted to local conditions nor have sufficient sensory quality. Currently, the working group consists of approximately 15 organic Austrian farmers, 5 research institutions, and the seed association ARCHE NOAH as a coordinator. The goal is the development of tasty and open-pollinating tomato varieties, featuring resistance to plant pathogens, by means of crossing heirloom varieties with modern varieties. The group’s primary focus is breeding varieties for high tunnel production systems - with resistance to the fungal pathogen *Cladosporium fulvum*, Tobacco Mosaic Virus and common root diseases. A second area of focus is the development of varieties for open field production. The breeding objective is creating varieties resistant to the fungal pathogen *Phytophthora infestans*, as well as to Early Blight (*Alternaria* spp.) and Septoria leaf spot disease (*Septoria lycopersici*). An additional emphasis is put on a low susceptibility to fruit cracking and blossom end rot. The main target group for new outdoor varieties are home gardeners, but also professional gardeners may use these new varieties for selling or processing the fruits. Each year, the plants are evaluated in the field for the occurrence of abiotic and biotic diseases. In 2024, many breeding lines were tested with markers for the resistance genes Ph-2 and Ph-3, to determine the genetic background of resistance to *Phytophthora infestans*. Breeding lines with preferably both resistance genes will be stabilized and tested on several sites in the following years, prior to the group decision which lines should be registered as varieties. The appearance of the fruits turned out to be less important for outdoor productions; most important for the farmers are vigorous plants (preferred are plants with indetermined growth), little cracking and good taste of fruits. Over the course of the last years, we observed more and more symptoms of Early Blight and Septoria Leaf Spot in our breeding fields. Regarding Septoria Leaf Spot, resistant varieties developed in the United States revealed resistance in the field; for Early Blight, however, no complete resistances are available and varieties with intermediate resistance did not differ significantly from susceptible varieties in their phenotypical susceptibility to the disease. Therefore, optimizing production practices seems to be a more effective approach than resistance breeding. Crop rotation and thermal seed treatment will be tested in 2025, to minimize the damages of Early Blight.

RESULTS ON SOME IMPROVEMENT APPROACHES OF SPRING BARLEY HETEROGENEOUS POPULATIONS

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Abstract Text:

Heterogeneous populations can provide large diversity within a single crop field and are able to evolve within the time and adopt to a specific cultivation environment. The research history on evolutionary barley (Hordeum vulgare L.) populations starts back in the beginning of 20th century with the work of Harry Harlan. Nowadays heterogeneous material is topical due to development of organic agriculture and its advantages found especially under unfavourable growing conditions with biotic and abiotic stress factors.

Our work aims at development facilitation and further improvement of composite cross populations (CCPs). We applied following approaches: (1) application of male sterility (ms) to reduce workload during crossing and extend diversity, (2) selection of best-performing lines from CCP and combining them in a mixture, (3) selection for resistance by molecular marker from CCP, (4) crossing of CCP to several parents to improve some traits, (5) mass selection under extreme growing conditions. Agronomic testing was done during 2021 – 2024 in one to six environments. Traits assessed involved grain yield, stability, characteristics related to competitiveness against weeds, nitrogen use efficiency (NUE), disease severity and grain quality.

Comparing two populations created using the same set of 11 parents by using (a) dialell crosses and (b) pollination of eight ms lines with the same 11 genotypes each in six environments, resulted in on average 10% lower yield for ms CCP. The differences were smaller under low yielding environments and ms CCP was more stable, had slightly lower early vigour and weed suppression ability, higher infection with powdery mildew (Blumeria graminis), lower grain volume weight but higher protein and NUE in some environments.

Mixtures from 10 best performing lines selected out of three CCPs using regular breeding procedure were compared to the initial CCPs. Yield advantage of the mixtures in four environments was between 8 and 11% with significant differences in a few cases. Two mixtures were more stable and one with adaptation to unfavourable environments. There were overall trends for shorter plants and higher grain weight, as well as higher WSA and volume weight in some cases.

Selection for loose smut (Ustilago nuda) Un8 resistance gene was done from a CCP and seeds of resistant plants bulked. While comparing to the unselected CCP, we found a 5% yield reduction and similar stability over five environments. The selected population had better WSA and low smut infection but higher leaf disease severity.

Crossing of CCP Mirga to three advanced pure lines from organic breeding to further improve yield, resistance to loose smut, NUE and other agronomic characters and comparison to Mirga was performed. The yield of the new population over six environments varied between 90 to 135% of Mirga with no significant differences and similar stability. Improvement in early vigour, WSA and related traits, powdery mildew and loose smut severity and NUE was found.

Selection of productive barley spikes from two CCPs was done on a farm under extreme pressure of buckwheat and from one CCP in research field with low soil pH. Preliminary testing in one environment resulted in insignificant yield improvement in two populations selected from CCP Mirga (6 and 12%) with superiority of WSA and traits related to it. The selection from other CCP yielded slightly lower with not clearly pronounced advantages in WSA.

Concluding, application of male sterility can bring in a population some undesirable traits and affect negatively yield performance, however, in later generations and unfavourable environments it becomes less pronounced. Selecting lines from CCPs to build line mixtures requires comparatively large efforts but the obtained agronomic gain was not clearly significant whereas the diversity is reduced. This approach can be used in case of some specific limiting traits. Instead of selecting in population for only one resistance gene, a complex selection for resistance to several most devastating diseases could be a more effective strategy reducing a possibility to increase susceptibility to other diseases. The advantages of improved populations by crossing CCP to several genotypes could not be clearly approved due to difference in generations and possible heterosis effect, however, the observed superiority in traits related to weed suppression ability, NUE and disease severity encourages to continue using this approach. Mass selection from CCPs in extreme environments can provide improved competitiveness against weeds.

CARROT IMPROVEMENT FOR ORGANIC AGRICULTURE: LEVERAGING ON-FARM AND BELOW GROUND NETWORKS

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Abstract Text:

Organic growers need vegetable varieties that are adapted to organic growing conditions and have market qualities demanded by organic consumers. In carrots, nutrient acquisition, nematodes, disease pressure, and weed competition are particularly critical challenges to both fresh market carrots and carrot seed production, while flavor, appearance, and nutrition are key market qualities. The Carrot Improvement for Organic Agriculutre (CIOA) project is a long-term, ongoing project, initiated in 2011, with the goals of delivering improved carrot varieties for organic; improved understanding of how carrot genotypes interact with the root microbiome to access promote plant health and suppress pathogens; and a participatory breeding model that may be adapted to other crops for organic cultivar development.

Project breeding efforts are evaluating diverse germplasm from the USDA collection and breeding new populations and cultivars based on participatory trials and input from framers and organic seed companies. Breeding activites to date advanced more than 50 new populations with various combinations of priority traits including improved flavor, nutrient concentration, color, top growth size and vigor, Alternaria Leaf Blight (ALB) resistance, nematode resistance, and cavity spot resistance. Researchers released nine cultivars and breeding lines with a diversity of pigments, superior flavor, resistance to Alternaria dauci, resistance to root-knot nematode (Meloidogyne incognita and M. javanica). Three additional lines are set for release in 2025 including sources of durable resistance to Cavity Spot and root-knot nematode (M. incognita). Efforts are currently underway to develop marker assisted selection (MAS) for both nematode species. Several organic cultivars including red, rainbow, and orange types, developed or derived from CIOA breeding lines, are commercially available through participating farmers and organic seed companies.

Microbiome research is expanding our understanding of the potential to evaluate and breed carrot gentoypes for enhanced plant-soil microbial interactions. A study to determine whether four carrot cultivars preferentially recruit AMF communities under organic management was carried out on five organic vegetable farms and the University of

Wisconsin (UW). Mean root colonization was significantly greater for one open-pollinated variety, which aligns with previous research, where modern varieties of several crops demonstrate a loss of response to colonization by AMF. Project studies also identified carrot roots were colonized by an abundant and diverse assortment of bacteria and fungi with greater diversity in organic management than conventional soils (Abdelrazek et al. 2020a). Carrot genotype affected endophyte abundance in taproots and researchers identified differences in the potential for individual isolates to affect seed germination, seedling growth, and A. dauci (Abdelrazek et al. 2020b). Benefits of endophytes on carrot growth were greatest when plants were subjected to ALB stress, highlighting the importance of environmental conditions and the potential functional role of endophytes. Current research is expanding field trials to assess resistance to A. dauci and associated microbial communities in diverse environments. Using insights from the field trials, a greenhouse experiment will aim to verify the role of microbiomes in mediating nutrient uptake, A. dauci resistance, and end-use quality of roots. Additional studies evaluating carrot root microbiome effects on response to water-stress, nitrogen scavenging and heavy metal uptake are also underway.

Flavor is a priority trait necessary for the successful adoption of new cultivars. Sensory analysis, including flavor, texture and culinary quality, is being conducted on advanced materials. Carrot texture analysis methodology development is underway with the use of two high-resolution texture analyzers in evaluation of multiple factors that may affect phenotyping, especially root handling variables and tissue puncture logistics.

The CIOA project is advancing our understanding of the genetic and environmental influences on carrot performance in organic systems and providing insights into breeding for improved cultivars. New cultivars adapted to organic conditions will enhance organic carrot production and organic farmer economic returns, thus facilitating expansion of organic carrots. Publically available breeding lines, including germplasm with nematode and Alternaria resistance, support organic seed industry development of additional new cultivars. The development of improved carrot varieties with greater tolerance to biotic and abiotic stress bring broad environmental benefits by reducing the need for off-farm inputs. Organic seed companies, producers, and consumers will benefit from access to new cultivars.

Reference:

Abdelrazek, S., Simon, P., Colley, M., Mengiste, T., Sulba, Jyothi *Hoagland, L., 2020. Changes in the core endophytic mycobiome of carrot taproots in response to crop management and genotype. Scientific Reports, 10 (13685). http:doi.org/10.1038/s41598-020-70683-x.

Abdelrazek, S., Simon, P., Colley, M., Mengiste, T., *Hoagland, L., 2020. Crop management system and carrot genotype affect endophyte composition and Alternaria dauci suppression. PLOSOne. http:doi.org/10.1371/journal.pone.0233783.

DEVELOPMENT OF A NEW PUMPKIN VARIETY ENRICHED WITH HIGH CAROTENOID LEVELS

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Abstract Text:

Carotenoids are considered bioactive components in the human diet, offering a range of health benefits due to their powerful antioxidant properties. They play a crucial role protecting against oxidative stress and inflammation. Among the most important carotenoids, β-carotene is a provitamin A compound, meaning it can be converted into vitamin A in the body. Vitamin A is vital for maintaining healthy vision, promoting immune function, and supporting growth and development. A deficiency in this nutrient can lead to serious health issues, particularly in developing regions, where vitamin A deficiency (VAD) remains a major public health concern. Addressing this deficiency through increased consumption of carotenoid-rich foods, such as pumpkins, presents an effective strategy for improving global nutrition and preventing related health problems.

Pumpkins, especially *Cucurbita maxima, Cucurbita moschata,* and *Cucurbita pepo*, are rich sources of carotenoids, particularly β-carotene, which is abundant in the orange flesh of the fruit. These pumpkins also contain other essential nutrients, including sugars, starch, vitamin C, vitamin E, and dietary fiber, making them an excellent addition to a healthy, balanced diet. *Cucurbita maxima*, in particular, is widely cultivated across both developed and low-income regions, where it serves as a critical source of vitamins and minerals, particularly for populations at risk of nutrient deficiencies. This makes pumpkins a highly valuable crop for addressing vitamin A deficiency, which can have serious implications for public health, especially in young children and pregnant women.

In line with this, one of the key objectives of this initiative is to promote sustainable agricultural practices that support the production and processing of plant-based foods with superior nutritional profiles. A breeding program based on the "pedigree method" is being employed to develop new pumpkin varieties with enhanced carotenoid content, improved sensory qualities, and increased consumer acceptability. Pumpkins, with their significant genetic diversity, offer tremendous potential for breeding varieties with optimized nutritional traits. By focusing on *Cucurbita maxima*, which is the most commonly grown species worldwide, the breeding program aims to improve carotenoid levels and other valuable nutrients, ensuring that the crop meets the nutritional needs of diverse populations.

This work highlights the latest advancements in the breeding program, which are already showing promising results in developing pumpkin varieties with increased carotenoid content and improved sensory attributes. Preliminary analyses of the resulting products have demonstrated their potential to meet both nutritional and market demands. By improving

the carotenoid profile and consumer appeal of these pumpkins, this initiative not only aims to combat vitamin A deficiency but also contributes to the development of more sustainable and health-promoting food systems.

FROM FIELD TO FORK: CONSUMER PREFERENCES GUIDING IDEOTYPE SELECTION FOR TOMATO

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Abstract Text:

Integrating consumer preferences into crop breeding is essential for developing market-aligned, sustainable varieties (Sanchez et al., 2024). The aims of the present work focus on identifying ideotypes that combine superior appearance with exceptional sensory profiles. To achieve this goal, we evaluated a composite cross population (CCP), obtained by crossing 4 tomato landraces (COMAV-UPV seedbank), was first evaluated and mass selected in 2023 spring-summer season open field, under Mediterranean organic farming conditions (Valencia). Then, seed lots of the offspring were shared for double evaluation and selection in 2024 in two different organic conditions: i) Valencia (again spring-summer 2024 open field Mediterranean) and ii) Coimbra (Portugal, under agroforestry conditions).

Based on the evaluation conducted in Portugal, six ideotypes were developed based on observed differences in fruit size, color, and shape, ensuring that every harvested fruit in the CCP could be assigned to one of these six representative groups. Following this, fifty-two customers from the ESAC organic shop evaluated these ideotypes by voting for their preferred one. Ultimately, these ideotypes were further evaluated by 30 consumers in a tasting panel conducted at the sensory analysis laboratory at ESAC, Portugal, using the SEEDLINKED mobile app. The panel assessed thirteen sensory attributes, including Acidity, Sweetness, Umami, Purchase Intent, Bitterness, and Skin Thickness. Data were analyzed using Principal Component Analysis (PCA) to identify key drivers of variation, supplemented by ANOVA and Tukey tests to determine significant differences among ideotypes.

ESAC customers chose Plant 484 as their preferred shape and color. In the tasting trial, PCA reduced dimensionality, with PC1 (49.2%) and PC2 (27.6%) accounting for 76.8% of the total variation, revealing extensive phenotypic diversity. Key traits driving differentiation included Acidity and Bitterness. Distinct ideotypes emerged: Plant 631, characterized by high Acidity, appealed to consumers favoring tangy profiles; Plant 117 exhibited pronounced Bitterness, and Plant 797 displayed elevated Sweetness and Overall Flavor. Intermediate ideotypes demonstrated balanced sensory profiles, highlighting the complex interplay of attributes. ANOVA and Tukey tests confirmed significant differences ($p<0.05$) among ideotypes for Acidity and Sweetness.

These results underscore the value of participatory sensory analysis in breeding programs, linking consumer preferences to genotype selection. Future steps will focus on further refining these ideotypes for broader market options.

Reference:

Sánchez, A. S., Flores, P., Hernández, V., Sánchez, E., Molina, E., López, N., Rodríguez-Burruezo, A., Fenoll, J., & Hellín, P. (2024). Fruit Agronomic and Quality Traits of Tomato F1 Hybrids Derived from Traditional Varieties. Horticulturae, 10(5), 440. https://doi.org/10.3390/horticulturae10050440

BREEDING FOR DIVERSITY, NUTRITIONAL VALUE AND FARMERS' NEEDS – A NOVEL, PARTICIPATORY APPROACH FOR IMPROVED DURUM AND EMMER CULTIVARS

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Abstract Text:

In the face of a changing climate and shifting consumers preferences, modern plant breeding encounters numerous challenges. While maintaining a strong emphasis on high (processing) quality, nutritional value, and productivity—alongside yield stability—breeding must also adapt to the growing demand for diversity, both in agricultural fields and on consumers' plates. Furthermore, the increasing restrictions on pesticide and mineral fertilizer use necessitate the development of new cultivars that exhibit both enhanced resistance to diseases, weeds and pests, as well as improved nutrient use efficiency. However, these multifaceted requirements often exceed the scope of mainstream breeding, which primarily prioritizes widely adaptable, high-market-share varieties optimized for intensive cultivation. In contrast, the specific needs of consumers, farmers, or unique local growing conditions—critical factors influencing cultivation success—are more effectively addressed through decentralized, participatory breeding approaches. At the Research Institute of Organic Agriculture (ÖMKi), participatory approaches are integral to both our research initiatives and our recently launched breeding programme. Our on-farm system, embedded within ÖMKi's Living Lab network, offers a valuable platform for the early-stage testing and participatory selection of new breeding materials. After the initial difficulties, we can now work with a more stable and dedicated group of farmers. As a non-profit organization independent of market-driven constraints, we can integrate neglected and underutilized crops, as well as alternative cultivars such as promising landraces and organic heterogeneous materials (OHM), into the range of options available to farmers. This approach may both contribute significantly to the enhancement of agrobiodiversity and imply a higher adaptation capacity of the cultivars. Emmer (Triticum turgidum ssp. dicoccum), an ancient wheat species but now only a minor, alternative crop, possesses both advantageous and less favourable agronomic traits. Its ease of cultivation—stemming partly from its adaptability to diverse growing conditions, combined with its good resistance to weeds, pests, and most diseases—as well as its high nutritional quality (Bencze et al. 2020 - Čurná & Lacko-Bartošová 2017, Dinu et al. 2018) makes it a promising candidate for organic and low-input agricultural systems. However, its lower yield, susceptibility to lodging and the hulled nature of its grains render it less popular among organic farmers compared to spelt. Conversely, durum wheat (Triticum turgidum ssp. durum), despite its superior processing quality and higher yield potential, exhibits poorer disease tolerance, particularly to Fusarium species. Given that emmer and durum wheat belong to the same species but represent distinct subspecies, their genetic

compatibility presents an opportunity to combine their desirable traits through targeted hybridization efforts. This work started in 2020 with the crossing of spike-type lines selected in Hungary from the EPO durum OHM population (developed and maintained by INRAe) with emmer ('dicoccum') landraces, resulting in the 'EPO×DIC' population. Our primary goals for emmer breeding included the development of naked-grained OHMs and variety candidates, addressing a major limitation in emmer cultivation—the need for de-hulling processing step. Excellent disease resistance and weed suppression were also aimed, as emmer in general exhibits above-average features in these areas but lacks effective rust resistance. Selection under organic conditions allows the identification of lines with the best possible combination of resistance traits. Given the high impact of low-input conditions and climate extremes on actual yield, breeding for high yield and yield stability remain essential. Additionally, we aim to improve grain quality for bread and pasta production, ensuring stable traits even under extensive conditions, for which the EPO×DIC population also serves as a valuable source. Finally, lodging resistance is a key focus, we counterselect against unfavourable traits but can also make use of shorter-straw types resulting from the crosses. For durum wheat, our breeding efforts prioritize stable, high-yielding and -quality materials with strong adaptability, alongside germplasm selection carried out for improved disease resistance traits, particularly against Fusarium. This ongoing work has resulted in a diverse array of parameter combinations and remains far from complete. Nevertheless, numerous promising OHMs and selected lines have already emerged. Early-stage farmer involvement enables the dynamic maintenance and adaptation of materials to their specific conditions, supporting both natural selection processes and farmer-led breeding initiatives. This approach also fosters the use of organic seeds and promotes seed sovereignty. Additionally, small-scale farmers gain access to high-performing OHMs and organic variety candidates, enhancing their potential for success and profitability.

Reference:

Bencze S, Makádi M, Aranyos TJ, Földi M, Hertelendy P, Mikó P, Bosi S, Negri L, Drexler D (2020) Re-Introduction of Ancient Wheat Cultivars into Organic Agriculture—Emmer and Einkorn Cultivation Experiences under Marginal Conditions. Sustainability 12 (4):1584. https://doi.org/10.3390/su12041584 Čurná V, Lacko-Bartošová M (2017) Chemical composition and nutritional value of emmer wheat (Triticum dicoccon Schrank): A review. J Cent Eur Agric 18 (1):117-134. https://doi.org/10.5513/JCEA01/18.1.1871 Dinu M, Whittaker, A, Pagliai G, Benedettelli S, Sofi F. (2018) Ancient wheat species and human health: Biochemical and clinical implications. J Nutr Biochem 52:1-9.

ENHANCING FARMER SEED SYSTEMS FOR HEATHY AND SUSTAINABLE FOOD SYSTEM TRANSFORMATION: 25 YEARS' ACTION RESEARCH IN CHINA

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Abstract Text:

Small - scale farmers are crucial for global food security and the protection of agrobiodiversity. In the global South, indigenous and rural communities rely on their own seeds, which have cultural significance and genetic diversity advantages. There are still around 478 million small - scale farmers globally, contributing to 35% of the world's food production. In China, small - scale farmers accounted for over 98% of agricultural business entities and managed 70% of cultivated land in 2016, and are expected to remain dominant by 2050. They depend on self - run seed - saving and exchange systems, including seed selection and neighbor - to - neighbour exchanges to maintain genetic diversity, which is vital for sustainable agriculture.

However, these seed systems are under threat. Climate change, the decline of small farms, market pressures, and seed privatization make them increasingly vulnerable. Commercial seeds are often unsuitable for small - scale farmers and require costly agrochemicals that harm the ecosystem and human health. Seed regulatory frameworks also tend to discriminate against small - scale seed producers. As a major follower of the Green Revolution, China faces severe food safety and environmental issues due to overuse of pesticides, fertilizers, etc. The expansion of monocropping and the narrowing of the genetic base threaten food security, and the rapid disappearance of local seeds and the degradation of farmers' seed - related knowledge pose significant challenges.

To address these issues, solutions cantered on local seeds, indigenous knowledge, and farmer - scientist collaboration are essential. The Centre of Chinese Agricultural Policy (CCAP) of the Chinese Academy of Sciences (CAS) launched a Participatory Plant Breeding (PPB) action - research initiative in 2000. The Key methods include:

- Participatory Plant Breeding (PPB): Farmers and scientists work together to breed varieties adapted to local conditions.
- Community Seed Banks (CSB): Preserve local crops and landraces, along with biocultural knowledge.
- Farmer Field Schools (FFS): Share knowledge on seed saving and diverse farming practices.
- Field and laboratory analysis: Assess local crop biodiversity and nutritional value.
- Market linkages: Connect producers and consumers to support landrace conservation.

Some scientific and technical results are:

- 56 Community Seed Banks have been established in 12 provinces, promoting seed conservation and exchange.
- 436 local crop varieties have been evaluated, blending traditional wisdom with scientific knowledge.
- Over 180 soybean varieties, 160 rice varieties and 120 millets varieties have been introduced to farmers through PPB collaborations in different regions.
- 5 local soybean producers have been linked to processors.
- Lab analysis of 53 local soybeans reveals their genetic diversity and nutrition - enhancing potential.
- Farmers' nature-friendly agroecology practices benefit the ecosystem biodiversity and services in pilot communities in national biodiversity conservation parks

The 25 - year exploration has achieved substantial results. Community Seed Banks have become hubs for seed conservation and knowledge sharing by farmers in different ecoregions in China. The integration of traditional and scientific breeding knowledge has spurred crop improvement. Linking soybeans' producers to processors has increased the value of native crops.

These efforts underscore the importance of farmer seed systems. However, continued support is needed. We must scale up successful models, deepen stakeholder cooperation, and raise public awareness. This will drive the sustainable transformation of the food system and secure the future of rural communities.

This article aims to demonstrate the significance and possibility to enhancing farmer seed systems with the following objectives:

- Highlight the pivotal role of farmer seed systems for sustainable food with 25 years' continue enhancing actions in China
- Exhibit the collaborative methods, like PPB, community seed banks etc, between farmers and scientists through co-implementing, exchange nand sharing in knowledge and materials for complementary and mutual benefit in resilience community
- Elucidate the nutritional, ecological, and cultural values of local seeds abd native crops, using soybeans as an exam

Reference:

Sarah Sensen, Yiching Song, Ronnie Vernooy *2024, The Conservation and Sustanable use of Agrobiodiversity in China nd Germany: Advance the policy Agenda

Lammerts van Bueren ET, Struik PC, van Eekeren N, and Nuijten E (2018). Towards resilience through systems-based plant breeding.

Song, Y. and Vernooy, R. (Eds.) 2022. Seeds that give revisited: Participatory plant breeding and rural revitalization. China Agriculture Press, Beijing

Song, X. Li, G., Vernooy, R., Song Y. 2021. Community seed banks in China: achievements, challenges and prospects. Frontiers in Sustainable Food Systems 5:630400. doi: 10.3389/fsufs.2021.630400

EXTENDING PARTICIPATORY BREEDING TO MULTI-ACTOR INVOLVEMENT TO CO-CONSTRUCT VALUE CHAINS FOR NEGLECTED AND UNDERUTILISED CROPS: QUESTIONS AND METHODS

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Abstract Text:

Participatory Plant Breeding (PPB) is an approach to develop genetic material informed by the perceptions and experiences of end-users. The main advantages are the insights into trait importance and genotype evaluation in the real conditions of cultivation and use, which is connected to direct adoption prospects. Many successful PPB initiatives were implemented in the Global South, where resource constrains make it a viable alternative to big professionalized breeding programs. In Europe, PPB is increasingly emerging with several initiatives in place. Participation activities tend to focus on farmer involvement in selection, with experiences and attempts to engage other stakeholders often including much less structured approaches and less direct influence on the breeding outcome.

However, as urging challenges such as climate change, (agro)biodiversity loss, land degradation and the environmental footprint of agricultural and food production call for a systematic shift in the whole agri-food system towards diversity, resilience and input reduction, it becomes obvious that the development of future genetic material and associated agricultural practices demands a holistic approach involving all concerned parties of the agri-food system.

After a century of scientific and economic specialization, segmentation and optimization, a perspective of re-learning and re-connecting to ecologically valuable agroecological practices such as the cultivation and consumption of neglected and underutilised crops (NUCs) is taken, supported by the pressure of the organic and agroecological movement and environmental and social activists.

In the light of these developments, it is important to extend the concept of Participatory Plant Breeding to the methods of multi-actor value chain creation, with the objective to fully involving all stakeholders in the value chain, including farmers, food producers, chefs, retailers, consumers, citizens and even policy makers in the development and use of genetic material. While it is easy to understand the need for this truly multi-actor approach, the development of the concept and its implementation are emerging together with the attempts to combine PPB and suitable value chain co-creation for the genetic material outcome of these programs.

To contribute to this discussion, this research has collected information on participatory activities in six Living Labs of the EU-Project DIVINFOOD (Co-constructing interactive short and mid-tier food chains to value agrobioDIVersity IN healthy plant-based FOOD). The project focus is on the re-integration of neglected and underutilized crops (NUCs) into farming and food systems in 9 European countries by including a range of stakeholders across the value chain. The data was collected in semi-structured interviews in 2024.

A first result is the identification of three domains of action for multi-actor breeding to co-construct NUCs value chains: (i) awareness-raising, (ii) capacity building and (iii) Evaluation/Selection. Regarding Awareness-raising, field days are the most common activity. In the Capacity building domain, activities such as conducting a workshop for processors to engage with new products and recipes or working collaboratively with farmers on the question of a suitable NUC crop for a certain region have been mentioned. Evaluation/Selection activities have taken place on-field with different actor groups, but also in the form of culinary evaluations with consumers. Different pathways and methods have been worked out and will be presented with the focus specifically on the consumers and citizens actor group.

General awareness for agrobiodiversity and the value of the respective NUC can be seen as a prerequisite to any action of the different actors. For going a step further and gain profound knowledge on the traits and breeding aims needs of the actors along the value chain, a focus on activities collecting evaluation data in a systematic way and measuring the impact of the performed activities in the germplasm adaptation / cultivar development is envisioned.

40 YEARS OF PARTICIPATORY PLANT BREEDING IN PORTUGAL. THE VASO PROGRAM

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Abstract Text:

The VASO project started 40 years ago, originally to address challenges like enhancing yield, utilizing traditional genetic resources, and adjusting to agroclimatic conditions and production systems.

The history of the VASO Program is a living history that upholds the belief that adapted maize seed can be developed, that a good grain can be generated from the seed and that a good flour can be created from the grain and utilized in our cuisine (e.g. broa or maize bread), establishing a value chain with history and culture. Organic farming has become the focus of the VASO Project since 2007, even if sustainability issues have been a major part of it since the start.

Throughout VASO's history, we have been able to evaluate the genetic gain from selection in certain improved populations (Mendes-Moreira et al, 2017; Alves et al, 2018), make sure farmers continue to sow traditional varieties and employ indicators (such as triadic and ear value) to aid in selection and evaluation (Mendes-Moreira et al, 2014). We were able to determine if selection had reduced genetic diversity, as well as the link between the many traditional kinds of maize and their organoleptic quality. We were also able to gain a deeper understanding of the composition (Alves et al 2019), and flavors associated with different types of maize. Additionally, the emergence of synthetic and composite populations, population adaptability to monoculture or polyculture systems, and how production methods may alter the microbiome composition (Ares et al, 2021).

Several meetings, interviews, and training of the value chain's components are also part of the socio-economic process, which is essential to developing the value chain from seed to plate.

The VASO program has enabled us to continue using and sowing the offspring of selections from our populations, and this study aims to provide a clearer explanation of our operations.

Reference:

Alves, M. L., Brites, C., Paulo, M., Carbas, B., Belo, M., Mendes-Moreira, P., Brites, C., Bronze, M. R., Šatović, Z., & Vaz Patto, M. C. (2018). Long-term on-farm participatory maize breeding by stratified mass selection retains molecular diversity while improving agronomic performance. Evolutionary Applications, 11(2), 254-270. https://doi.org/10.1111/eva.12549

Alves, M. L., Carbas, B., Gaspar, D., Paulo, M., Brites, C., Mendes-Moreira, P., Malosetti, M., van Eeuwijk, F., & Vaz Patto, M. C. (2019). Genome-wide association study for kernel composition and flour pasting behavior in wholemeal maize flour. BMC Plant Biology, 19, 123. https://doi.org/10.1186/s12870-019-1729-7

Ares, A., Costa, J., Joaquim, C., Pintado, D., Santos, D., Messmer, M. M., & Mendes-Moreira, P. M. (2021). Effect of low-input organic and conventional farming systems on maize rhizosphere in two Portuguese open-pollinated varieties (OPV), "Pigarro" (improved landrace) and "SinPre" (a composite cross population). Frontiers in Microbiology, 12. https://doi.org/10.3389/fmicb.2021.636009

Mendes-Moreira, P., Fernandes, A., Mendes-Moreira, J., Vaz Patto, M. C., Hallauer, A. R., & Pêgo, S. E. (2014). Is ear value an effective indicator for maize yield evaluation? Field Crops Research, 161, 75-86. https://doi.org/10.1016/j.fcr.2014.02.015

Mendes-Moreira, P., Satovic, Z., Mendes-Moreira, J., Santos, J. P., Santos, J. N., Pêgo, S., & Vaz Patto, M. C. (2017). Maize participatory breeding in Portugal: Comparison of farmer's and breeder's on-farm selection. Plant Breeding, 136(6), 861-871. https://doi.org/10.1111/pbr.12551

BUSINESS BIRDVIEW AS AN INNOVATIVE CONCEPT FOR ACCELERATING ORGANIC FARMING

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Abstract Text:

According to Eurostat, the organic farming area in the EU expanded by 56% between 2012 and 2020, reaching over 14.7 million hectares. In line with the expansion of organic agricultural land, consumer demand for organic products continues to rise. This growing market is driving higher demand for organic seeds. Under current EU legislation, organic farmers are required to use organic seeds when available. However, due to limited supply, they can still rely on conventionally bred and/or produced seeds under specific derogation systems.

To find a way to bring the organic sector closer to farmers as well as consumers and to start developing this sector, the organic seed market and cultivar testing networks were analysed as part of a LiveSeeding project as a broader effort to identify key obstacles and opportunities for scaling up at the national and European levels. All the information collected through the survey, workshops and the SWOT interviews among organic and conventional seed producers/traders or breeders were systematised through the "Business Birdview" tool. The "Business Birdview" template provides a streamlined, holistic view of a business by integrating internal and external challenges, opportunities and key strategic elements. Insufficient data about organic seed production and use is among the key factors affecting the current development of the organic seed market in the EU. Seed suppliers, producers, and breeders need the information to make appropriate investment decisions.
These investments in developing new supplies of organic seed will be made only if the possibility of derogations does not stifle demand. To determine these gaps, analysed fields are divided into four categories: type of activity (organic seed production and cultivar testing network), type of organisation (company, initiative, research centre), type of crops (arable, vegetable), and type of production (organic and organic&conventional).

The "Business Birdview" combines insights from SWOT analysis and the Business Model Canvas into three sections: "Challenges of Today", which identifies internal and external bottlenecks; "Sounds Like Opportunity", which highlights growth opportunities, unique selling propositions and customer strategies; and "Future is Organic", which focuses on profitability and strategic recommendations.

To conclude, different business models and innovative financial and governance models are needed to sustain breeding initiatives and business models for organic seed. Business Birdview tool not only simplifies complex business analysis, making insights easily digestible for stakeholders and aiding in more informed decision-making, but it can also inspire farmers and consumers to start demanding the organic sector's development to make the agriculture climate robust.

Reference:

EU Agricultural Economic briefs

https://agriculture.ec.europa.eu/document/download/df01a3c7-c0fb-48f1-8eca-ce452ea4b8c2_en?filename=agri-market-brief-20-organic-farming-eu_en.pdf

Future of EU rules on plant and forest reproductive material

https://food.ec.europa.eu/plants/plant-reproductive-material/legislation/future-eu-rules-plant-and-forest-reproductive-material_en

Špicnagel AM, Đumbir M, Maričić D, Dlačić I, Mrkšić S (2024) Report on bottlenecks and opportunities for the horizontal proliferation and scaling-up of the organic seeds and cultivar testing network. Deliverable 5.1 LiveSeeding. https://liveseeding.eu/wp-content/uploads/2025/01/LiveSeeding_D5.1_Bottleneck-opportunities_FINAL.

THE INTERNATIONAL TREATY'S BENEFIT-SHARING FUND AS INNOVATIVE FUNDING MODEL

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Abstract Text:

The International Treaty on Plant Genetic Resources for Food and Agriculture is a legally binding international agreement on the conservation and sustainable use of plant genetic resources for food and agriculture (PGRFA) and the fair and equitable sharing of benefits arising from their use. Hosted by the Food and Agriculture Organization of the United Nations (FAO), the International Treaty is a fully operational global system mandated by 154 Contracting Parties.

Key to achieving these objectives is the International Treaty's Multilateral System of Access and Benefit-sharing (MLS) that facilitates the exchange of a wide range of plant genetic resources for research, breeding, and training. Benefits arising from the use of the Multilateral System are shared in the Treaty's Benefit-sharing Fund (BSF), an innovative, financial mechanism sustaining small-scale and local breeding initiatives.

The BSF supports projects working with small-scale farmers in developing countries to improve livelihoods, food security and adaptation to climate change. This is achieved by enhancing the on-farm management and improvement of plant genetic diversity, strengthening local value chains and supporting communities of practice to conserve and sustainably use plant genetic materials and related knowledge. So far, over 100 projects have been implemented in almost 80 developing countries, reaching more than 1 million people, including small-scale farmers, researchers, breeders, genebank curators, government officials, students and academics (FAO, 2023)

The extent to which the BSF operates worldwide and unites over 500 institutions in all global regions creates unique opportunities for exchange of knowledge and practices on various aspects of plant genetic resources management and innovation. Diverse institutions exchange experience and expertise on topics such as participatory plant breeding and on-farm cultivar testing, integration of (participatory) breeding into value chains, and inclusion of farmer managed PGRFA, including heterogeneous material, in policy and frameworks.

Since its establishment in 2009, participatory plant breeding (PPB) has featured prominently in the BSF. Almost half of the projects in the first three funding cycles focused on PPB while this increased to almost 80% in the fifth and most recent cycle. This prominence is explained by the fact that PPB supports realization of important BSF priorities such as on-farm management, sustainable use, improving livelihoods and knowledge exchange.

Over the past decades, PPB programmes – including the BSF and other global programmes such as those implemented by Oxfam Novib, IFAD, the Global Environment Facility, Bioversity

– have increasingly demonstrated their positive impact on the livelihoods of small-scale farmers and the relevance of PPB to addressing intertwined challenges of biodiversity loss, food insecurity and climate change adaptation. While this makes a strong case for financial support to PPB for sustainable development, there is much more information available that can be leveraged for documentation of lessons and good practices and reflection on challenges and opportunities on institutionalizing and mainstreaming PPB initiatives (Toledo, 2020).

Evidence can be used to apply for new funding opportunities, including in response to expanding international donor finance for climate change and new global funds such as the Global Biodiversity Framework Fund. The experience gained from PPB programmes in response to climate change and biodiversity loss provide a strong basis for approaching several climate-change and other financing institutions that have not yet supported work on PGRFA.

However, next to support and funding from international organizations, a transit is needed towards a more diversified approach to ensure local sustainability of initiatives, together with better national policy and budgetary planning. There are some ongoing national efforts to take note of in this regard and the International Treaty also supports mainstreaming efforts at national to sub-regional levels in BSF projects and other capacity building activities (idem).

Constraints and opportunities presented above stress the call for the PPB and PGRFA community – with its wide range of stakeholders – to discuss failures and bottlenecks, share lessons and disseminate success stories. The BSF is taking initiative to facilitate this in its Community of Practice, and to make knowledge gained available to global platforms to support the further growth of successful approaches to PGRFA conservation and use.

Reference:

FAO (2023). The Benefit-sharing Fund: 2022–2023 report. https://doi.org/10.4060/cc8123en

Toledo Á (2020). Funding participatory plant breeding. Outlook and challenges. In Westengen O, Winge T (eds) Farmers and plant breeding. Current approaches and perspectives, [263-276].

Website International Treaty on Plant Genetic Resources for Food and Agriculture: https://www.fao.org/plant-treaty

AN IMPROVED FRAMEWORK TO CLASSIFY SEED SYSTEMS IN THE ORGANIC SECTOR

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Abstract Text:

Organic farmers obtain their seeds from various seed systems. In the scientific literature, seed systems are differentiated according to how they are embedded into legal frameworks, organisational approaches and governance structures. The first classification distinguishes between formal and informal seed systems whether farmers buy seeds from seed suppliers (« formal seed systems ») or produce seeds themselves on the farm or exchange seeds with other farmers (« informal seed system » also sometimes called « farmers' seed system ») (Bocci and Chable, 2009; Edith T. Lammerts van Bueren et al., 2018; Louwaars, 2007). A more recent, complementary, classification distinguishes between « Commons » seed systems characterised by common ownership and collective management and « Conventional » seed systems, characterised as private-property-based seed production (Kliem et al. 2021). We compare these frameworks to mappings of the seed supply from two case studies of organic production in France and Belgium (Antier, 2021; Antier, 2025). These mappings showcase information flows and material flows of seeds and seedlings between actors of vegetable sector. The mappings indicate that farmers' seeds choices result from complex ethical, technical, economic, practical and social factors. Additional dimensions are found important to describe actual seed supplies accurately. In complementarity to existing classifications, seed systems can also be assessed by the length of value chains between breeding and use of seeds. This additional axis, measurable as direct, short or long seed value chain, can be useful to clarify further the coexistence, within the formal seed system, of small to medium-size seed companies aiming at providing organic, open-pollinated varieties in consistency with the organic sector standards, side to side with seed companies aiming at highly productive varieties, no focus on reproducibility, and mostly bred for conventional farming. This assessment is also useful for highlighting the critical roles of seed producers (multipliers) who work upstream of seed companies and have rarely been included in the classification of seed systems. This improved mapping of seed systems can be used as a framework to study risks and opportunities for the organic sector and help direct effort to the seed value chains most aligned with the organic sector standards.

ORGANIC FROM THE START – WHY DOES IT MATTER? BENEFITS AND COSTS OF ORGANIC HETEROGENEOUS MATERIAL IN ORGANIC WHEAT CULTIVATION

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Abstract Text:

The benefits of organic breeding (e.g. contribution to the overall objective of organic farming to conserve and enhance biodiversity, development of locally adapted and resilient cultivars that help to reduce the use of agrochemicals, environmental pollution and greenhouse gas emissions) span the entire food system. However, organic breeding currently plays a niche role in the organic sector and needs to be promoted more strongly. There is an undersupply of organic varieties, which is linked to a lack of awareness among value chain actors, including consumers. The aim of this study was to assess the benefits of organic heterogeneous material (OHM) as a cultivar type promoted by the EU Organic Regulation (2018/848).

We explored the economic, social and environmental benefits and costs of breeding, growing and processing OHM using the Furat tenero Floriddia bread wheat population in Tuscany, Italy, as a case study. Interviews were conducted with stakeholders of short, local value chains of the OHM bread wheat cultivar Furat tenero Floriddia. These stakeholders, including breeders, multipliers, farmers and processors, have been using OHM cultivars for several years and therefore gathered knowledge and experience about its benefits and costs. Additionally, external researchers working with OHM were interviewed. In total, 17 interviews were conducted in 2023 and were analysed through a structured content analysis. The results from the interviews were validated in 2 stakeholder workshops which took place in 2024 hosted by Rete Semi Rurali Italian seeds network. During the stakeholder workshops the interview results were discussed, validated and, where possible, quantified.

The analysis of the interviews and the workshops shows that key benefits and costs of OHM derive from the genetic diversity of these materials. Agronomic benefits of using OHM cultivars as perceived by the participants to the case study include: adaptation to the local growing conditions, high nutrient use efficiency, good weed competition, high disease resistance, and beneficial effect on the soil quality. The participants linked these factors to a better spatial exploitation of plants above and below ground and a to a higher yield stability potential over time. The technical aspects linked to population conservation (e.g. maintaining an appropriate genetic diversity level), seed production and traceability (e.g. preventing seedborne diseases in farm saved seeds), emerged as challenging factors in our study, meaning that OHM handling is a knowledge and responsibility intensive activity for farmers. The independence from the seed and cereal commodity market, which is considered as an

opportunity by the farmers using OHM, requires however local value chains, specifically adapted to the food products based on OHM grain, in order to ensure fair and stable revenues for all the actors involved. More benefits perceived as important for OHM wheat processing, include good baking quality and stability, good nutritional value, as well as distinctively good and unique aroma and taste. On a system level, using populations leads to seed sovereignty because of the absence of IPRs on OHM. On the other hand, the funding of OHM breeding programmes is a challenge. In conclusion, stakeholders and experts working in the Furat tenero Floriddia wheat population value chains in Italy confirmed a great potential of using OHM cultivars in organic farming, especially when grown in marginal areas and when integrated in short and artisanal value chains.

BREEDING WITH CROP WILD RELATIVES: POSSIBILITIES FOR AN AGROECOLOGICAL AND SOCIAL TRANSITION

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Abstract Text:

Industrial agricultural practices, including the breeding and dispersion of high-yielding cultivars and associated agronomic methods, have contributed to a significant erosion of genetic diversity in cultivated plants worldwide. In parallel with these trends, the continuous extension of intellectual property rights over plant reproductive material since the 1970s has also resulted in an extensive consolidation of power over the production and sale of seeds. Today, only four companies control more than 60% of the world's seed sales and more than 40% of the food commodity market (Howard 2016, Barber and Ngu 2019). This has led to eroding control over the price of plant reproductive materials and the technologies of seed conservation and improvement by smaller market actors. In turn, the homogenization in plant genetic material threatens the resilience, productivity, and adaptive capacity of agroecological systems and poses a major threat to food and nutrition security (Khoury et al. 2021).

To counter the degradation of diversity at the genomic, variety, and species level, breeders as well as policymakers are increasingly turning to Crop Wild Relatives (CWR), the progenitors or close relatives of cultivated species. Due to their longtime adaptation to local environmental conditions and their escape from domestication bottlenecks, CWRs present immense genetic variability, making them hardy and resilient plants. CWRs today represent critical resources of genetic information for major food crops. While they are lesser known in modern agricultural systems, they have been instrumental in farmer-led crop improvement and genetic enrichment for millenia, supplying nutrition, income, and cultural resources (Altieri and Merrick 1987, de Wit 2016, Pawera et al. 2017). CWRs also play an important role in the resilience of agricultural systems by enhancing biodiversity on farm, improving soil quality, and strengthening the resilience of food crops (Nabhan 2009, Nazarea et al. 2013). However, CWRs are also highly vulnerable to private capture by powerful market actors and are threatened by a logic of extraction that limits their ability to serve a genuine agroecological transition (de Wit 2016). Often, CWRs are chiefly considered for their capacity "to give [commercial] crops a genetic helping hand," infusing them with resilient CWR traits to adapt the industrial agricultural system to new conditions (Guarino and Lobell 2011, 374).

This paper examines the work of small-scale CWR breeders who use crop wild relatives for the enhancement of the social and ecological resilience of agricultural systems. Through a collection of in-depth interviews with breeders from diverse political, socioeconomic, and ecological contexts in Europe, it studies the goals, practices, and paradigmatic orientations that these breeders adapt to enhance agrobiodiversity in situ while countering systemic socio-economic challenges in the sector (van Bueren 2018).

Adopting an environmental social science perspective, this study explores how these actors see their role in the context of an increasingly consolidating seed market economy and evaluates their capacity to expand the role of CWRs beyond the extraction of their value for the enhancement of already dominating crops. By understanding the varied and diverse ways that these actors see their own practices in the wider breeding context, the paper identifies success factors and areas for improvement in addressing the above challenges and circumventing existing market pressures. This work is based on research done in the EU-Horizon project COUSIN with breeding partners from Italy, Hungary, Spain, Switzerland, the UK, and the Netherlands. The paper is part of a broader research effort within COUSIN which aims to understand the extent to which current breeding and management practices of CWRs can contribute to more sustainable and democratically managed agricultural systems, and whether there are measures and modes of organization that could be adopted to maximize CWRs' potential in this regard.

Reference:

Altieri, M. A., & Merrick, L. C. (1987). In situ conservation of crop genetic resources through maintenance of traditional farming systems. Economic Botany, 41(1), 86–96. https://doi.org/10.1007/bf02859354

Barber, D., & Ngu, A. (2019, June 11). Opinion | Save our food. Free the seed. The New York Times. https://www.nytimes.com/interactive/2019/06/07/opinion/sunday/dan-barber-seed-companies.html

Guarino, L., & Lobell, D. B. (2011). A walk on the wild side. Nature Climate Change, 1(8), 374–375. https://doi.org/10.1038/nclimate1272

Howard, P. H. (2016). Concentration and power in the food system. Bloomsbury. https://doi.org/10.5040/9781474264365

Khoury, C. K., Brush, S. B., Costich, D. E., Curry, H. A., De Haan, S., Engels, J., Guarino, L., Hoban, S., Mercer, K. L., Miller, A. J., Nabhan, G. P., Perales, H., Richards, C. M., Riggins, C. W., & Thormann, I. (2021). Crop genetic erosion: understanding and responding to loss of crop diversity. New Phytologist, 233(1), 84–118. https://doi.org/10.1111/nph.17733

Nabhan, G.P. (2009). Where our food comes from: Retracing Nikolay Vavilov’s quest to end famine. Washington, DC: Island Press/Shearwater Books.

Nazarea, V.D., R.E. Rhoades, and J. Andrews-Swann, eds. (2013). Seeds of resistance, seeds of hope: Place and agency in the conservation of biodiversity. Tucson, AZ: University of Arizona Press.

Pawera, L., Łuczaj, Ł., Pieroni, A., & Polesny, Z. (2017). Traditional plant knowledge in the White Carpathians: ethnobotany of wild food plants and crop wild relatives in the Czech Republic. Human Ecology, 45(5), 655–671. https://doi.org/10.1007/s10745-017-9938-x

de Wit, M. M. (2016). Stealing into the wild: conservation science, plant breeding and the makings of new seed enclosures. The Journal of Peasant Studies, 44(1), 169–212. https://doi.org/10.1080/03066150.2016.1168405

Van Bueren, E. T. L., Struik, P. C., Van Eekeren, N., & Nuijten, E. (2018). Towards resilience through systems-based plant breeding. A review. Agronomy for Sustainable Development, 38(5). https://doi.org/10.1007/s13593-018-0522-6

FROM ORGANIC BREEDING TO MARKET: LIVING LABS TO ADVANCE ORGANIC SEEDS IN ORGANIC VALUE CHAINS

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Abstract Text:

Organic plant breeding (OPB) supports the transition toward agroecological, resilient and sustainable food systems by providing appropriate cultivars for organic agriculture. Despite its impact, OPB is underrepresented in the organic sector due to the low acceptance and awareness among farmers and all actors in the supply chain, including consumers (Petitti et al., 2024). This hinders the potential scaling up of organic farming and actions are needed to overcome these lock-ins. Research on sustainable and agroecological transitions emphasizes that a transition requires radical changes toward new types of socio-technical systems (Geels et al., 2010; Oliver et al., 2019). Transition is the process of reconfiguring the regime under the action of the landscape and the ability of niches to be integrated into the dominant socio-technical regime. Niches can drive changes in the dominant system, by promoting innovation, overcoming lock-ins and transforming socio-technical regimes.

In the context of agroecological transition, Living Lab (LL) has emerged as an effective innovation ecosystem. It is defined as "*an open innovation ecosystem in real-life settings, in which user-driven innovation is the co-creation process for new services, products and societal infrastructures*". Agroecology LLs adopt a transdisciplinary approach which involves farmers, researchers and other stakeholders in the co-design, monitoring and evaluation of agricultural practices and technologies in working landscapes (MACS 2019). Within the EU Horizon LIVESEEDING project (www.liveseeding.eu) 17 Living Labs in different European countries representing the main pedoclimatic areas, offer a constellation of ecosystem and different actors involved in OPB-based value chains, from seed to plate. These LLs are experimenting with innovations, such as organic heterogeneous material (OHM) and organic varieties (OV) using participatory selection methods and testing new agroecological practices, as well as engaging in the development of new markets and organic food value chains.

The present study aims to investigate how the LL can provide a pathway to advance organic breeding and the organic sector for different crops. In particular, the study aims to: (i) map the challenges faced by Living Labs, (ii) identify key success factors for organic breeding innovations, (iii) analyse the role of co-creation in improving and expanding organic sectors, and (iv) provide recommendations to increase the use of organic cultivars and seeds. To achieve these objectives, the study uses a mixed-method approach, including workshops, questionnaires and in-depth interviews. Three co-creation workshops were held integrating different methodologies such as dynamic presentations in the Pecha Kucha format and

interactive working groups involving different actors of the LLs. Qualitative data was also collected through questionnaires, while semi-structured in-depth interviews are ongoing.

Preliminary results show that LIVESEEDING Living Labs are successfully implementing several innovations based on organic breeding, in spite of time and resource constraints and, in some contexts, limited institutional involvement and support. The participation of very diverse actors with different roles within the LLs emerges as a key success factor that allows cross-fertilisation between different sectors, increasing awareness about the use of organic seeds, particularly among conventional or mixed actors such as farmers, seed companies, retailers and citizens.

In conclusion, a discriminating factor in becoming an innovation-catalyst for organic seeds and breeding, is the type of organisational structure within the Living Lab. A good governance is essential to maintain the focus on the objective and foster the active participation and motivation of all the stakeholders involved. This empowers the Living Lab to effectively exploit innovations and achieve impact on organic value chains and the wider food system.

Reference:

Geels FW (2010). Ontologies, socio-technical transitions (to sustainability), and the multi-level perspective. Research Policy 39 (4):495-510. http://dx.doi.org/10.1016/j.respol.2010.01.022

International Agroecosystem Living Laboratories Working Group (2019). Agroecosystem Living Laboratories: Executive Report. In: G20 Meeting of Agricultural Chief Scientists (G20-MACS).

Ollivier G, Magda D, Mazé A, Plumecocq G, & Lamine C (2018). Agroecological transitions: what can sustainability transition frameworks teach us? An ontological and empirical analysis. Ecology & Society, 23(2).

Petiti M, De Santis G, Ceccarelli S, Stentella R, Salvan M, Bussi B, Bocci R, Ponzini D (2024). Rice Diversity from Seed to Fork: a Living Lab for Organic Rice in Northern Italy. Journal Of Integrated Field Science 21:37-39 – Graduate School of agricultural Science, Tohoku University https://doi.org/10.50974/0002002001

SUPPORTING MASS SELECTION WITH THE MICROBIOTA: PARTICIPATORY AND TRANSDISCIPLINARY RESEARCH WITH BORDEAUX VINEYARDS

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Abstract Text:

Viticulture is addressing more and more challenges, especially in the Bordeaux region: vineyards are facing climate instabilities, more frequent and aggressive pathogens (e.g mildew) as well as consumers' concerns about pesticides' use and biodiversity. This context requires a shift in practices: an increasing number of wine estates engage in an ecologisation process, considering among other leverages agroecology, agroforestry, crops diversification, and varietal adaptation. In this study, we focus on vine (Vitis vinifera subsp vinifera L.) mass selection within four estates in the Bordeaux region. We consider participatory breeding as a facilitation tool between practitioners and researchers to address a biological issue regarding the transmission and stability of vine microbiota in mass selection. The diversity of partners involved in this kind of project is often associated with asymmetries of knowledge, expectations and different stances towards living beings. To face this challenge, we discuss the biological questions within a larger framework, not only using a molecular ecology approach but also a socio-anthropological one. In this presentation, we aim at showing the complementarity between these academic fields, and how they support participatory breeding.

Our project is articulated in three axes, each one giving a special highlight to our research question. We first consider mass selection in the Bordeaux region with a socio-anthropological approach to bring forward its specificities in comparison to other on-farm breeding initiatives. We interviewed nine members of four vineyards (Château Latour, Château Lafite, Château Leoville las Cases and Château Palmer), either in the executive committee or research and development team. By linking micro-structural evolutions to macro-structural dynamics (i.e agricultural modernisation and knowledge reputation), we show how mass selection is implemented in coherence with each estate historical identity. In our field of study, we also demonstrate how mass selection is a first step out of the plantacionocene (Haraway, 2015), which leads to a more inclusive conception of viticulture. Then, we focus more on the vine microbiota itself with a metagenomic approach, using 16S and 18S DNAs. Samples of soil, roots, leaves and berries undergo DNA extraction, PCR using primers NS22b and SSU817 for fungi (Lê Van et al., 2017), and 799F and 1223R for bacteria (Vannier et al., 2018). After purification, quantification and normalisation, amplicons are then sequenced with Illumina MiSeq. Sequence data are then processed with the FROGS pipeline (Escudié et al., 2018) before further statistical analysis. First, a community ecology approach will describe the microbiotic assemblages. Intra- and inter-vineyard microbiotic diversity of the mother plants will be estimated by calculating diversity indices, in order to describe and

compare them with that of the daughters plants lines. In addition, the effects of environmental factors (biotic and abiotic) will be estimated using multivariate analyses (Canonical Correspondence Analysis) and univariate models. These analyses will be carried out at the level of all bacterial and fungal communities and for the main phyla. Secondly, community assembly processes will be studied using different methods - DESeq (Anders & Huber, 2010), Beta Nearest Taxon Distance (Stegen et al., 2012) and Normalized Stochasticity Ratio (Ning et al., 2019) - in order to determine their stochastic and deterministic dimensions depending on the selection method, as well as identifying potentially characteristic microorganisms of mass selection. These analyses will be carried out on mother plants, daughter plants and controls from clonal selection.

Finally, we discuss the metagenomic process in regard of translation sociology (Callon et al., 2006) and Science and Technology Studies approaches (i.e. political ecology and anthropology of microbes). We analyse the trade-off between increased interpretability and loss of biological relevance through each step of the process, from sampling to data analyses. We suggest collaborative research as a reflexive tool between scientists and practitioners, in order to consider the microbiota in an integrative way, rather than within a reductionist paradigm.

Reference:

Anders, S., & Huber, W. (2010). Differential expression analysis for sequence count data. Nature Precedings, 1-1. https://doi.org/10.1038/npre.2010.4282.1 Callon, M., Akrich, M., & Latour, B. (2006). Sociologie de la traduction. Textes fondateurs. Presses des MINES. ⟨hal-03597436⟩ Escudié, F., Auer, L., Bernard, M., Mariadassou, M., Cauquil, L., Vidal, K., ... & Pascal, G. (2018). FROGS: find, rapidly, OTUs with galaxy solution. Bioinformatics, 34(8), 1287-1294. https://doi.org/10.1093/bioinformatics/btx791 Haraway, D. (2015). Anthropocene, capitalocene, plantationocene, chthulucene: Making kin. Environmental humanities, 6(1), 159-165. https://doi.org/10.1215/22011919-3615934 Lê Van, A., Quaiser, A., Duhamel, M., Michon-Coudouel, S., Dufresne, A., & Vandenkoornhuyse, P. (2017). Ecophylogeny of the endospheric root fungal microbiome of co-occurring Agrostis stolonifera. PeerJ, 5, e3454. https://doi.org/10.7717/peerj.3454 Ning, D., Deng, Y., Tiedje, J. M., & Zhou, J. (2019). A general framework for quantitatively assessing ecological stochasticity. Proceedings of the National Academy of Sciences, 116(34), 16892-16898. https://doi.org/10.1073/pnas.1904623116 Stegen, J. C., Lin, X., Konopka, A. E., & Fredrickson, J. K. (2012). Stochastic and deterministic assembly processes in subsurface microbial communities. The ISME journal, 6(9), 1653-1664. https://doi.org/10.1038/ismej.2012.22 Vannier, N., Mony, C., Bittebiere, A. K., Michon-Coudouel, S., Biget, M., & Vandenkoornhuyse, P. (2018). A microorganisms' journey between plant generations. Microbiome, 6, 1-11. https://doi.org/10.1186/s40168-018-0459-7

PROTECTING ORGANIC SEEDS: RESEARCH ON SEED TREATMENTS FOR ORGANIC FARMING

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Abstract Text:

Seeds represent the fundamental basis of agricultural production, accounting for approximately 90% of the world's food crops. However, seeds can also serve as a vehicle for the transmission of plant pathogens that pose a threat to food production. Seedborne pathogens infect seedlings after seed germination, causing diseases that affect both yields and crop quality, and therefore have a significant impact on farmers' incomes and food security. Furthermore, seedborne pathogens can disseminate within agricultural fields, infecting other plants, and they can often survive in the soil for long time periods until they encounter new hosts and initiate further infections. Despite the implementation of preventive measures to avert the transmission of diseases, the presence of pathogens on seeds and in soil can be inevitable.

In conventional agriculture seeds are treated with chemical fungicides to protect against both seed-borne and soil-borne diseases. However, organic agriculture demands alternative approaches avoiding the use of artificial inputs and that should adhere to European organic regulations. These treatments primarily involve the use of natural compounds (e.g., plant extracts, plant oils, chitosan), physical treatments (e.g., mechanical, thermal), or the application of beneficial microorganisms. While these treatments can be highly effective against certain diseases in specific crops, some crops or crop-pathogen systems still need solutions suitable for an organic production. Furthermore, treatments that are effective eradicating seed pathogens can sometimes have unintended negative effects on seed health, such as reducing seed vigor, or negatively impacting the natural seed microbiome, which can also have beneficial roles in seeds. Consequently, further research is necessary to identify novel seed treatments against specific diseases affecting organic crop production.

At the Research Institute of Organic Farming (FiBL) we are investigating new organic seed treatments. Our two primary areas of focus are protecting seeds against soil-borne pathogens, and disinfecting seeds infected by seedborne pathogens. In the SeednSoil project, which is funded by Fenaco, the focus is on investigating seed treatments that protect wheat seeds from soil-borne infections, such as common bunt disease (caused by *Tilletia caries*) and snow mold disease (caused by *Microdochium nivale*). These diseases have the potential to cause considerable yield losses in organic farming. In the EU-funded project LiveSeeding, the objective is to investigate novel seed treatments to sanitize seeds of various vegetables, and thereby, provide protection against seedborne diseases. These treatments

are developed to be compatible with the facilities of seed companies, by working together with seed companies in Switzerland (Sativa Rheinau AG), Germany (Bingenheimer Saatgut AG) and Greece (Oikos seeds). Seed treatments with protective potential against plant pathogens have been identified in both projects. These results will be presented.

Reference:

Spadaro, D., Herforth-Rahmé, J. and van der Wolf, J. (2017). Organic seed treatments of vegetables to prevent seedborne diseases. Acta Hortic. 1164, 23-32

Klaedtke, S.M.; Rey, F.; Groot, S.P.C. (2022). Designing a Seed Health Strategy for Organic Cropping Systems, Based on a Dynamic Perspective on Seed and Plant Health. Sustainability 2022, 14, 10903. https://doi.org/10.3390/su141710903

PRE-BREEDING: LATVIA'S HORTICULTURAL CROP BREEDING PROGRAM ADDRESSING MODERN AGRICULTURAL CHALLENGES

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1 - Institute of Horticulture (LatHort), Latvia;

Abstract Text:

The Institute of Horticulture in Dobele, Latvia (LatHort), founded in the 1950s by P. Upītis, has a long history of introducing and breeding horticultural plants. This legacy includes evaluating hybrid materials, establishing breeding collections, and developing new cultivars. Over the years, these efforts have led to the registration of more than 70 horticultural plant cultivars. Current horticultural practice faces interconnected challenges such as abiotic and biotic stresses, adaptation to climate change, yield stability, sustainability and environmental impact, genetic diversity, pollination and self-fertility. Consumer expectations of improved fruit quality and storage properties are essential. To adapt to environmental challenges, as well as market demands, the efficiency and speed of breeding are increasingly important. Currently, LatHort is engaged in breeding activities under the project "Horticultural Crop Breeding Programme to Promote the Introduction of Conventional, Integrated, and Organic Cultivation Technologies" (No. 10.9.1-11/24/1654-e), funded by the Ministry of Agriculture. The project aims to develop cultivars resistant to biotic and abiotic stresses and well-suited for Baltic region climate conditions, catering to diverse uses. Developing new cultivars is a complex, long-term process comprising several interconnected stages. Pre-breeding is a crucial but often underestimated stage, which plays a pivotal role in laying the groundwork for achieving successful outcomes. Pre-breeding aims to explore key traits for breeding, select suitable donors, and enhance breeding methodologies. In the Latvian breeding program, pre-breeding activities are carried out for apple trees, raspberries, blackcurrants, Japanese quince, domestic plums, European pears and sweet cherries. The selected pre-breeding directions are related to the leading breeding challenges - resistance to biotic stresses and stability of fruit production, which includes resistance to apple scab (*Venturia inaequalis*), virus complexes of *Rubus* and *Ribes*, *Cecidophyopsis* gall mites of *Ribes*, European pear rust (*Gymnosporangium sabinae*), *Pseudomonas syringae* on sweet cherries and the genetics of self-incompatibility of *Chaenomeles*. The diverse *Malus* germplasm, *V. inaequalis* strain collection, and *V. inaequalis* races differential *Malus* genotypes are used for selecting resistant genotypes and long-term monitoring of *V. inaequalis* virulence changes within the Vinquest network (https://www.vinquest.ch/index.html) to aid sustainable resistance breeding in Latvia, tracking potential new races and resistance gene breakdown. Research includes characterizing pathogen interactions and atypical disease responses and identifying possible new resistance sources. Pre-breeding selects scab-resistant forms from over 300 genotypes, using molecular markers for *Rvi* genes and identifying resistant forms

lacking known genes. Pre-breeding activities for *Rubus* and *Ribes* focus on refining virus diagnostic methods, identifying virus complexes in germplasm and breeding material, and assessing their role in symptoms like raspberry syndrome of bushy dwarf and crumbly fruit and a severe form of blackcurrant reversion. This research aims to clarify the impact of various viruses and enhance breeding strategies for resistant varieties. Research on *Ribes* resistance to *Cecidophyopsis* gall mites includes studying phenological, structural, and morphological bud differences among *Ribes* species and genotypes and developing diagnostic methods for *Cecidophyopsis* species and genetic variants in the breeding material. Additionally, Nanopore sequencing of samples from blackcurrants with severe reversion form has begun to identify specific pathogens, aiding in refining breeding strategies. European pear breeding for resistance to *G. sabinae* focuses on identifying resistance donors and understanding plant-pathogen interactions. Pre-breeding activities at LatHort include field resistance evaluation of germplasm and seedling collections, microscopic interaction studies, and gene expression analysis. Genome sequencing of resistant and susceptible genotypes has also been initiated to identify potential resistance genes. Due to climate change and associated pathogen expansion risks, sweet cherry resistance to *P. syringae* is nowadays also considered in the breeding program. Pre-breeding activities include developing reliable bioassay techniques for testing genotype resistance under controlled conditions, searching for resistance sources, and understanding host-pathogen interaction. Whole-genome sequencing of selected *P. syringae* strains is underway to support understanding host-pathogen interactions and aid further resistance breeding. Molecular markers, including newer species like Japanese quince (*Chaenomeles japonica*), are essential for modern fruit plant breeding. Due to limited genome knowledge, pre-breeding research focuses on self-incompatibility heritability, transferring *S*-gene markers from related species, and identifying compatibility patterns in new cultivars.

COLLECTING CROP WILD RELATIVES OF FORAGE SPECIES TO INCREASE THE AGROBIODIVERSITY

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Abstract Text:

Genetic resources of cultivated plants are the irreplaceable wealth of our planet, created by nature and later by the purposeful creative work of man. Crop wild relatives (CWR) are one of the plant genetic resources components, and an essential item in the attempt to introduce greater diversity into cropping systems (Halewood et al., 2018). Collecting and evaluation of CWR has a long tradition in Serbia and Czech Republic, but common activates started in 2011. Researchers from the Institute for Forage Crops in Kruševac and the Agricultural Research in Troubsko collaborated to collect wild relatives of fodder crops in both of their countries (Petrović et al., 2024). In this contribution we present the results of collecting plant genetic resources from the territory of Southern Serbia during the period 9. 8. – 12. 8. 2021. This region is environmentally significantly different from the rest of the country. These differences are caused by the effect of the Mediterranean climate. The vegetation cover is characterized by Sub-mediterranean plant communities in the lower altitudes, which are thermophilous and xerophilous, containing many annual plant species. The vegetation at higher elevations is more mesophilous, containing mostly species typical of the Central European floristic zone. We gathered 45 seed samples throughout a more than 1000-meter elevation gradient, beginning at 450 meters and ending at 1600 meters above sea level. The database containing passport data for each collected sample was created. Gathered samples belong to the Fabaceae family: 13 species of genus Trifolium (T. aureum Pollich., T. repens L., T. medium L., T. pratense L., T. alpestre L., T. pannonicum Jacq., T. hybridum L., T. angustifolium L., T. lappaceum L., T. campestre Schreb., T. striatum L., T. retusum L., T. vesiculosum Savi), Lathyrus sylvestris L., Anthyllis vulneraria L., Vicia cracca L., Coronilla scorpioides (L.) W. D. J. Koch, Medicago minima L., Dorycnium germanicum (Gremli) Rikli and two Poaceae species – Dasypyrum villosum (L.) Borbás and Aegilops ovata L. Samples are stored in active collections in both institutes in Kruševac and Troubsko. As soon as the sufficient amount of seed has been multiplied, the samples will be stored in the gene banks of both countries. Collected seed samples of fodder wild relatives are a very valuable source of genetic variation that is a key element in any breeding process (Vymyslický et al., 2023).

Reference:

Halewood M, Chiurugwi T, Sackville-Hamilton R, Kurtz B, Marden E, Welch E, Michiels F (2018). Plant genetic resources for food and agriculture: opportunities and challenges emerging from the science and information technology revolution. New Phytol., 217(4), 1407–1419. doi: 10.1111/nph.14993.

Petrović M, Zornić V, Lugić Z, Nedeljko R, Vymyslický T. (2024). Collecting and evaluation of Serbian and Czech genetic resources of fodder species in order to increase the diversity in agriculture. In: Book of Abstract 15th Symposium on Forage Crops of the Republic of Serbia, Kruševac, 26. - 27. 9. 2024, pp. 27–28. ISBN 978-86-82165-04-0.

Vymyslický T, Raab S, Frei I, Hutyrová H (2023). Grass and forage legume genetic resources in the Czech Republic and their practical utilization. – In: Book of Abstracts of the 35th Meeting of the EUCARPIA Fodder Crops and Amenity Grasses Section „Novel technologies, strategies and crops to sustain forage production in future climate", 10. – 14. 11. 2023, Brno, Czech Republic, pp. 28–30.

ORGANIC BREEDING OF MULTI-PARENT POPULATIONS (MPP) OF WINTERPEAS

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Abstract Text:

Introduction: Winter peas have been bred for organic cultivation in Germany for about 15 years. Winter peas are sown in autumn. Winter peas show only stout growth above-ground over the winter, but develop a strong root system. As soon as the day length reaches over 12 h in spring, length growth begins. Winter peas are better adapted to spring droughts. They are also better adapted to foot diseases due to the harsh conditions in which they grow. However, winter peas, like all other grain legumes, also show large yield fluctuations. Timeaus et al. (2022) found higher yield stability, yield gains and quality improvements under high environmental variability in wheat populations and wheat varieties grown in mixtures with winter peas. There, the mixtures showed agronomic advantages with heterogeneous populations. These were more stable than the varieties. However, there were also varieties that outperformed the heterogeneous populations in yield or protein content. According to Döring (2011), the success of crop diversity lies in "complementation, cooperation, compensation and capacity" and especially under uncertain environmental conditions. Populations of self-pollinators, also called composite cross populations (CCP) or multi-parent populations (MPP), have mainly been studied in cereals and especially in wheat (Brumlop et al. 2017, Döring et al. 2011). However, the diversity of CCP consists of bulked recombinant inbreed lines from single crosses. To generate a diverse population with a broad genetic background through recombination and also to use the possibility of pyramiding quantitative traits, the multi-parent population approach could be more suitable. For winter pea, no CCP or MPP has been generated yet. Advantages of MPP could lie in the pyramidisation of quantitative traits such as winter hardiness, tolerance to pathogens and yield or yield stability. MPP are based on a more sophisticated crossing scheme of at least 8 parental lines brought together by cross-breeding, rather than just bulking of single crosses (Cavanagh et al. 2008). Studies have shown that winter peas for organic cultivation should only be grown in a mixture (Quendt&Haase 2014). Therefore, the development of MPP is carried out from the beginning in a mixture with triticale or rye. Mixed cultivation also increases the interspecific diversity in field cultivation. **Hypothesis:** 1. The concept of multi-parent population (MPP) can be adapted to winter pea breeding. 2. Diverse populations can be developed by positive respectively negative mass selection. 3. Populations already in development from multiple crosses show higher and more yield stability than the initial varieties and new winter pea lines. 4. Pyramidisation of different alleles for winter hardiness and field resistance to diseases lead to improved population performance. 5. New lines can be developed from populations if needed. Method: The project will test the developed MPP against the initial lines and other winter pea varieties and lines for yield performance, yield stability, winter hardiness and growth habit in mixed cultivation with triticale. The MPP are to

be further developed by means of positive and/or negative mass selection and led to an agronomically meaningful uniformity in growth height and maturity. In addition to their use as a population, they are to become the starting point for new line varieties and form a diversity pool for further population breeding of winter peas. The winter pea MPP will be made available for further selection and use for different locations. **First results of 2024:** When analysing the group averages, a significant higher yield was determined for the MPP compared to the initial varieties and the new breeding lines. This initially confirmed the observation, that bulks have a higher yield than line varieties. An improved winter hardiness was shown in the MPP, as well as a higher vigor. Only in lodging were MPP inferior. The aims of winter pea breeding are winter hardiness, vigorous, not too tall, determinate growth types that have sufficient standing ability, are competitive in mixed cultivation and produce an appropriate yield overall. The prerequisites for the selection of these characteristics are present in the bulks. However, how selection for the preferred traits should be carried out and what influence this has on the positive characteristics of the bulks must be investigated in the next steps. Further results of the first test year will be presented at the conference.

Reference:

Brumlop, S, Pfeiffer, T, & Finckh, MR (2017): Evolutionary Effects on Morphology and Agronomic Performance of Three Winter Wheat Composite Cross Populations Maintained for Six Years under Organic and Conventional Conditions. Organic Farming, 3(1), 34–50.

Cavanagh, C, Morell, M, Mackay, I, Powell, W (2008): From mutations to MAGIC: resources for gene discovery, validation and delivery in crop plants. Current Opinion in Plant Biology. Vol. 11, Issue 2, 215-221

Döring, TF, Knapp, S, Kovacs, G, Murphy, K, & Wolfe, MS (2011): Evolutionary plant breeding in cereals-into a new era. Sustainability, 3(10), 1944–1971.

QUENDT, U.; HAASE, T. 2014: Breeding winter peas in diversity for diversity. In Book of Abstracts: Diversity Strategies for organic and low input agriculture and their food systems, 41-42.

Timaeus, J, Weedon, OD and Finckh, MR (2022): Harnessing the Potential of Wheat-Pea Species Mixtures: Evaluation of Multifunctional Performance and Wheat Diversity. Frontier Plant Science 13:846237

ASSESSMENT OF CROSSABILITY AND AGRONOMIC TRAITS OF F1 PROGENY IN WHEAT-RYE SUBSTITUTION LINE × COMMON WHEAT HYBRIDIZATION

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Abstract Text:

Rye (Secale cereale L.) is one of the important sources that have been extensively explored by breeders for bread wheat improvement due to its elite genes. Due to the high collinearity of the genomes of both cereal species, it is possible to obtain interspecific chromosomal translocations and substitution lines (Moskal, K. et al. 2021). However, despite the numerous advantages, the transfer of large fragments or whole chromosomes has been quite often accompanied by a decrease in end-use quality (Efremova, T. T. et al. 2022). This paper presents the assessment results of crossability and agronomic traits of F1 progeny in reciprocal wheat-rye substitution line × common wheat hybridization. The parental stable hexaploid wheat-rye substitution lines used in our hybridization work were the next 4 lines: 378/3SD (1R/1B, 2D/2R, 3D/3R, 6D/6R), 383/1SD (1R/1D, 2R/2D), 384/1D and 384/2D with the same substitution 1R/1D. These lines were created in our lab through traditional hybridizations between triticale and wheat varieties, and for the first time included to the crosses with the common wheats in order to improve their agronomic traits. The parental 9 common wheats used in crosses with our wheat-rye substitution lines were the next: the 4 bread wheat cultivars – Triticum aestivum cv. Absheron (Azerbaijan), Triticum aestivum cv. Rumeli (Turkey), Triticum aestivum cv. Bezostaya-100 (Russia), Triticum aestivum cv. Chinese Spring (China) and the 5 local common wheat lines - 171ACS, 172ACS, 626AO, TG-3, 225DKh-86. Overall, a correlation was observed between seed-setting rate and the number of rye chromosome pairs in all hybrid combinations of wheat-rye lines with the common wheats, i.e. the more pairs of rye chromosomes in the parental line, the lower the rate of seed setting (from 50.45% to 15.15%, respectively) obtained with their involvement. However, as expected, the seed-setting percentage was higher in combinations with cultivars compared to those with wheat lines. Unlike seed-setting rate, no relationship was observed between the number of rye chromosome pairs and the germination ability of the obtained hybrid seeds. The highest germination ability of hybrid seeds were recorded for combinations with Absheron (with mean value of 78.95%) and Chinese Spring (with mean value of 95.24%). The F1 plants derived by using of lines 384/1D, 384/2D, and 383/1SD as maternal parents exhibited heterosis effect on spike length, but the advanced fertility rate compared only with maternal plants. The F1 plants obtained with the participation of the 378/3SD line, revealed the superiority in traits of spike length, number and weight of grains per spike compared only to the line itself.

In conclusion, the hybridization work of wheat–rye substitution lines with common wheat (especially with wheat cultivars) showed the effectiveness of such crosses in improving traits related to yield potential.

Reference:

Moskal, K., Kowalik, S., Podyma, W., Łapiński, B., & Boczkowska, M. (2021). The prosand cons of rye chromatin introgression into wheat genome. Agronomy, 11(3), 456. https://doi.org/10.3390/agronomy11030456

Efremova, T. T., Chumanova, E. V., & Zhukova, I. M. (2022). Winter hardiness analysisof wheat-rye 5R (5A)-substituted lines in Western Siberia.Cereal Research Communications,1-11. https://link.springer.com/article/10.1007/s42976-021-00147-z

PHENOPHASE SHIFTS OF LENTIL ACCESSIONS FROM THE UKRAINIAN GENEBANK IN RELATION TO CLIMATE CHANGE

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Abstract Text:

Adaptation to climate change represents a major challenge for agriculture. The innovation of novel crop rotations represents a potential solution, offering the prospect of increasing agrobiodiversity, enhancing food security and improving environmental health. The incorporation of legume crops into rotations has been demonstrated to contribute to a reduction in pesticide usage whilst simultaneously enhancing soil quality through the residual nitrogen accumulation. The innovation of new rotations is the goal of the TRANSFORM project, funded through the Horizon Mission Adaptation to Climate Change, as part of support for arable agriculture in its adaptation to the challenges of climate change. The lentil collection of the National Centre for Plant Genetic Resources (NCPGRU), located in Kharkiv (Ukraine), can be used as a model data-set for adaptability under climate change. Over the course of research (1993-2024), an annual total of 46 to 383 accessions from 53 countries were sown, thereby establishing a model population with high level of diversity (Simpson diversity index ranging from 0.55 to 0.94). The field research was conducted at the Plant Production Institute na V.Ya.Yuriev National Academy of Agrarian Sciences of Ukraine (PPI NAAS). Evaluation of the impact of climate change on the lentil ontogenesis was realised according to indicators list built in the TRANSFORM project. Such as a Simpson's index, indicators on meteorological conditions (number of days with extreme minimum and maximum temperatures), and duration of lentil phenophases. An evaluation of the weather conditions over the first three months of each year revealed a trend of increasing temperature and precipitation. The timing of lentil sowing in the Kharkiv region, over the period from 1993 to 2024, ranged from 25th March to 4th May, with a predominance of sowing done in April. Duration of seedling phase (from sowing to germination) variated from 6 to 12 days with average sum of effective temperatures (> 10°C) is 156°C. Physiologically, lentil seeds begin to germinate at a temperature of 4−5 °C (optimum 7−10°C) with the sum of effective temperatures is 110-127 °C. The date of maturation of lentil accessions was noted as July in many years, with variation from 26th June to 11th August. The average duration of the growing season from germination to full maturity was recorded as 79 days (sum of effective temperature is 1541°C). The frequency of extremely hot days (> 25°C) increased over time, the percentage in pod filling period varied from 21% to 100% (average 58,47%). The optimal temperature for the formation of generative organs is 17−21 °C. As result, a shift in the phenophases of lentil genotypes was observed, with a shortening of the

pod filling period. This indicates that in the Forest-Steppe zone of Ukraine starting conditions of terminal droughts. Trend lines of precipitation show an increase in precipitation during the growing season, with a marked shift in the timing of precipitation over the growing season and transition to less frequent bouts of rain (two or three) of very high intensity (more than 50 mm), which do not replenish soil moisture reserves effectively. We observed possibility to shift lentil sowing dates to earlier that enables seeds to use the moisture persisted from the winter-spring period. However, it is noteworthy that cold weather and frosts in spring are a characteristic of the Kharkiv region. Given that lentil is a cold-resistant crop, their seedlings can withstand frosts down to -6 °C. Thus, earlier sowing dates are not a critical factor in survival. The early start of the growing season would also allow other phases of growth, such as flowering and fruiting, to be shifted to more favourable periods. Lentils could be used as part of new rotations, expanding the range of regions where this crop can be grown – notably into more northerly regions of Europe. The introduction of a new crop into a rotation will require the selection of cultivars with germination and growth characteristics appropriate to local conditions, based upon detailed data, as provided by the genebank, and models of germination and growth. The data from the genebank experiment will therefore be used in the design of new crop rotations in the TRANSFORM project, as part of support for arable agriculture in its adaptation to the challenges of climate change.

ENHANCING PEPPER (CAPSICUM SPP.) DIVERSITY THROUGH LOW INPUT BREEDING AT IFVCNS: CHALLENGES AND ACHIEVEMENTS

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Abstract Text:

Pepper (*Capsicum* spp.) is a key vegetable crop with important nutritional and economic value, particularly in the Southern parts of Europe. The Institute of Field and Vegetable Crops (IFVCNS) in Novi Sad, Serbia, has been actively involved in the breeding and development of pepper varieties for 50 years.

With a focus on improving agronomic traits, enhancing resilience to biotic stresses, and adaptation to regional environmental conditions, the breeding programs at IFVCNS successfully use local and broad genetic resources, utilizing classical breeding methods to develop new pepper cultivars. Despite resource limitations, these efforts have resulted in the development of 16 pepper varieties to date, demonstrating the continued relevance and potential of traditional breeding methods for farmers in Serbia.

One of the core objectives of the IFVCNS breeding program has been to enhance the disease tolerance of pepper varieties, particularly for bacterial leaf spot, and to improve fruit quality. This work has involved the use of simple effective strategies, such as pedigree selection, to improve traits such as fruit shape, weight and pungency.

The latest pepper varieties developed at IFVCNS exhibit distinct features in terms of fruit morphology, taste, and storage characteristics. Hot pepper varieties like NS Vatrena, a variety with high levels of dihydrocapsaicin, and NS Ljutica, show significant improvements in fruit size, and pungency. While NS Vatrena is suited for drying and pickling, NS Ljutica is well-suited for fresh consumption and pickling. NS Prva, a sweet pepper variety, has demonstrated high postharvest storage ability, with minimal weight loss after several weeks of cold storage. Tomato-shaped variety NS Kruna one of the newest, has a thick pericarp fruit. The fruits of this variety are intended for fresh consumption and pickling. In addition to developing improved cultivars, the IFVCNS has also focused on enhancing fruit characteristics such as soluble solids content. These characteristics make them promising for the Serbian fresh market and export.

Consumer preferences also play a critical role in shaping breeding priorities. In Serbia, different pepper types are preferred across regions, with the most popular being kapia and bell peppers. The results of consumer surveys reveal a distinct preference for red-colored peppers, and among hot peppers, a tendency for medium heat levels. This information is valuable in guiding the breeding process to cater to market demands while ensuring the

viability and competitiveness of Serbian pepper varieties in both local and international markets.

Our research underscores the importance of maintaining genetic diversity within the pepper gene pool and its critical role in supporting sustainable agricultural practices. The IFVCNS breeding efforts emphasize the necessity of aligning breeding objectives with both market trends and environmental resilience, ensuring that the developed varieties meet the needs of farmers and consumers. These achievements demonstrate the potential of classical breeding techniques in contributing to the long-term sustainability and competitiveness of pepper production in Serbia.

ENHANCING ORGANIC SEED PROVISION AND VARIETAL DIVERSITY IN LATVIA: CHALLENGES AND RECOMMENDATIONS

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Abstract Text:

The EC 2018/848 regulation stipulates that from 2036, only organic seed will be allowed in organic farming systems. Certified organic seed is an essential part of the supply, alongside organically produced home-saved seed, local variety seed, and heterogeneous material in organic farming. Although diversity is crucial in organic farming systems, this includes the use of specially bred organic varieties, heterogeneous materials, and local varieties, even diversity of varieties in crop organic seed offer. If organic seed is not available, derogations for using non-organic seed are currently acceptable.

The study contributes to understanding the impact of the quantity offered by the National Organic Seed Database (NOSD) on the provision of crop sowing areas with ocertified organic seed. The number and diversity of offered varieties were evaluated, as well as the amount of granted derogations for non-organic seeds concerning the quantity and diversity of varieties. The selected crops included in the study were spring and winter wheat (Triticum L.), spring oat (Avena sativa L.), and spring field pea (Pisum sativum L.) in the period 2018-2022.

Locally produced organic certified seed ensures only part of the sowing area under organic conditions, from 1.6% (spring oat area in 2019) to 24.6% (field pea area in 2020). The production of organic seed failed for winter wheat in 2018. The amount of organic seed offered by NOSD constituted only part of the locally produced certified seed, from 6% (winter wheat in 2019) to 53% (spring oats in 2021), except in cases where certified seed material produced in previous years or imported from another country by seed distribution companies was included in NOSD. The offered amount of seed in the database varied from year to year. The number of varieties in NOSD was very low, mostly offering certified seeds of only one variety, and rarely 2 or 3 varieties during a year. The insufficient supply of organically produced seed was a reason for granting derogations. The number of derogations varied from 160 (spring oats in 2020) to 9 (spring wheat in 2021), but even the use of certified non-organic seed did not provide a sufficient amount for the sowing area of the crop. The certified organic and non-organic seeds provided sowing for less than half of the crop's total organic sowing area each year, except spring wheat, spring oat, and field pea in 2018 when about 80% of the sowing area was covered with certified seed. The derogations were provided for non-organic certified seeds of a wide range of varieties for each crop (7-21). In many cases, varieties had not been tested in the growing conditions of Latvia or similar, posing a risk of yield losses for farmers. Foreign seed distribution companies offered non-organic certified seed with instructions for applying for derogations.

Authorities had to accept derogations because the offer in NOSD was very low and there was no choice of varieties.

The supply of organic certified seed for studied crops is very low, and the number of offered varieties is negligible; state support for seed producers and certified seed users is essential. The functionality of NOSD must be improved with the aim to include all produced-in-country organic certified seed. The organic certified seed and variety diversity offer could be enlarged by joining the Router database, involving offers from other countries, but the varieties offered must be tested in local or similar growing conditions. Derogations should be granted by authorities only for varieties tested in Latvia or similar growing conditions. This requirement could impose an obligation to test crop varieties in the target location before importation into the country.

INNOVATIVE BUSINESS MODEL FOR AN INNOVATIVE SMALL SCALE ORGANIC AND DIVERSITY-BASED BREEDING INITIATIVE

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Abstract Text:

Organic breeding needs crucial changes in France: IFOAM states that breeding should be done in organic conditions and cultivars should include genetic diversity. Indeed, the actual context of climate change, political tensions and of the organic market crisis underline the necessity to operate a paradigm shift not only regarding the agronomical production, neither than the market organization, but to have a holistic vision on how we interact from seed to plate with the ecosystems. We make the hypothesis that the concept of diversity as a factor of resilience must be applied to breeding, but also to the economic models for organic adapted seeds. Until now, European seed system is based on genetic homogeneity and return on investment financing through royalties generated by plant variety certificates. Since January 2022, seed regulation has been opened to the concept of genetic diversity through the possibility of selling Organic Heterogeneous Material (OHM). However, this new type of cultivar, based on genetic diversity and improving farmers' seed autonomy, does not rely on intellectual property and need therefore completely different economical models to support the cost of research and development programs. Some initiatives like participatory breeding programs try to develop such populations, based on public grants that are decreasing. In this change of paradigm, without property rights, pre-financing of breeding is absolutely necessary instead of post-financing, to accelerate the efficient use and adaptation of agrobiodiversity. In this context, D'une graine aux autres (DUGA), a French small-scale company, tries to develop small-scale and multi-actor organic breeding programs, based on genetic diversity with an innovative pre-financing system involving all the actors along the food system, sharing a vision of cooperation. The breeding scheme tested by DUGA relies on experiences of several EU projects since 2007, and especially Diversifood). It starts from the individual observation of genetic resources (landraces) for 3 to 5 years on station. Then, these accessions are assembled to create diversified populations based on one or more common criteria. The created populations, called DOPs (Diversified Oriented Populations) or PEPs in French (Populations Evolutives Pré-Sélectionnées) are evaluated on station and then on farm, under different conditions, for the maintenance of the criteria chosen. The business model steps closely follow the breeding steps. It is based on the financial participation of all the actors of the food system, considering that they are all committed in the production of the raw material. During the « on-station » phase of the program, the actors pay an annual subscription which is calculated according to the size of the company. DUGA also provides a coordination service which is paid for too. On the "on-farm" stage, DUGA only provides project management. This private funding is completed by public grants rather during on-station stages. Breeding method and business model are still under test by DUGA. Two

breeding programs are going on with two species: oat (Avena sativa L.) and lentils (Lens culinaris), both are still at on-station stage. For oat, different PEPs are under evaluation, and one cooperative and one food processor are financing the program. For lentils, the accessions characterization enters its third year. We benefit from a public grant and we are consolidating a group of interested actors of the food chain. At this stage of the experiment, the multi-actor funding is not covering all the costs. So the question is how to convince more customers to get involved. Moreover, the length of the breeding program (10 years) can be a bottleneck in finding partners in the actual economical context. Some questions arose by exchanging with the partners: how to manage the seeds collectively? How to welcome new partners later on during the breeding process (populations and knowledge created within a project will be available to anyone after the project...)? Can we bring together in one breeding program the actors that are ‘competitors’ on the market? This breeding program based on a new vision of breeding is still under testing and needs to be discussed further with the partners. However, it’s a promising example in a context where the research institutions are not sufficient anymore to scale up the urgent use of genetic diversity.

Reference:

Chable V, Rossi A, Nuijten E, Rey F, Bocci R and Kovács T (2018). A paradigm shift. Diversifood innovation factsheet #16. https://diversifood.eu/wp-content/uploads/2018/05/Diversifood_IF16_Paradigm_shift-1.pdf Serpolay E (2020). Shaping Diversity for On-farm Organic Plant Breeding of Wheat (and Other Cereals) in France. In Hubbard, K. (editor). 2020. Organic Seed Growers Conference Proceedings. February 12 - 15, 2020, Corvallis, OR. Organic Seed Alliance, Port Townsend, WA. 110 pp: 43-48

ORGANIC AGRICULTURE IN PORTUGAL: INSIGHTS FROM ASSOCIATIONS AND COMPANIES

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Abstract Text:

In recent years, there has been growth in the organic agriculture sector in Portugal. To understand whether this trend will persist in the future and how the sector is perceived, it becomes important to gather insights from experts in the field about prospects, potential challenges faced, and key strategies for the continued development of organic agriculture.

The work carried out aimed to gather different perspectives on the organic agriculture sector from leaders of companies and national organic agriculture associations. The methodology adopted the construction and dissemination of an online questionnaire with 43 questions. The study was firstly approved by the Ethics Committee of the Polytechnic Institute of Coimbra (reference Nº 81_A_CEIPC/2021).

A total of 237 national organic agriculture entities were contacted, of which 40 completed questionnaires that were considered for descriptive statistical analysis. Among the surveyed entities, 35% reported producing fruits; 25% focused on aromatic, medicinal, and seasoning plants, while 23% produced vegetables. Additionally, 11% reported producing other foods, such as olive oil, olives, wine, mushrooms, acorns, cereals, and legumes. Finally, 4% were involved in raising livestock. The majority of the farms surveyed have less than 2 hectares, and these farms showed the greatest diversity of food produced. As for the location of the production units, 23% of the entities surveyed were concentrated in the Braga district, followed by Coimbra with 13%. Of the entities that responded to the survey, no production units were located in the Madeira archipelago or in Azores. Preserving ecosystems (27%), improving public health (25%), increasing biodiversity (24%), and preserving species (23%) were the aspects most frequently highlighted by the organizations where organic farming can make a difference. The organizations pointed out some aspects considered to be limiting for those who choose to adopt organic farming, particularly the bureaucracy involved in obtaining financial support (49%); the difficulties in applying for bank loans (24%) and the difficulty in acquiring organic seeds (20%). Finally, online sales (37%), distribution and home delivery of food (27%), and the grouping of producers (16%) were the strategies most often highlighted to meet consumer needs.

In summary, the study highlighted the diversity of products, sustainability benefits, and strategies to strengthen the organic agriculture sector in Portugal and address consumer requirements but it also stressed organic seeds as an important constraint that is also an opportunity for the sector.

HIGH THROUGHPUT PHENOTYPING ENABLES BREEDING FOR PROFITABLE SUGAR KELP PRODUCTION IN THE NORTH SEA.

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Abstract Text:

The European seaweed sector has high potential for producing sustainable biomass. Currently we use almost half of the global land surface to produce plant- and animal-based food and this percentage even has to increase to ensure food security in the future. At the same time, agricultural yields are expected to decrease due to soil degradation, depletion of natural resources, and extreme weather events, requiring even more of the limited land surface. To mitigate these challenges, utilizing the sea for seaweed production offers a more sustainable and resilient way of food production without relying on irrigation and high quality arable land. Additionally, seaweed is beneficial for natural ecosystems by reducing ocean acidification and providing habitat for other species. Although seaweed is a versatile resource for various different industries including the food and feed, as well as the pharmaceutical and medical sectors, seaweed farming in the North Sea is not yet economically feasible. The challenge of making the North European seaweed sector profitable is twofold – high production costs and unpredictable, low yields. To reduce these production costs, the European seaweed sector wants to adopt a so-called direct seeding method, however farmers have observed high losses of up to 90% of the seeding material due to poor attachment to cultivation ropes. Moreover, these losses not only reduce yield, but also affect yield stability due to large variation in losses between years, environments and genotypes. By enhancing the attachment properties of seaweed via breeding approaches, a reduction of the aforementioned losses can be achieved. To assess early stage attachment properties of seaweed, we developed a high-throughput, image based, phenotyping system in a laboratory setting. To process the large amount of image data, a machine learning model was trained. This phenotyping system allows testing for the effect of genotype, substrate, and seeding age on attachment. Furthermore, the data show the effects of traits, such as the rhizoid number (root like structures), sporophyte morphology, and bouquet (cluster of sporophytes) size on attachment properties. From this phenotypic data, we will identify genetic markers for attachment efficiency by phenotyping and genotyping over 100 sugar kelp (Saccharina latissima) genotypes. These are the first steps undertaken in breeding for improved attachment, consequently increasing the profitability of seaweed production in the North Sea and providing sustainable and versatile biomass.

EXPLORING TRITICUM MONOCOCCUM DIVERSITY AS A SOURCE OF DISEASE RESISTANCE FOR ORGANIC FARMING

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Abstract Text:

Triticum monococcum L. (einkorn wheat) is a minor crop particularly suited for organic farming due to its adaptability to marginal and low-input conditions. An interesting crop per se, it also represents an underutilized genetic resource with high potential for common wheat improvement as a source of breeding traits including resistance to biotic stresses. Indeed, fungal disease outbreaks are increasingly affecting crop productivity and represent a major concern worldwide also considering the current climate change scenario affecting fungal distribution and infection conditions. This is particularly relevant in organic farming systems where crop protection, by means of synthetic chemical use, is quite strictly regulated. Magnaporthe oryzae H. (MoT), the causal agent of wheat blast, and Blumeria graminis f.sp. tritici S. (Bgt), the causal agent of powdery mildew, are responsible of significant losses worldwide potentially causing up to 100% and 30% losses, respectively. The aim of this study was to investigate the potential of einkorn as a source for disease resistance traits. To the purpose a collection of 192 einkorn wheat pure lines were derived from accessions sampled across the entire distribution area of the species using the Single Seed Descent method. The collection includes both wild (T. monococcum subsp. boeoticum) and cultivated (T. monococcum subsp. monococcum) forms offering a comprehensive representation of the genetic variability within the species; most of the cultivated accessions in the diversity panel are landraces. Resistance characterisation was performed focusing on both MoT and Bgt. Seeds germination and plant growth were conducted under controlled conditions. Resistance assessment was performed from the second leaf stage using high-throughput platforms based on the Detached Leaf Assays (DLA). Resistance to both pathogens was evaluated using standard infection and diseases scales and at different number of Days Post Inoculation (DPI). Statistical analysis was performed to identify patterns of disease resistance in the collection as well as accessions of particular interest for the resistance to both pathogens. A high frequency of Bgt resistance was observed, 64.8% of the tested genotypes showed robust resistance. Response to Mot was more variable with only the 17.44% of cultivated accessions showing robust resistance; cultivated accessions were significantly more resistant to MoT than wild forms. According to correlation analysis results, no significant overall correlation exists among the two resistances; noteworthy a positive significant correlation occurs when only genotypes showing extreme phenotypes are considered (i.e. highly resistant or highly susceptible). This evidence suggests that resistance to the two pathogens may involve complex, not completely distinct, genetic pathways. In conclusion, this study underscores Triticum monococcum as a promising source of disease resistance traits, especially for powdery mildew (Bgt), with potential applications in breeding

programs aimed at developing wheat varieties that are better suited for organic farming systems. The high frequency of resistance among landraces further emphasizes the importance of their conservation and use in plant breeding as well as for direct cultivation in more sustainable forms of agriculture including organic farming.

DARKWIN: A NEW PHENOTYPING PLATFORM THAT INTEGRATES POLLINATORS' DECISIONS FOR TOMATO BREEDING UNDER CLIMATE CHANGE

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Abstract Text:

Food security is threatened by abiotic stresses such as water scarcity combined with rising temperatures, conditions exacerbated by climate change. Those factors mainly disrupt the delicate balance in ecosystems, affecting crop physiology during flowering and ecosystem services such as plant-pollinator interactions. Today's digital phenotyping platforms are typically based in genetic traits expressed in leaves, that reflect the physiological status of the plant. However, the transport of photo-assimilates from the leaf (source) to the flower (sink) is reduced in plants with low resilience. Indeed, the metabolism of flowers, and thus the quantity and quality of floral rewards (pollen and nectar), which serves as food for pollinators, change in response to the environment. Targeting floral traits can help to increase crop tolerance to abiotic stresses and would ensure food security through resilient crops and pollinator services. We hypothesize that tracking and ranking pollinators' preferences for flowers under environmental pressure could be used as a marker of plant quality for agricultural breeding to increase crop stress (Pérez-Alfocea et al., 2024). DARkWIN offers a pollinator-assisted phenotyping and selection platform for automated quantification of Genotype × Environment × Pollinator interactions through a RFID-based insect geo-positioning system. A 30-lines tomato NIL mapping population from Solanum lycopersicum (cv. Moneymaker) x S. pimpinellifolium (acc. TO-937) was evaluated under control and climate change conditions, and the pollination activity of managed bumblebees (Bombus terrestris L.) was monitored. While tomato genotypes showed differences in their adaptation capacity to stress and in the level of pollinators' visitation, models are being developed for linking pollinator preferences with agronomical, physiological and molecular traits in leaves and flowers to select the most resilient lines and to assist breeding decisions for increasing tomato crop resilience under climate change.

Reference:

Pérez-Alfocea, F., Borghi, M., Guerrero, J.J., Jiménez, A.R., Jiménez-Gómez, J.M., Fernie, A.R. and Bartomeus, I. (2024), Pollinator-assisted plant phenotyping, selection, and breeding for crop resilience to abiotic stresses. Plant J, 119: 56-64. https://doi.org/10.1111/tpj.16748

EXPLORING THE ROLE OF THE FLC GENE IN CAMELINA SATIVA: INFLUENCE ON FLOWERING TIME AND SEED SIZE

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Abstract Text:

Camelina sativa L., also known as camelina or false flax, is a promising cover crop with significant potential for climate change mitigation, a critical global challenge demanding urgent and sustainable solutions to ensure food security, environmental protection, and energy sustainability. This oilseed crop, native to Europe and Central Asia and belonging to the Brassicaceae family, is notable for its resilience across diverse climates, including arid and semi-arid regions, making it highly adaptable to various environments with minimal agricultural inputs. Its ability to thrive in nutrient-poor soils, coupled with its relatively short growing cycle, makes it an attractive candidate for cultivation in marginal lands where other crops may struggle. Beyond its potential as a biofuel crop, camelina is being explored as a novel source of both protein and oil, with increasing interest in its applications for human nutrition, animal feed, and industrial purposes. The seeds boast an oil content of approximately 40%, rich in polyunsaturated fatty acids (including 30-40% α-linolenic acid, 15-25% linoleic acid, 15% oleic acid, and around 15% eicosenoic acid), making it a valuable crop for producing high-quality edible and industrial oils with potential health benefits.

In this work, there were studied six winter and five spring varieties of *C. sativa* and some lines generated both by the crossing of spring lines and by the crossing of a spring line for a winter line (Ghidoli et al. 2024).

An agronomic characterization was carried out regarding parameters such as yield, weight of 1000 seeds and flowering time, and regarding this, flc gene (flowering locus c) was studied for all the genetic materials.

The data obtained showed that spring varieties exhibited early maturity, high seed weight of 1000 seeds comparable to winter varieties. A strong negative correlation between 1000 seed weight and days to flowering ($r = -0.91$; $p = 3.87E-5$) suggests a physiological and/or genetic relationship between these two traits. This result agrees with previous work, in which spring and winter genotypes were differentiated by most seed shape descriptors and in particular seed weight, furthermore, the main QTL associated with flowering period is located on Chr8 (chromosome 8) linked to a strong QTL associated with seed size.

Finally, flowering time and seed size are important characteristics to consider in breeding programs to develop cultivars with desirable flowering characteristics and a seed size that can facilitate the cultivation, harvesting and processing of camelina seeds, making this precious crop more accessible and economically sustainable for farmers.

Reference:

Ghidoli M, Geuna F, De Benedetti S, Frazzini S, Landoni M, Cassani E, Scarafoni A, Rossi L and Pilu R (2024). Genetic study of Camelina sativa oilseed crop and selection of a new variety by the bulk method. Frontiers in Plant Science, 15. https://doi.org/10.3389/fpls.2024.1385332

DEVELOPMENT OF NEW VARIETIES OF CAMELINA SATIVA L. AND EXPLORATION OF ITS POTENTIAL AS AN INTERMEDIATE CROP

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Abstract Text:

Camelina sativa (L.) Crantz, an oilseed crop belonging to the Brassicaceae family, has gained increasing interest due to its high adaptability to marginal lands, low input requirements, and valuable oil composition rich in omega-3 fatty acids. Its potential applications span multiple sectors, including biofuel production, animal feed, and the food industry. Moreover, its use as a cover crop and in crop rotation systems contributes to sustainable agricultural practices by improving soil health, reducing erosion, and enhancing biodiversity. Despite these advantages, the genetic improvement of camelina remains underdeveloped, primarily due to its low genetic variability, the presence of antinutritional compounds such as glucosinolates, and its historical neglect in favor of more widely cultivated oilseed crops like rapeseed.

This research focused on the genetic enhancement of camelina through two complementary breeding strategies: (i) the development of a synthetic population derived from the crossbreeding of two spring varieties, evaluated for agronomic traits, bromatological parameters, and glucosinolate content, and (ii) the implementation of a marker-assisted breeding program to develop new lines with improved yield, enhanced oil quality, and reduced levels of antinutritional compounds. The results demonstrated that autumn-winter cultivation of camelina in Northern Italy can significantly increase yield compared to spring sowing, with an average production of 2 t/ha versus 0.6 t/ha. Additionally, a negative correlation between spring and winter yields was observed, indicating that varieties performing well in winter conditions tend to have lower productivity in spring. The synthetic population tested in this study showed remarkable adaptability across different environments and contained lower glucosinolate levels (around 17 mmol/kg), making it a promising candidate for future commercial applications.

Furthermore, a second breeding approach combined molecular characterization using SSR markers and genotyping-by-sequencing (GBS) techniques to distinguish winter and spring varieties at the genetic level. Based on this analysis, selected parental lines were used to create new genetic variability through the bulk method. Among the lines developed, the most promising genotype, C1244, exhibited early maturity similar to spring varieties, a high thousand-seed weight (1.46 g), and an oil content of 33.62%, comparable to winter varieties. These characteristics make it particularly suitable for intermediate cropping systems and valuable for both human consumption and animal feed industries.

The findings of this research highlight the potential of *Camelina sativa* as a sustainable energy and rotational crop, providing both agronomic and environmental benefits. The

combination of classical breeding, molecular-assisted selection, and advanced genome editing techniques such as CRISPR-Cas9 offers promising opportunities to further optimize camelina's genetic traits. Future studies should focus on refining these approaches to enhance the crop's yield stability, disease resistance, and industrial viability, ensuring its successful integration into modern agricultural systems.

PRELIMINARY CHARACTERIZATION OF A WORLDWIDE COLLECTION OF CASTOR BEAN (RICINUS COMMUNIS L.) GERMPLASM

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Abstract Text:

Castor bean (*Ricinus communis* L.) presents a compelling opportunity as a multi-faceted crop with diverse applications, spanning industrial uses like lubricants, coatings, and chemical feedstocks, agricultural applications such as biofuel production, and crucial environmental roles in phytoremediation and soil stabilization. Due to its adaptability to a wide range of climatic and soil conditions, including arid and semi-arid regions, castor bean holds promise for cultivation in marginal lands that are often unsuitable for staple crops. This research investigates its potential for sustainable agriculture, with a particular focus on optimizing its agronomic performance and economic viability in challenging environments.

A central challenge in realizing castor bean's full potential is the presence of ricin, a highly toxic ribosome-inactivating protein found in the seeds, which necessitates strict safety measures, careful handling, and advanced processing techniques to ensure its safe utilization. Additionally, the development of improved, non-toxic or low-ricin varieties, as well as genotypes with enhanced agronomic traits, is essential for expanding its commercial viability. Another key factor in the large-scale adoption of castor bean cultivation is the need for varieties that are well-suited to mechanized harvesting, as traditional manual harvesting methods remain labor-intensive and economically restrictive (Landoni et al. 2023).

This study presents a preliminary characterization of a diverse worldwide collection of castor bean germplasm, aiming to explore its genetic potential for crop improvement. A comprehensive collection of accessions from the GRIN (Germplasm Resources Information Network) germplasm bank, representing diverse geographic origins and potentially diverse genetic backgrounds, was analyzed to assess key morphological and agronomic traits. This initial characterization focused on evaluating traits outlined by the CPVO (Community Plant Variety Office), including plant height, branching architecture, leaf morphology, flowering time, and seed characteristics, which are essential parameters for breeding programs.

The aim of this preliminary evaluation was to establish a foundational dataset that informs future breeding and selection programs specifically for the Italian country, while also contributing to broader global efforts in castor bean improvement. The phenotypic variation observed within the collection highlights the extensive genetic diversity available for enhancing castor bean productivity, stress tolerance, and oil quality. These initial findings will serve as a reference for identifying promising accessions for further research, including molecular characterization, genetic mapping, and large-scale field trials. Ultimately, this work contributes to the selection of castor varieties with yield potential, oil composition and

environmental adaptability for the development of future breeding programs, positioning castor as a sustainable and versatile crop with far-reaching industrial and ecological benefits. This research marks a crucial first step towards unlocking castor's full potential.

Reference:

Landoni M, Bertagnon G, Ghidoli M, Cassani E, Adani F and Pilu R (2023). Opportunities and Challenges of Castor Bean (Ricinus communis L.) Genetic Improvement. Agronomy, 13, 2076. https://doi.org/10.3390/agronomy13082076

MORPHO-PHENOLOGICAL AND GENETIC CHARACTERIZATION OF WILD AND CULTIVATED EINKORN TO BOOST CULTIVATED DIVERSITY

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Abstract Text:

The domestication of wheat marks a pivotal transition in agricultural history, facilitating the shift from foraging to farming and ensuring food security for early human societies. Einkorn wheat is one of the earliest domesticated cereals; considered a minor crop today, it still serves as a critical genetic and agronomic foundation for modern wheat breeding. In this study we evaluated and compared wild (Triticum monococcum subsp. boeoticum Boiss.) and cultivated (Triticum monococcum subsp. monococcum L.) accessions for morpho-phenological and genetic diversity to identify useful diversity for breeding existing in the wild and in landraces. Both quantitative and qualitative phenotypic traits were considered while genetic diversity was explored taking advantage of next-generation sequencing genotyping base on double digest restriction-site associated DNA (ddRADseq) to examining genetic differentiation between wild and domesticated forms ascertaining the existence of origin-related patterns. A comprehensive sampling strategy allowed to compile a diversity panel including 192 cultivated and wild Einkorn accessions. To ensure the selection of wild accessions with the broadest possible genetic diversity, an Ecogeographic Land Characterization (ELC) analysis was initially performed using the CAPFITOGEN3 toolbox on all the accessions available in global genebanks (Parra-Quijano et al. 2012). This approach enabled to predict the potential diversity of wild Einkorn accessions representing the widest ecogeographic and genetic variability, reflecting diverse environmental conditions across eight countries of origin. The selection of 96 wild accessions was then based on CWR-Eco units, which integrate ecogeographic categories and genetic diversity, ensuring a robust representation of adaptive traits. Included cultivated accessions, mainly landraces, represent a wide geographical range of landraces diversity across Europe. According to analysis results, a collection of 192 pure lines was then derived from the retrieved accessions using the Single Seed Descent method. Plants were grown in pots under protective net in open field. A total of 179 single plants were successfully morpho-phenologically characterised. Morpho-phenological analysis results revealed distinct differentiation in qualitative and quantitative traits between wild and domesticated forms, particularly in flag leaf dimensions, heading date, and spikelet characteristics, which are key domestication traits. A wider diversity in the wild was observed for several tratis (e.g. days to heading, plants growth habit, awn length, spike colour). Genotyping was successfully achieved on 184 wild and cultivated accessions allowing the identification of 1.7 million polymorphic sites; 5,540 high-quality SNPs were retained for analysis after a strict Quality Control. Population structure analysis affirmed three distinct genetic races within wild Einkorn, with the Beta subgroup showing the closest

genetic proximity to domesticated forms (Ahmed et al. 2023). Result of Principal Component Analysis (PCA) further supported these findings, highlighting latitude-related genetic diversity and adaptive divergence, suggesting environmental factors play a significant role in shaping wild populations. This study highlights the existence of a wide morpho-phenological and genetic diversity in the developed einkorn diversity panel that is pivotal in boosting wheat diversity and building more resilient agricultural systems through an improved use of diversity in wheat breeding. Indeed, traits like early flowering and more prostrate growth habit, only observed in wild accessions, could be of great potential for breeding new varieties that are better suited to organic farming where varietal ideotype can be quite different in comparison to what has been bred for under conventional agriculture. Findings also reveal how ecogeographic and latitudinal factors shape genetic diversity, favoring targeted conservation and, on the other hand, facilitating use of wild Einkorn resources. This work aligns with the need for programs to focus on enhancing temporal and spatial diversity by benefitting from plant genetic resources to address challenges such as pest epidemics and nutrient runoff, while promoting self-regulating agricultural systems that is crucial in breeding for organic farming.

Reference:

Ahmed, H. I., Heuberger, M., Schoen, A., ... & Krattinger, S. G. (2023). Einkorn genomics sheds light on history of the oldest domesticated wheat. Nature, 620(7975), 830-838. https://doi.org/10.1038/s41586-023-06389-7

Parra-Quijano, M., Iriondo, J.M., Torres, E. (2012). Ecogeographical land characterization maps as a tool for assessing plant adaptation and their implications in agrobiodiversity studies. Genet Resour. Crop Evol. 59, 205–217. https://doi.org/10.1007/S10722-011-9676-7.

SOIL-PLANT INTERACTIONS IN UNDERVALUED NATIVE MEDITERRANEAN LEGUMES AS A WAY TO REGENERATE ERODED SOILS FOR SUSTAINABLE AGROFORESTRY

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Abstract Text:

Symbiotic interactions between plants and microorganisms, particularly legumes and Rhizobium bacteria, are crucial for sustainable agroforestry due to their ability to fix atmospheric nitrogen, enhancing plant nutrition and providing environmental benefits. Orphan crops, especially legumes, are valued for their drought tolerance, soil fertility enhancement, and nutritional and medicinal benefits, though they remain undervalued (Popoola et al., 2022). Intercropping promotes a diverse plant community, enhances root growth, and improves soil processes, along with microbial abundance and diversity. This results in increased resource use efficiency, which benefits plant growth and production. The design of agroecology-based cropping systems enhances sustainability and reduces reliance on chemical inputs. Legumes are key in many agroecological services, such as the recovery of soils subjected to drastic abiotic stress, the production of large masses of food or the mitigation of climate change (Harman et al., 2021; Anas et al., 2025).

This work aimed to study the growth and nodulation capacity of two Mediterranean leguminous plants, Coronilla varia and Coronilla juncea, in the soil of the Sierra Calderona, which, although it represents one of the most valuable enclaves of the Valencian Community with great ecological interest, has been subjected to continuous environmental aggressions such as quarrying, illegal dumps and fires.

To carry out this study, seedlings were cultivated in mixtures containing different proportions of universal substrate and soil from the Sierra Calderona. Growth measurements, microbiological analyses of the rhizosphere, and characterization of the nodules were performed at various intervals. Throughout the study, it was observed that both legume species could grow and form nodules in the Sierra Calderona soil. Notably, C. varia demonstrated significantly greater root development, with growth 57% higher than that of C. juncea. Both legume species exhibited nodulation capacity; however, C. varia produced 74% more nodules than C. juncea.

In agreement with these results, microbiological analysis of the rhizosphere associated with C. varia was higher than that obtained from the rhizosphere of C. juncea, with values an order of magnitude higher in the number of viable aerobic mesophiles and 45 % higher in the count of moulds and yeasts.

The results suggest that while both legumes examined can successfully establish symbiotic relationships with the microorganisms in the studied soil, C. varia appears to be the more effective in establishing symbiotic relationships with soil microorganisms, making it a promising candidate for soil regeneration and sustainable agroforestry. The enhanced microbial activity associated with C. varia supports its potential to improve soil fertility, enhance ecological diversity, and contribute to sustainable land management practices in eroded and climate-affected areas.

Reference:

Anas, M., Khalid, A., Saleem, M. H., Ali Khan, K., Ahmed Khattak, W., & Fahad, S. (2025). Symbiotic Synergy: Unveiling Plant-Microbe Interactions in Stress Adaptation. Journal of Crop Health, 77(1), 1-21.). https://doi.org/10.1007/s10343-024-01070-z

Harman, G., Khadka, R., Doni, F., & Uphoff, N. (2021). Benefits to plant health and productivity from enhancing plant microbial symbionts. Frontiers in Plant Science, 11, 610065. https://doi.org/10.3389/fpls.2020.610065

Popoola, J. O., Aworunse, O. S., Ojuederie, O. B., Adewale, B. D., Ajani, O. C., Oyatomi, O. A., ... & Obembe, O. O. (2022). The exploitation of orphan legumes for food, income, and nutrition security in Sub-Saharan Africa. Frontiers in Plant Science, 13, 782140. https://doi.org/10.3389/fpls.2022.782140

SEED SIZE AND PROTEIN CONTENT IN DRY GRAINS OF THE FABA BEAN (VICIA FABA L.) LINES OIGINATED FROM SERBIAN LOCAL POPULATIONS

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Abstract Text:

In the past, the faba bean (Vicia faba L.) was an important legume in the Mediterranean diet for both humans and livestock. Today, however, it has largely been forgotten in Serbia. The Serbian Ministry of Agriculture currently recognizes only two commercial varieties of faba bean for animal feed (var. minor). Faba beans intended for human consumption are grown on very small plots of land, primarily for family use. The key factor for the survival of tiny local faba bean populations is the traditional preparation of faba bean tied to Lenten practices observed by Orthodox Christians. During this time, guests are offered a vegan, hummus-style dish made from faba beans. However, this dish is not prepared in all regions of Serbia, or every village. Seeds are infrequently transferred between farmers and are rarely found at the farmer's markets, so it is feasible to believe that faba bean biodiversity in Serbia is high because maybe every farmer, which produces faba bean, has his own population.

The Institute for Forage Crops Kruševac (IKBKS) has launched a research program to collect and evaluate native faba bean populations in Serbia. This collection now has approximately 30 original populations and about 60+ inbreed derived lines. According to preliminary assessments, the grain quality and grain bioactive material content are both a quite high (Milenković et al., 2024, Mitić et al., 2024). In this research, the lines were divided into two groups depending on seed size: major and equine-minor, to evaluate if grain size affects protein content. Because in Serbia the majority of local populations have a major grain size, the lines with equine and minor grain types are joined. The two-year experiment was conducted on the IKBKS plot in two repetitions using a randomized block system. The crude protein content was chemically analyzed using the Kjeldahl method. In this exploratory study, the crude protein content of the dry grain of faba bean lines was investigated in order to choose material for future work on the development of a new high-protein faba bean variety. According to the findings of this study, the protein content of the examined lines ranged between 26-31%, indicating that there is need for future research into the development of high-quality varieties for human or animal consumption.

Low-input agriculture is consistent with sustainable farming goals in Serbia, and it can be especially beneficial for smallholder farmers trying to save costs while minimizing their environmental impact. Collecting and cultivating neglected and old species in conventional and organic agriculture can make a significant contribution to healthy food.

Reference:

Milenković Jasmina, Anđelković Snežana, Petrović Mirjana, Zornić Vladimir (2024): Grain quality of local faba bean populations collected in Serbia. Proceedings of the VII Congress of the Serbian Genetic Society, Zlatibor, Serbia, October 2 to 5, 2024

Mitic, Violeta, Nikolic, Jelena, Andjelkovic, Snezana Petrovic, Mirjana, Stankov Jovanovic, Vesna, Milenkovic, Jasmina (2024): Antioxidant Activities, Total Phenols, and Proanthocyanidin Changes during Storage of Fourteen Faba Bean (Vicia faba L.) Populations from Serbia–A Chemometric Approach. Analytical Letters, Volume 57, Issue 4, Pages 607 – 627. https://doi.org/10.1080/00032719.2023.2217713

UTILIZATION OF BIOACTIVE SUBSTANCES FROM SUNFLOWER: A SUSTAINABLE APPROACH IN THE CIRCULAR ECONOMY

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Abstract Text:

Helianthus annuus L. is one of the main oilseed crops worldwide. The cultivation area of sunflower has expanded 15 times in recent decades, reaching 25 million hectares. Since its introduction to the European continent, numerous varieties and hybrids characterized by high oil content (28-50%) and productivity have been created, contributing to a global seed yield of 38 million metric tons. While sunflower is primarily cultivated for its seed oil, other plant components, notably the floral organs (petals, receptacle, and tubular flowers), represent a largely untapped resource. Although containing a diverse array of valuable bioactive compounds, these floral organs are significantly underutilized in industrial applications. However, in 2011, 0.76 and 3.8 metric tons of petals and, respectively, tubular flowers were collected. Harvesting these floral organs is considered economically viable, as potential revenues can match those from seed sales.

The purpose of the present study was to determine the chemical composition of the reproductive organs in order to identify compounds with potential use in the food, biopharmaceutical and other industries. Reproductive organs from a single hybrid were collected at the flowering stage from three Moldovan localities (Soroca, Pelenia, Bacioi) with varying climates.

Using standard extraction methods (including Steam Extraction with a Clevenger-type apparatus and Soxhlet extraction), various plant extracts were obtained, including volatile oil from petals (0.19% yield), fatty oil from pollen (~9.23%), triterpene compounds from petals (6.47% nonpolar, 26.42% polar), and phenolic acids from petals (~40.9%) and tubular flowers (~34.03%).

Gas chromatography-mass spectrometry (GC-MS) analysis revealed quantitative and qualitative variations in the extracts depending on organ type and the area from which the plant material was collected. The diverse components extracted from sunflower petals, tubular flowers, and pollen offer various bioactive properties that can be utilized in multiple fields such as pharmaceuticals, cosmetics, and functional foods. Thus, triterpenes are widely recognized for their antioxidant, anti-inflammatory, antimicrobial, and anticancer activities. Sunflower petals and tubular flowers are rich in phenolic acids, which are well-known for their antioxidant and anti-inflammatory activities. These substances can contribute to innovative natural products with therapeutic and nutritional value, positioning sunflower as a key component of a sustainable, circular economy.

EFFECTS OF STRESS FACTORS ON SUNFLOWER MORPHOLOGICAL, BIOCHEMICAL, AND YIELD TRAITS

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Abstract Text:

Helianthus annuus L. is an economically important oilseed crop, but its productivity is often threatened by various biotic and abiotic stress factors. Among these, *Orobanche cumana* Wallr. (broomrape) stands out as a devastating parasitic weed in different sunflower cultivating countries, including the Republic of Moldova.

This study investigated the effects of broomrape infection on the morphological, biochemical, and yield-related traits of 11 sunflower hybrids (both sensible and resistant to *O. cumana*) across infested and non-infested fields over two growing seasons - one characterized by a severe drought and the other by the amount of annual precipitation corresponding to the requirements for the sunflower growth and development.

Our findings revealed a significant impact of broomrape on sunflower productivity, with yield losses reaching up to 65.6% in susceptible hybrids, a strong negative correlation (r=-0.81) being established between yield and attack intensity. When comparing data from infested and non-infested fields, a reduction in plant height, leaf area, and leaf area index was observed, with reductions ranging from 24-29%, 16-48%, and 25-51%, respectively. Additionally, the chlorophyll content in the leaves, an indicator of photosynthesis efficiency, decreased by 11-15%.

The ANOVA analysis revealed a greater influence of genotype on yield variation in sensitive hybrids (45.9%) compared to resistant ones (30.8%). This trend was also observed at the genotype-location (GxL - 26.9%) and genotype-year (GxA - 12.9%) interaction levels. Various morphological and biochemical parameters associated with productivity also show a wide range of variation depending on environmental conditions. As expected, the determining factor for the number of leaves is the genotype, both in resistant hybrids (44.5%) and in sensitive ones (71.6%). Additionally, sensitive hybrids differ from those resistant to *O. cumana* by the greater influence of genotype, including in biometric parameters: plant height, leaf area index, and only in the case of leaf area, the influence of genotype and location does not differ based on infestation presence. It is noteworthy that the impact of environmental conditions is surprisingly low (3-12%) in the variation of values for most morphological factors, regardless of whether they are affected or unaffected by the parasite.

The impact of the broomrape parasite on the growth and development of sunflower plants is evident at the level of chlorophyll pigments (Chla and Chlb) and carotenoids. The variation in pigment content is predominantly determined by genotype, with its influence being greater than that of environmental factors, both in affected and unaffected hybrids. However, in the case of compatibility interaction and pathogen establishment, the modification of the

Chla/Chlb ratio is primarily determined by the GxM interaction (69.1%), in contrast to the reaction of unaffected hybrids, where environmental conditions (45%) are the main factor determining Chla/Chlb variation, with the GxM interaction factor contributing less (21%).

In summary, our study highlights the importance of integrating genetic resistance to *O. cumana* with environmental adaptation in sunflower breeding programs to ensure stable productivity under challenging conditions. The observed genotype-by-environment interactions emphasize the need for multi-location and multi-year testing to identify truly resistant and high-yielding hybrids.

EXPLORATORY EVALUATION OF A COMPOSITE CROSS POPULATION OF PEPPERS UNDER ORGANIC FARMING

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Abstract Text:

The global trend toward more sustainable and environmentally friendly agricultural practices requires not only the adaptation of cultivation techniques and systems, but also the development of resilient varieties or populations suited to low – input management and variable climatic conditions. In this context, as part of the LIVESEEDING Project, the development of heterogeneous sweet pepper (Capsicum annuum L.) populations was initiated.

The process began with the creation of two simple hybrids through manual and controlled crosses. These were then crossed to produce a double hybrid, building the initial composite cross population (G0). This population was evaluated under organic farming conditions in an open field trial in 2023 (Horta Sud, Valencia, Spain). A total of 215 plants were evaluated for traits such as yield, average fruit weight, plant vigor, fruit foliage cover and soluble solids content (SSC) of fruits. Open-pollinated mass selection of the best individuals was performed based on these traits and additional factors, such as fruit shape, resulting in the first generation (G1).

In 2024, G1 population was cultivated in the same location and under organic farming conditions, with an additional 25% reduction in irrigation, introducing water use efficiency as additional selection factor. A total of 218 plants were evaluated for the same traits, and a new selection of the best individuals was performed.

To assess population evolution, traits were compared across both years. Results showed a positive effect of selection on traits such as vigor, foliage cover and fruit weight. Mean vigor increased from 2.9 (≈ 3, “intermediate”) in G0, with a coefficient of variation (CV) of 33%, to 4.2 (≈ 4, “high”) in G1, with a CV of 18%. Leaf coverage followed a similar trend, with G0 showing a mean of 2.7 (≈ 3, “intermediate”), with a CV of 34%, while G1 reached 3.4 (≈ 3), with a CV of 18%. Fruit weight also increased from 74.4 g (CV 23%) in G0 to 100.5 g (CV 30%) in G1. However, yield remained similar between generations, increasing slightly from 1.1

kg·plant^{-1} in G0 to 1.8 kg·plant^{-1} in G1, showing similar CVs (37%-38%, respectively). SSC values were also stable, measuring 8.7 ºBrix (CV 11%) in G0 and 8.6 ºBrix (CV 13%) in G1.

Notably, G1 traits, particularly vigor, foliage cover, yield and fruit weight, were more similar to the parental lines than to G0. However, environmental differences between evaluation years may have influenced some observed results.

These results support the effectiveness of selection, particularly for fruit size and overall plant appearance. Next steps will continue mass selection across different agronomic conditions and regions using a "shuttle breeding" approach, aiming to develop a resilient heterogeneous population that maintains minimum requirements for yield, fruit weight, appearance and quality.

IMPORTANCE OF ORGANIC POST-REGISTRATION TRIALS IN HUNGARY THROUGH THE EXAMPLE OF SPELT WHEAT

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Abstract Text:

According to the EU's strategy, a significant increase in the share of organic agricultural land is expected by the end of the decade, reaching 25%. This is followed by the Hungarian organic action plan aimed at increasing this ratio to 10% from the current 6% until 2027. The expansion of the group of organic farmers necessary for this can best be achieved by making farming as successful and profitable as possible, for which it is essential to ensure the availability of appropriate plant cultivars and cultivation technologies. Organic crop production, being more exposed to the environmental conditions, critically relies on the availability of detailed information about cultivar performance, including biotic and abiotic resistance, stable yield and high quality values. To ensure this, the Organic Seed Working Group of the Hungarian Seed Association was established 5 years ago, to improve domestic organic seed production and plant breeding. The current EU organic regulation classifies cultivated plant species (in some cases, cultivation types of species) into three categories according to the applicable seed source: only organic seed can be used for the cultivation of species belonging to category I; organic farmers must request a case-by-case permit for species of category II; while the use of chemically untreated, conventional seed is generally permitted in category III. In Hungary, currently all plant species fall under category II, so their cultivation from non-organic seeds requires an individual permit in each case. This creates an administrative overload both for the organic certification bodies and organic farmers. In addition, this practice prevents the increase of organic certified seed use, thus indirectly endangering the sustainability of organic plant breeding and the long-term profitability of organic farms. The national organic seed database serves as a control point when granting a permit for category II species, therefore filling it with as many cultivars and as many seed lots as possible is of utmost importance. The goal of the organic small-plot post-registration trials, launched by the working group and now in its fifth year, is to identify cultivars suitable for organic cultivation and to boost their organic seed trade. When sufficient amount of seed lots involving a suitable number of cultivars of a given species is uploaded, the pathway for transferring that species to category I can be explored. Spelt wheat (Triticum aestivum subsp. spelta (L) Thell.) in Hungary can provide an example to follow: the experience of the post-registration trials of spelt, which entered into its 4th year in 2025, and comparing its results with the derogation lists of non-organic spelt seed lots received from the two organic certification bodies, will be sufficient to propose the gradual transfer of spelt to category I soon. During the process planned for 3 years, farmers (and seed production companies as well) can prepare for the new conditions, when farmers will only be able to produce certified organic spelt (e.g. grain, straw, germ, feed) using seed of organic origin (certified or farm

saved). The three-year results of the national small-plot experiments running at 7 locations revealed relatively small average differneces in yield and protein content among the 7 tested spelt varieties (originated from Hungary, Austria, Germany and France). The Mv Martongold variety had the highest values with 4.12 t/ha grain yield (std: 0.19 t/ha; cv: 5%); 16.04% protein content (std: 0.38%, cv: 2%); and 35.92% gluten content (std: 1.43%, cv: 4%). The quality traits were high regarding all spelt varieties tested and standard deviation between the varieties was low regarding all traits, therefore all spelt varieties can be recommended for organic cultivation in Hungary. Based on the last 5 years, 43 derogation applications concerning 7 spelt varieties were received by the organic certifying bodies on yearly average, accounting for nearly 1,300 hectares annually. This area could be supplied with certified organic seeds of several spelt varieties within a few years with proper organization, so that the permanent transfer of spelt to category I could be realized. The detailed results of the small-plot cereal trials are available on ÖMKi's website (in Hungarian): https://biokutatas.hu/tudastar/kisparcellas-fajtatesztek-eredmenyei/

PRELIMINARY EVALUATION OF A SET OF PEPPER CULTIVARS (CAPSICUM ANNUUM L.) COMBINING ORGANIC MANAGEMENT AND REDUCED IRRIGATION

Marisa Jiménez Pérez[1]; Estela Moreno Peris[1]; Elena Hinojal Vicente[1]; Ana María Adalid Martínez[1]; Miguel Díaz Riquelme[1]; Alicia Iborra López-Milla[1]; Mireia Romans Escrivà[1]; María Pallardo Maravilla[1]; Monica Tereza Boscaiu Neagu[2]; Ana Fita[1]; Adrián Rodríguez Burruezo[1];

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Abstract Text:

The COMAV Institute is dedicated to the recovery, improvement and valorisation of traditional and local varieties of various horticultural crops. At COMAV, the Capsicum Breeding Team works on the breeding of Capsicum peppers both for quality, due to its high content of antioxidants, especially ascorbic acid, and for adaptation to sustainable agriculture in the context of climate emergency. In particular, water scarcity is a major challenge in the Mediterranean region (Tramblay et al. 2020), making water-efficient crop management essential for low-input farming systems.

In the present work, we evaluated seven pepper landraces under organic farming in open field conditions (Horta Sud area, Valencia, Spain), combined with three different water regimes: 100% of the usual water dose (T100), corresponding to 400 mm applied throughout the crop cycle, 75% (T75, moderate water deficit) and 60% (T60, extreme water deficit). Fruit weight, yield, flesh thickness and key quality traits were assessed. Sugars (fructose and glucose), ascorbic acid and flavonoids were quantified by High-Performance Liquid Chromatography (HPLC) (Rosa-Martínez et al. 2021), while red and yellow-orange carotenoids were analyzed by spectrophotometry (Hornero-Méndez and Mínguez-Mosquera, 2001).

In general, irrigation reduction did not significantly affect yield (ranging from 2.92 $kg{\cdot}m^{-2}$ in T100 to 3.19 $kg{\cdot}m^{-2}$ in T60) or fruit weight (ranging from 108 g in T100 to 122 g in T60), indicating stable production under moderate and severe water deficit. Flesh thickness (mm) was largely unaffected, except for the Bola genotype which showed a significant reduction under water deficit, 3.3 mm in T60 compared to 4.15 mm in T75.

For quality traits, ascorbic acid levels were not significantly different between treatments in four of the seven genotypes, while three showed higher concentrations under the T60 treatment (from 1069 $mg{\cdot}kg^{-1}$ in T100 to 1180 $mg{\cdot}kg^{-1}$ fw in T60). Flavonoid content followed a similar trend, increasing in some genotypes under T60 or T75 compared to T100 (from 12.8 $mg{\cdot}kg^{-1}$ in T100 to 16.2 $mg{\cdot}kg^{-1}$ fw in T60). In contrast, carotenoid content declined with water deficit, especially the red carotenoids (from 121 $mg{\cdot}kg^{-1}$ in T100 to 79

mg·kg^{-1} fw in T60). Finally, the fructose and glucose profiles were also analysed and showed a general increase in glucose content under T75 and/or T60 conditions (from 21.7 g·kg^{-1} in T100 to 29.4 g·kg^{-1} fw in T60), which may increase fruit sweetness.

These results demonstrate the potential of traditional pepper landraces for low-input and organic farming, as they maintain yield stability while exhibiting desirable quality traits under water stress. These findings highlight the importance of landrace conservation in the transition to more sustainable agriculture. They also support future breeding programmes to develop new varieties that are more resilient and better adapted to changing environmental conditions.

Reference:

Hornero-Méndez D and Mínguez-Mosquera MI (2001). Rapid spectrophotometric determination of red and yellow isochromic carotenoid fractions in paprika and red pepper oleoresins. Journal of Agricultural and Food Chemistry, 49(8), [3584–3588]. 10.1021/jf010400l

Rosa-Martínez E, García-Martínez MD, Adalid-Martínez AM, Pereira-Dias L, Casanova C, Soler E, Figàs MR, Raigón MD, Plazas M and Soler S (2021). Fruit composition profile of pepper, tomato and eggplant varieties grown under uniform conditions. Food Research International, 147, [110531]. https://doi.org/10.1016/j.foodres.2021.110531

Tramblay Y, Koutroulis A, Samaniego L, Vicente-Serrano SM, Volaire F, Boone A, Le Page M, Llasat MC, Albergel C, Burak S, Cailleret M, Kalin KC, Davi H, Dupuy JL, Greve P, Grillakis M, Hanich L, Jarlan L, Martin-StPaul N, … and Polcher, J (2020). Challenges for drought assessment in the Mediterranean region under future climate scenarios. Earth - Science Reviews, 210, [103348]. https://doi.org/10.1016/j.earscirev.2020.103348

GWAS STUDY OF YELLOW RUST TOLERANCE IN A TRITICALE EUROPEAN COLLECTION

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Abstract Text:

Triticale (x Triticosecale Wittmack) is a potential alternative to other small cereals since it is a double-purpose grain and forage crop, thriving even on marginal soils with lower nutrient inputs. Since its introduction, triticale has been considered a healthier option than its progenitors. However, with its introduction in cultivation, triticale has begun to show susceptibility to several fungal diseases, including powdery mildew, fusarium head blight, septoria leaf blotch, and rust, adversely affecting yield and grain quality. One of the primary goals of triticale breeding is to develop resistance to these diseases, such as yellow rust, caused by the pathogen Puccinia striiformis f. sp. tritici (Pst), which is recognized as one of the top 10 crops fungal pathogen (Dean et al., 2012), and new aggressive isolates began to spread.

In this study, 280 triticale genotypes, 112 commercial varieties, and 170 breeding lines were cultivated over two to three seasons at five locations. To ensure uniform infection, the plots were surrounded by a highly susceptible triticale cultivar. The accessions were primarily evaluated for their tolerance/susceptibility to yellow rust. Still, other interesting phenotypic traits not influenced by the disease were recorded, such as soil cover, plant height, and flowering time. Genetic variation was assessed using DArT (Diversity Arrays Technology) markers. The final number of single nucleotide polymorphisms (SNPs) included in the study after filtering was around 15’000. Those were aligned to a synthetic triticale genome, constructed from the A and B subgenomes of the IWGSC wheat cultivar ‘Chinese Spring’ v2.1 and the R genome of the rye inbred line ‘Lo7’ v3. Later, the SNPs were used to assess the population structure and associated with the phenotypic traits, and a genome-wide association study (GWAS) was performed.

The phenotypic screening of triticale showed considerable variation in yellow rust incidence across different years, locations, and triticale genotypes. The infection levels were significant in six environments, and the infection scores displayed a strong correlation between these environments, providing a solid foundation for this study. The GWAS identified six significant SNPs associated with the phenotypic traits of yellow rust tolerance, of which half are

positioned on the rye subgenome. After, the candidate genes were identified within the candidate regions defined by linkage disequilibrium (LD) surrounding each significant marker. Additionally, the tolerant genotypes were derived from various breeders, suggesting the presence of multiple sources of resistance within this population.

Reference:

Dean, R., Van Kan, J.A.L., Pretorius, Z.A., Hammond-Kosack, K.E., Di Pietro, A., Spanu, P.D., Rudd, J.J., Dickman, M., Kahmann, R., Ellis, J. and Foster, G.D. (2012), The Top 10 fungal pathogens in molecular plant pathology. Molecular Plant Pathology, 13: 414-430. https://doi.org/10.1111/j.1364-3703.2011.00783.x

ESTIMATION OF PRODUCTIVITY OF PEAS VARIETIES IN PEA-BARLEY INTERCROPPING IN ORGANIC FARMING

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Abstract Text:

For sustainable agricultural practices, legume-cereal intercropping allows the use of functional diversity of the species and increases yields and stability (Annicchiarico et al. 2021). One of the additional advantages of legume-cereal intercropping is weed control, especially in an organic growing system. The main problem with growing semi-leafless pea genotypes under organic growing conditions is their low competitiveness against weeds. The solution could be intercropping with cereals. However, the share of peas in the total yield is usually significantly lower; it depends on the pea proportion in the seed material and due to a decrease in yield components that are negatively affected by intercropping (Neugschwandtner & Kaul 2014). Using pea-cereals intercropping, farmers are interested in obtaining a higher pea yield. In addition, when performing selection in intercropping, the amount of seeds obtained from pea genotypes is important for establishing following breeding nurseries.

The aim of the study was to evaluate the share of peas in the total crop yield and compare it to the yield of peas in pure stands. The additive design was used for peas and barley intercropping. The seed rate was 130 seeds m^{-2} for the pea in pure stand and intercropping and 120 seeds m^{-2} for barley, which is 30% of barley sowing rate in pure stand. The seeding ratio for pea and barley was 100:30. The trial was set up in an organic field and included five semi-leafless pea varieties in 2023 and seven varieties in 2024. The varieties were sown in intercropping with medium-early, medium-tall advanced barley line PR-9275, which was selected in the organic breeding program. The harrowing was performed for weed control in both years of the study. During the study, pea field emergence estimated in scores, crop ground cover at the flowering stage, pea yield components, lodging, total yield, and pea share in the total yield were evaluated.

The results showed that in 2023, under extremely dry conditions, the average total yield (peas + barley) was twice as high as the pea yield in pure stand. In comparison to pea yield in pure stand, the share of the yield of peas in intercropping with barley ranged from 20% to 50% by weight, depending on the variety. In 2024, the yield of peas in crops mixture with barley ranged from 10% to 81% compared to pea pure stand. Field emergence could partly influence pea yield in intercropping with barley, as it was significantly lower for some pea varieties. Low field emergence also affected the crop ground cover at the pea flowering stage. Overall, in both years of the study, crop ground cover in intercropping was higher compared to the pure stand. The intercropping significantly affected the yield components for peas, and they were lower compared to the pure stand, which consequently affected the ratio of pea yield to the total yield. Resistance to lodging was particularly relevant in 2024

when heavy rainfall occurred in the ripening stage. Lodging was less pronounced in the pea-barley intercrop compared to the pea pure stand.

Although the sowing rate of peas in intercropping with barley was the same as in the pure stand, the addition of barley in the sowing rate in order to improve competitiveness with weeds did not maintain the pea yield at the level of the pure stand. However, despite this, testing of organically bred pea and barley (or alternatively oats or wheat) genotypes for their suitability to be intercropped can be recommended.

Reference:

Annicchiarico P, Nazzicari N, Notario T, Monterrubio Martin C, Romani M, Ferrari B, & Pecetti L (2021). Pea breeding for intercropping with cereals: variation for competitive ability and associated traits, and assessment of phenotypic and genomic selection strategies. Frontiers in plant science, 12, 731949.

Neugschwandtner R W, & Kaul H P (2014). Sowing ratio and N fertilization affect yield and yield components of oat and pea in intercrops. Field Crops Research, 155, 159-163.

ZUG – BREEDING OF RESISTANT ROOTSTOCK CULTIVARS TO SOIL-BORNE PATHOGENS FOR ORGANIC CUCUMBER PRODUCTION SYSTEMS

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Abstract Text:

Introduction The cultivation of greenhouse cucumbers in organic farming faces significant challenges due to soil-borne pathogens, particularly *Fusarium* wilt and *Fusarium* root rot (caused by *Fusarium oxysporum* f. sp. *cucumerinum*, *F. oxysporum* f. sp. r*adicis-cucumerinum*, *F.oxysporum* f. sp. *niveum*, as well as , among others, *F. solani*, *F. culmorum* and *F. redolens*) and root-knot nematodes (*Meloidogyne* spp.). Grafting onto resistant rootstocks has been the primary strategy to mitigate yield losses, but the currently available rootstocks are exclusively F1 hybrids from conventional breeding programs, limiting their suitability for organic systems. The ZUG project aims to develop open-pollinated (OP) rootstock cultivars that enhance the resilience of organic cucumber production while reducing market dependency on a few dominant F1 hybrids. Objectives The primary objectives are: (i) breeding and selection of genetically stable, open-pollinated *Cucurbita moschata* and *Cucurbita ficifolia* rootstock lines, (ii) screening these lines for resistance to soil-borne pathogens and nematodes under controlled and on-farm conditions, and (iii) evaluating the agronomic performance of grafted cucumber plants using selected rootstocks in organic production systems. The breeding program integrates classical selection methods with resistance screenings conducted in collaboration with research institutions and organic seed company. Materials & Methods Breeding lines of *Cucurbita* spp., will be screened for their resistance to soil-borne pathogens and root-knot nematodes, followed by a multi-stage selection process. Resistance screening against *Fusarium* wilt and root rot disease and root-knot nematodes is conducted under greenhouse conditions using inoculated substrates. Promising genotypes are further tested in naturally infested soils in greenhouse and on participating organic farms. In on-farm agronomic trials plant vigor, grafting compatibility, yield, and fruit quality of selected rootstocks will be assessed and measured under real cultivation conditions. Results Preliminary results indicate a high variability in resistance among tested accessions. Several *C. moschata* and *C. ficifolia* lines show promising resistance to wilting disease, with some also exhibiting tolerance to *Meloidogyne* spp. Early-generation lines are currently being advanced through selfing and selection, with further testing planned to validate their agronomic performance and resistance stability. Conclusions While F1 hybrids provide consistent performance, their reliance on hybrid seed production limits their accessibility in organic systems. The development of open-pollinated, resistant rootstock cultivars offers a viable alternative to conventional hybrids, enhancing the resilience of

organic cucumber production systems. This work contributes to the broader goal of increasing biodiversity, resilience, and self-sufficiency in organic vegetable production By developing OP rootstocks, the ZUG project addresses a crucial gap in organic breeding, supporting long-term sustainability and reducing the vulnerability of organic growers to external seed supply chains.

UNLOCKING LEAF PROTEIN POTENTIAL: GENETIC DETERMINANTS OF EXTRACTION EFFICIENCY AND YIELD IN SUGAR BEET

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Abstract Text:

Sugar beet (Beta vulgaris L.) leaves are an agricultural waste stream that can be further valorized through extracting leaf protein. Currently, leaf protein yield is too low to be economically viable. In this study, the potential to increase leaf protein yield through plant breeding is investigated, along with its impact on the beet root. Additionally, key genetic targets for enhancing leaf protein extraction and yield are identified through association mapping. A genome-wide association study was performed using a panel of 200 sugar beet accessions. The accessions were grown in four field trials in 2022 and 2023, and evaluated for total leaf protein content, extractable leaf protein, protein extraction efficiency, leaf yield, root yield and sugar content. The broad-sense heritability of the traits and the adjusted genotypic means were estimated to assess genetic variation and potential for selection.

Leaf protein content and extractable leaf protein content had considerable heritability, 0.65 and 0.48 respectively, but not as high as beet root sugar content (0.75) and root yield (0.88). Protein extraction efficiency and leaf yield were also found to be heritable, but lower at 0.26 and 0.27 respectively. Leaf protein content was negatively correlated with beet root sugar content, and positively correlated with root yield, suggesting that sugar beet “yield” types are more suitable for protein extraction than “sugar” types. Association mapping resulted in the identification of 33 QTL regions associated with leaf yield, total protein, extractable protein and extraction efficiency. Candidate gene analysis identified several cell-wall related (especially pectin) genes to co-localize with markers for extractable leaf protein content and extraction efficiency. These results confirm the role of the cell wall as a hurdle for leaf protein extraction. A QTL was detected on chromosome 9 which is associated with extractable leaf protein content and extraction efficiency, but not with total leaf protein content. For this QTL, REDUCED CHLOROPLAST COVERAGE 3 was proposed as a candidate gene, which plays a role in determining the cellular volume devoted to the chloroplast compartment. Our results suggest that it is possible to increase leaf protein extraction yields through the selection of sugar beet accessions with higher extractable leaf protein and extraction efficiency. The QTLs identified are key to accelerate the development of new varieties with improved leaf protein extractability. Furthermore, a list of putative candidate genes was provided which gives a valuable insight into the parameters involved in leaf protein extractability. These findings contribute to advancing whole-crop utilization strategies for sugar beet, reducing agricultural waste streams, and promoting more sustainable protein production systems

SENSORY ANALYSIS IN A PARTICIPATORY SELECTION OF TOMATO LANDRACES UNDER LOW INPUT CULTIVATION: KEYS FOR CONSUMERS' ACCEPTANCE

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Abstract Text:

Tomato (*Solanum lycopersicum* L.) flavor is determined by sugars, acids and volatile organic compounds (Tieman et al., 2017). Despite the relevance of flavor for consumption of non-processed foods, breeding programs have focused on improving yield and external appearance of the fresh fruits, which have led to less flavored cultivars through a negative indirect selection (Folta and Klee, 2016; Tieman et al., 2017). Several factors contributed to the loss of tomato flavor and the accumulation of beneficial compounds, including the complex genetic basis of these traits, the expensive phenotypic with specialized instruments, and the dependance to soil composition, environmental conditions, and cultivation techniques. Therefore, consumers are losing interest in commercial varieties and focusing on traditional varieties, produced under sustainable conditions, which show a good performance in the field and retain a better and more intense flavor (Figàs et al., 2015). Our main objective was to analyze the likeliness of tomato landraces grown under organic farming on the western coast of the Mediterranean Sea and to discuss their relevance to improve tomato flavor and overall diversity.

In this work, ten tomato traditional cultivars from Italy and Spain, representing different typologies were characterized by a consumer sensory panel for different parameters like external appearance, consistence, aroma intensity, flavor intensity, firmness, juiciness, acidity and overall acceptance, using a ten-point scale. The sensory panel consisted of 280 individuals with ages between 15 and 70 and a well-balanced representation of women and men. The relationships between sensory studied parameters and acceptance by the consumers is discussed. Regarding yield as an important parameter to select tomato cultivars, with a plant density of 2.5 plants per square meter, big differences were observed among tested varieties, with an average production of 6.2 kg m-2 and ranging from 3.59 kg m-2 to 10.83 kg m-2. Most of the analyzed traditional varieties were classified as "eye-catching" or "normal appealing" and any of the varieties was classified as "not original". Variability in tasting was observed for all the traits analyzed; however, juiciness and intensity of flavor were the most diverse in the studied landraces. Among the traits analyzed, juiciness seems to be drivers of liking, whereas a very high firmness showed the opposite influence in the sensory panel. These results represent a contribution to knowledge that could lead to more effective participatory breeding strategies aimed at improving tomato sensory quality while maintaining yield under low input conditions. Also, they show the variability existing in

landraces that can be exploited for breeding more sustainable crops. Moreover, our work underlines the importance of establishing an open conversation with farmers and consumers to include and value their contributions to the scientific process.

Reference:

Figàs, M.R., Prohens, J., Raigón, M.D., Fita, A., García-Martínez, M.D., Casanova, C., et al. (2015). Characterization of composition traits related to organoleptic and functional quality for the differentiation, selection and enhancement of local varieties of tomato from different cultivar groups. Food Chemistry 187(2015), [517-524]. https://doi.org/10.1016/j.foodchem.2015.04.083

Folka, K.M., Klee, H.J. (2016). Sensory sacrifices when we mass-produce mass produce. Horticulture Research, 3(2016), [16032]. https://doi.org/10.1038/hortres.2016.32

Tieman, D., Zhu, G., Resende, M.F.R., Lin T., Nguyen C., Bies D., et al. (2017). A chemical genetic roadmap to improved tomato flavor. Science, 355(6323), [391-394]. https://doi.org/10.1126/science.aal1556

REINTRODUCING FRENCH HIGH-PROTEIN LANDRACE MAIZE POPULATIONS TO SUPPORT BRITTANY'S PIG FARMERS' AUTONOMY

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Abstract Text:

Brittany's pig farmers heavily rely on imported plant proteins to supplement their livestock feed, with the nitrogen from this feed later being recycled as slurry to fertilize their grain maize fields. In response to local farmers' expressed interest in reducing their economic dependence on external inputs and promoting self-sufficiency, our experimental unit in Ploudaniel, France, initiated a research project to identify and evaluate protein-rich maize varieties suitable for local cultivation. Drawing from our national collection data, we identified 50 French maize populations that combined higher grain protein content with sufficient earliness for Finistère's growing conditions. These populations were evaluated for grain production during 2023 and 2024 at our Ploudaniel facility, specifically within a long-term organic rotation system plot. INRAE maize landraces genebank conducted a study to evaluate the protein content of the panel of French landraces from our national collection in two locations in the South of France. We were able to narrow down the candidat landraces for Britany conditions to 50 landraces which complain to the earliness requirement of these cool oceanic climate, to the protein content nearly doubling what is observed in commercial hybrids and not too small in plant height in order to expect suitable yield for a farmer. Many of these landraces proved to be far removed from a hybrid reference variety commonly grown by farmers in the region. The three best populations met the criteria for protein yield (protein content over 11% without nitrogen fertilization, compared with 7% for the commercial control), earliness at harvest (moisture at harvest equivalent to or lower than the reference control) and satisfactory stalk strength (less than 20% lodging).Through this comprehensive evaluation process, we successfully narrowed down the selection to three promising French maize populations.These landraces are now ready for on-farm testing with our neighboring pig farmers, directly addressing their need for more protein-rich maize alternatives to current commercial hybrids. This research demonstrates the potential of historical landrace varieties to address contemporary agricultural challenges, particularly in the context of increasing farm autonomy and reducing reliance on external protein sources. The selected populations offer pig farmers an opportunity to enhance their feed self-sufficiency while maintaining locally adapted, organic cultivation practices.

FARMERS ATTITUDE TOWARDS ADOPTION AND ON FARM SELECTION OF WHEAT GENETIC RESOURCES FOR LOW-INPUT CLIMATE RESILIENT AGRICULTURE – LESSONS LEARNT IN SERBIA

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Abstract Text:

The need to address global agricultural problems related to climate change, extreme weather events, soil degradation and contamination, water pollution, and loss of agrobiodiversity has been advocated by numerous researchers, activists, and national, international, community-based, and non-governmental organizations focused on food and agriculture. Some proposed actions aimed at contributing to solutions, such as raising awareness of pressing challenges, emphasizing knowledge transfer, and highlighting the benefits of adopting new technologies, are particularly focused on farmers. Despite good intentions, the implementation approach targeting farmers may include some misconceptions.

Firstly, preconceived assumptions and top-down impositions may ignore the fact that farmers are among the most aware of these challenges, as their very existence is directly threatened. The higher their stakes, the greater their interest in solving the causes of the problems. Thus, raising awareness of climate change effects on agriculture among farmers is unnecessary, even condescending and potentially counterproductive.

Secondly, in our experience, farmers' interest in acquiring the skills and know-how required to adapt to changing circumstances is evident. This is reflected in their regular and large attendance at various knowledge transfer events, such as winter schools, seminars, training sessions, lectures, fairs, field days, and demonstration fields. However, farmers' receptiveness requires clear, focused, evidence-based, and straightforwardly communicated solutions that address their needs, which are often lacking in practice. It is not uncommon for academic jargon to raise doubts and suspicion among pragmatic farmers, whose extensive experience and rich traditional knowledge demand concrete facts and arguments.

Thirdly, farmers are often labeled as reluctant and slow adopters of new practices, concepts, and technologies. However, researchers' eagerness to implement state-of-the-art solutions often fails to consider that uncertain and fluctuating climate, human, market, political, social, environmental, and economic factors strongly shape farmers' risk-taking behavior. These factors make them cautious with investments and push them to carefully balance inputs and outputs.

The GRAINEFIT project, funded by the Benefit-sharing Fund of the International Plant Treaty for Food and Agriculture, has been working on preserving, evaluating, and reintroducing local landraces and varieties of small grain genetic resources that are more resilient to

climate change, biotic and abiotic stresses, and capable of maintaining stable yields under low-input agriculture. Additionally, the project aims to revitalize these grains by redesigning their products to be recognized as traditional local foods with strengthened market links, creating opportunities for small-scale farmers in Serbia to generate additional income through a relationship-based approach.

The process involved several interlinked steps designed to build trust, provide tailored knowledge, and create market opportunities.

Engaging farmers and understanding needs: The first critical step involved visiting farmers to listen to their needs, challenges, and preferences. Understanding the local culture, traditions, agro-environmental conditions, and the farmers' perspectives was essential for designing relevant interventions.

Evaluating and characterizing local varieties: In parallel, over 60 traditional wheat varieties were evaluated in field trials for their agronomic traits (e.g., yield, nitrogen use efficiency, disease resistance, lodging), phenology, nutritional and end-use quality (e.g., protein and microelement content, antioxidant activity). This data helped identify varieties suitable for low-input, climate-resilient agriculture.

Providing access and support for on-farm testing: Based on the evaluation results, farmers were provided with access to seeds and detailed information on variety performance. Farmers then established 15 on-farm testing sites across different regions, selecting from 5 to 10 preselected varieties. This allowed them to assess the varieties' performance under local conditions and for specific needs (e.g. drought resistance, frost tolerance, high nutritional quality, disease resistance, organic cultivation, stone-milling, and straw crafts).

Strengthening market links and networking: To enhance adoption, farmers were supported through networking opportunities, such as seed fairs in cooperation with local seed banks, training sessions, demonstration fields and B2B events. These initiatives facilitated collaboration between farmers, local food processors, and entrepreneurs, helping expand market opportunities for the selected varieties.

Fostering trust-based relationships: Throughout the project, building trust with farmers was a central element. By focusing on their needs and offering concrete, evidence-based solutions, the project ensured that farmers were equipped with the knowledge, resources, and market links necessary to adopt climate-resilient agricultural practices successfully.

By following these interconnected steps, the GRAINEFIT project created a collaborative, farmer-centered process that facilitated the integration of traditional wheat varieties into low-input, climate-resilient farming systems.

ASSESSMENT OF GARDEN PEA INTERCROPPING WITH VEGETABLE CROPS

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Abstract Text:

Organic vegetable production in Bulgaria is developing on the principle of sole crop cultivation, which has its functions - better distribution of areas, crops and crop rotations. This method of farming is easier to implement by farmers, but it is more vulnerable to the imbalance of nutrients in the soil, easier multiplication of plant pests and threat to the harvest. The application of appropriate techniques to maintain the nutritional balance of the soil and crop rotation undoubtedly play a permanent role in the organization of the farm, but to ensure stable, productive and diverse production, it is necessary to add other growing technologies, as an example with mixed crops/intercropping. One of the early spring crops that can be used as a companion for potatoes, tomatoes and peppers is garden peas. The experiment was conducted in 2023-2024. in organic field of Maritsa Vegetable Crops Research Institute, with varieties that were created at the institute and have good adaptive and productive performances when grown in organic conditions. Garden peas are a new selection line, with very good qualities for organic production. The duration of the vegetation of the legume crop is from 113 to 122 days, according to the climatic conditions of the year. In mixed crops, the joint vegetation is shortest, almost the same with tomatoes (from 23 to 29 days) and pepper (from 24 to 29 days), and the longest with potatoes (from 107 to 122 days). The following indicators of garden peas were registered - stem length (cm); fresh weight of the above-ground part (kg); beans per plant (number); fresh weight of beans (g); fresh weight of grains (g) and seed yield from the experimental area (kg). It was established that the most suitable cultivation of peas is with tomatoes and pepper. Relay cultivation was applied, with the sowing of tomato and pepper seeds being carried out about 20-25 days before the harvesting of garden pea seeds. This time difference allows the peas plants to full use of the area from mid-March to the end of May and to be used as living mulch who preserve soil moisture and suppresses the development of weed vegetation. After harvesting the plants at botanical maturity soil space is freed up for the development of tomato and pepper plants. The results are not so good when grown together with potatoes. Two crops together are cultivated with almost similar sowing/planting dates and the competition for light and nutrient area negatively affects the growth and productive performance of the peas. Sole crop cultivation in organic field conditions undoubtedly increases seed yield, but the density of the crop is a prerequisite for the occurrence of plant diseases. The corresponding trend is also observed in intercropping with potatoes, where higher humidity is maintained and favourable conditions are created for the development of fungal pathogens in both crops.

ASSESSMENT OF GARDEN BEAN INTERCROPPING WITH VEGETABLE CROPS

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Abstract Text:

Garden beans, a representative of legumes, have a beneficial effect on soil fertility and are a desirable crop in organic vegetable production. The crop can be successfully grown as an accompanying crop with other vegetable species, but its role in this regard in Bulgaria is undervalued and its sole cultivation is still practiced on farms. According to its biological requirements and cultivation as an early crop, it is suitable for combination with early potatoes, and tomatoes and peppers for medium-early field production. In organic field of Maritsa Vegetable Crops Research Institute, in 2023-2024, an experiment was conducted with varieties created at the institute with good adaptive and productive performances when grown in organic conditions. The duration of the vegetation of the legume crop is from 93 to 103 days, according to the climatic conditions of the year. In mixed crops, the joint vegetation is shortest, almost the same with pepper (from 53 to 56 days) and tomatoes (from 54 to 58 days), and longer with potatoes (from 66 to 92 days). The following indicators of garden beans were registered - stem length (cm); plant fresh weight (g); beans per plant (number); fresh weight of bean per plant (g) and seed yield from the experimental area (kg). It was found that it is appropriate to use garden beans as a companion crop for the tested three vegetable species. Relay cultivation was applied, which allows for different periods of sowing/planting of the species and the creation of favourable development conditions of both of them. Sowing of beans was carried out at the end of April, planting of potatoes at the beginning of March, and sowing of tomatoes and peppers at the end of May. The crops do not compete for light and food area. The botanical maturity of beans occurs after the harvest of potatoes and before the end of tomatoes and peppers vegetation. After harvesting the seeds, the bean plants are left as living mulch, which suppresses weed growth and retains moisture on the soil surface. They do not have a negative impact on the main crop. Sole crop cultivation of bean in organic field conditions inevitably increases seed yield and facilitates soil cultivation during the vegetation. In intercropping systems of cultivation with two crops, the difference in their biological requirements requires more specific treatments, but has a positive effect on increasing biodiversity per unit area.

GENETIC STUDIES ON THE PRODUCTIVITY TRAITS OF ORGANIC SPINACH

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Abstract Text:

Organic spinach growers require varieties adapted to organic conditions with qualities organic buyers seek, including nutrient use efficiency and nutritional value. Baby-leaf spinach is planted at high density, and organic spinach seed can be expensive due to labor, input costs, and the risks of crop failures from extreme weather and disease (Formiga et al., 2023). There is a need for organic breeding initiatives to develop varieties with superior nutrition, agronomic productivity, and enhanced seed yields by assessing and utilizing crop phenotypic and genetic diversity. The U.S. project, Systems Approach to Manage Organic Spinach Productivity, funded by the USDA NIFA Organic Research and Extension Initiative, is establishing a foundation to create spinach varieties for organic producers and consumers that feature improved nutrient acquisition, a better understanding of how spinach leaf and root-associated microbiomes interact with organic fields dedicated to spinach production, and a breeding model to develop varieties with higher organic seed productivity (https://eorganic.info/node/35658).

The project's research team conducted field evaluations of spinach accessions sourced from the USDA germplasm repository in Uvalde, Texas, under organic conditions to assess photosynthetic performance, pigments (chlorophyll, carotenoids, and anthocyanins), leaf morphology, nitrogen use efficiency, and seed productivity at the Organic Seed Alliance field site in Washington State. Significant natural variations in productivity traits were noted across the spinach accessions. The processed data were employed for Genome-Wide Association Analysis (GWAS) to identify the underlying genetics using a previously established set of SNPs and multiple models (GLM, MLM, BLINK, and FarmCPU) in GAPIT 3. Candidate gene mining and genome prediction (GP) were conducted with the SNP loci using Ridge Regression Best Linear Unbiased Prediction (rrBLUP) and Bayesian A (BA) models. GWAS was applied to photosynthesis components such as anthocyanin and chlorophyll pigment content in 299 spinach accessions using 50,873 SNPs. Eight SNPs (three QTLs on chromosomes 3 and 4) were linked to anthocyanin content; ten SNPs (two major QTLs on chromosome 3) were associated with carotenoids, and nine SNPs were related to leaf texture and petiole lengths. GWAS was also performed for seed yield-related traits, including days to flower, gender distribution, and seed yield in 227 spinach accessions using 86,049 SNPs. Twenty SNP markers were correlated with days to flower, and five SNPs (QTL on chromosome 2) were identified for seed yield. Significant SNP loci demonstrated relationships with various traits and exhibited high prediction accuracy. The GWAS-derived

SNP marker set showed notable accuracy in GP, indicating its potential for selecting accessions with enhanced organic productivity for breeding varieties through marker-assisted selection (MAS) and genomic selection (GS). Project results will be published and shared through the Genetic Resources Information Network (GRIN), supporting ongoing public and private organic spinach breeding efforts.

Reference:

Formiga, A.; Joshi, V.; Colley, M. (2023) Challenges in the market for organic spinach seed. eOrganic. https://eorganic.org/node/35758

OAT (AVENA SATIVA L.) LITHUANIAN VARIETIES FOR INTENSIVE, EXTENSIVE AND ECOLOGICAL

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Abstract Text:

Oats (Avena sativa L.) are very suitable crop for ecological and extensive farming because of their morphological traits. They are dominant spring Poaceae crop in ecological farming in Lithuania. The total oat area in 2023 was 28.2% of spring Poaceae crops, while spring wheat was 33% and spring barley 35.7%. At ecological farms, oats made up 68 % of the total area in this group of cereals. Spring wheat accounted for 14%, spring barley 4%, and 14% consisted of various mixtures with the mentioned cereals.

The total oat area in Lithuania is increasing from 50 thousand ha in 1993 to 110.7 thousand ha in 2024. The area of oat crop in Lithuania in 2023 was about 93 thousand ha, and 32 percent of this area was at ecological farms. From 2015 to 2023, the number of ecological farms in Lithuania was about 2.5 thousand. The average area of ecological farms in 2023 was about one hundred ha.

The average yield in 2023 in Lithuania was 2.12 t ha-1 for oats, 2.93 t ha-1 of spring wheat and 3,40 t ha-1 of spring barley. The average yield in ecological farms in 2023 in Lithuania was 2.51 t ha-1 for oats, 2.11 t ha-1 for spring wheat and 1.94 t ha-1 for spring barley. If compare ecological yield with total, we have 118,4% for oats, 72.0% for spring wheat and 57.1% for spring barley.

During the last ten years 7 oat varieties were released at Lithuanian Centre for Agriculture and Forestry. Four of them – Viva DS (2015), Frekula DS (2019), Svaja DS (2023) and Simer DS (2024) - are hulled varieties, and three – Milija DS (2021), Agoda DS (2022) and Vainius DS (2025) are hulless varieties.

Every hulled variety shows good results growing under extensive and intensive management practices. The average yield under extensive cultivation methods in 2024 was 3.22 t ha-1 and under intensive treatments 4.60 t ha-1 and it there were no significant differences between varieties. In ecological farming, the best yield results were shown by varieties Svaja DS (2.24 t ha-1) and variety Viva DS (2.13 t ha-1). Other varieties showed significantly lower yields in ecological farming.

Hulless variety Vainius DS showed significantly higher yield, protein content and hectolitre weight results comparing with other hulless varieties Milija DS and Agoda DS.

ENABLING FACTORS FOR LONG-TERM SUSTAINABILITY OF COMMUNITY SEED BANKS IN INDIA

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Abstract Text:

Community seed banks (CSBs) are vital grassroots initiatives that strengthen access to and availability of diverse, locally adapted seeds, offering a powerful tool for agrobiodiversity conservation, climate change adaptation, and enhanced food security and sovereignty (Vernooy et al. 2024; Altieri et al. 2012). These community-managed repositories play a crucial role in preserving traditional crop varieties and knowledge, empowering local communities, and promoting resilience in the face of environmental changes (Duthie-Kannikkatt et al. 2019). While their benefits are well-documented, ensuring their long-term sustainability, particularly economic viability, remains a critical challenge. CSBs often struggle with limited resources, lack of technical support, and difficulties in accessing markets for their seeds. This can hinder their ability to effectively conserve and distribute seeds, which may have impact on their long-term effect. We conducted in-depth analyses of eight CSBs across India, strategically selected to represent diverse agroecological zones: two in West Bengal, three in Odisha, and three in Karnataka. These CSBs, established between 2012 and 2023 with support from non-profit organizations, were founded to conserve indigenous seeds and traditional agricultural practices. Our research employed a two-phased approach. First, we conducted a comprehensive literature review to establish a foundation for our empirical investigation. This review informed the development of a conceptual framework for understanding CSB operations and identifying enabling and hindering factors. Second, we conducted an empirical study involving semi-structured interviews and direct observations at each CSB. The findings from these case studies, analyzed in the context of existing literature, contribute valuable insights into CSB functioning and offer practical recommendations for improving their long-term sustainability. Our research validates and refines the conceptual framework, highlighting the crucial need for CSBs to prioritize building robust support networks for technical, financial, and human resources, alongside expanding their marketing activities. We conclude by recommending policy and regulatory adaptations to create a more supportive environment for CSBs.

References

Vernooy R, Adokorach J, Gupta A, Otieno G, Rana J, Shrestha P, and Subedi A (2024). Promising Strategies to Enhance the Sustainability of Community Seed Banks. Sustainability

2024, 16(19), 8665; https://doi.org/10.3390/su16198665 Duthie-Kannikkatt K, Shukla S, Sanyasi Rao ML, Sakkhari K, and Pachari D (2019). Sowing the seeds of resilience: a case study of community-based Indigenous seed conservation from Andhra Pradesh, India. The International Journal of Justice and Sustainability 2019, 24(9), https://doi.org/10.1080/13549839.2019.1652800 Altieri AM and Nicholls CJ (2012). Sustainable Agriculture Reviews. (SARV, volume 11)

INTELLECTUAL PROPERTY RIGHTS USED ON U.S. MAIZE, RESTRICTIONS ON PUBLIC RESEARCH, AND SOCIETAL CHALLENGES: BARRIERS TO BREEDING FOR DIVERSITY

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Abstract Text:

Breeding for agrobiodiversity is crucial to meeting societal goals of agricultural and environmental sustainability, diet diversification, and mitigation of climate change impacts (Ceccarelli & Grando 2020). Diverse participation of farmers, public researchers, and other actors in management of crop genetic diversity is recognized as a priority in achieving these goals by countering the impacts of extreme consolidation and privatization of seed systems (Lammerts van Beuren et al. 2018). Enabling public and independent breeding requires a concomitant effort to address public policies that restrict access to genetic diversity (Louwars 2018). The current state of restrictive intellectual property (IP) commonly used on U.S. seed is a direct barrier to meeting these sustainability goals. This is sharply evident with IP used on U.S. maize that restricts breeding, research, and parental background data from breeders and farmers, which is a barrier to broadening participation in the breeding process, including action of participatory plant breeding (PPB).

U.S. commercial maize (*Zea mays*) is based on one race and the genetic diversity of the standing crop has been in decline for at least 40 years. Because of this, the USDA's Maize Crop Germplasm Committee is concerned about crop vulnerability to disease, pests, and extreme weather events, and has recommended a molecular based assessment of genetic diversity of the standing crop. An assessment has not been conducted because of IP and licensing restrictions. We define this obfuscation designed through patents, contracts, non-disclosure agreements, and confidentiality agreements by patent holders as data blanks. These data blanks about genetic vulnerability on the maize landscape puts farmers at risk of crop failure and the public at risk of food and fuel insecurity. This empirical study is based on a subset (n=36) of semi-structured interviews conducted with maize genetic diversity experts (n=44) about their perceptions and analyses of maize standing genetic diversity in the Upper Midwest. Results indicate that IP and licenses restrict research on commercial maize genetic diversity by obfuscating molecular based assessments in the public sector. Interviewees were uncertain about the legality of genetic research on commercial maize seed, resulting in a chilling effect in public sector research on genetic diversity. Implications include a decline in public breeding programs which is perceived as reducing standing genetic diversity. Results also indicate public sector experts are concerned about the private control and management of nearly all U.S. commercial maize seed by two companies with little transparency or oversight.

Policies that establish alternative IP solutions are needed to situate society towards achieving the six international sustainability policy goals of agrobiodiversity, food security and safety,

food and seed sovereignty, social justice, ecosystem services, and climate robustness (Lammerts van Beuren et al. 2018). Organic Seed Alliance is convening the Intellectual Property Rights on Seed Symposium (February 2025) to advance efforts in developing alternative forms of IP that allow for continuous improvement and flourishing of standing genetic diversity. Proceedings and policy white papers will be produced from the Symposium to inform future recommendations that support organic seed growers, plant breeders, and researchers in navigating the complexities of and developing alternative to IP commonly used on seed.

Reference:

Ceccarelli S and Grando S (2020). Evolutionary plant breeding as a response to the complexity of climate change. iScience, 23(12):101815. https://doi.org/10.1016/j.isci.2020.101815

Lammerts van Beuren ET, Struik PC, van Eekeren N, and Nuijten E (2018). Towards resilience through systems-based plant breeding. A review. Agronomy for Sustainable Development, 38(5), [42]. https://doi.org/10.1007/s13593-018-0522-6

Louwars NP (2018). Plant breeding and diversity: A troubled relationship? Euphytica, 214(114). https://doi.org/10.1007/s10681-018-2192-5

GENOTYPIC VARIABILITY IN SEED YIELD AND QUALITY OF ONION (ALLIUM CEPA L.) FOR OPTIMIZED BREEDING AND SEED PRODUCTION IN TUNISIA

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Abstract Text:

Onion (*Allium cepa* L.) is one of the most important vegetable crops worldwide and is of great interest because of its nutritional and medicinal properties. Onion is allogamous crop, protandrous with anthers shedding pollen before the stigma of the flower becomes receptive. It is an entomophilous species that requires insect pollinators specially honey bee to ensure appropriate seed production. Although self-pollination between flowers of the same umbel is frequent. Being highly cross-pollinated with 2 years per generation life cycle and thermo-sensitive crop, breeding efforts in this crop are minimal. In this research, the genotypic differences in seed yield and quality among six onion genotypes were studied at the Sahline and Chott-Mariem Experimental Stations. Seed yield traits evaluated were the number of seeds per umbel, seed yield per plant, flowering time, number of umbel per plant, and seed set percentage. For seed quality, traits such as seed size, seed weight (1000-seed weight), germination rate, seed vigor, seed viability, moisture content, seed longevity and purity were evaluated. Significant genotypic variations were observed across all evaluated traits. Certain genotypes demonstrated superior seed yield potential, characterized by a higher number of seeds per umbel and greater seed weight per plant. Other genotypes excelled in quality traits (larger seed size, higher germination rates, improved seed vigor, and greater seed viability) making them particularly suitable for long-term storage and high-quality seedling production. These findings provide valuable insights for onion breeding programs and seed production strategies, emphasizing the importance of selecting genotypes that exhibit a balance between high seed yield and superior seed quality. The results offer valuable information for optimizing onion seed production in Tunisia. By identifying high-performing genotypes and understanding their interaction with the environment, these findings supports the development of more productive and resilient onion varieties, optimizing seed production in Tunisia.

APHANOMYCES ROOT ROT, A NEW POTENTIAL THREAT TO GRASS PEA

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Abstract Text:

Grass pea *(Lathyrus sativus* L.) is a legume cultivated for food, feed and fodder primarily in hot arid and semi-arid regions. It is considered a resilient crop, characterized by high yield stability and tolerance to stresses. Still, as any crop, it might suffer from pests and diseases (Ellis et al. 2022), the relative impact of some of which might increase with climate change. One of the most devasting legume disease nowadays is Aphanomyces root rot (ARR), caused by *Aphanomyces euteiches*, rising major concern for pea (*Pisum sativum*) and lentil (*Lens culinaris*) producers, but also affecting alfalfa (*Medicago sativa*), faba bean (*Vicia faba*) and vetch (*Vicia sativa*) (Beacking et al. 2022). ARR is regarded a major constraint in the affected areas as there are no effective control methods and little genetic resistance is available in any crop. Although *Lathyrus* genus is phylogenetically very close to *Pisum* and *Lens*, little is known on the susceptibility of *L. sativus* to ARR, probably because it is a minor or even negligible crop in the regions where the disease is predominant. However, the current interest in introducing grass pea into new areas and the continued geographical expansion of ARR calls for the need to assess its host status to ARR and to explore the availability of sources of resistance and evaluate its potential impact on it.

In a preliminary test with 3 grass pea accessions inoculated under controlled conditions, we observed severe root symptoms confirming that grass pea crop can be severely affected by the disease. To further characterize the susceptibility status and to identify sources of resistance, a collection of 174 *L. sativus* accessions was tested. Four plants per accession were sown in 200 mL plastic pots using perlite as substrate and inoculated after 10 days of growth, by pipetting 5 mL of a 1,000 oospores/mL solution of the RB84 isolate at the base of each plant under controlled conditions (Moussart et al. 2024). Twenty days post-inoculation, foliar symptoms were assessed using a 0-5 foliar symptom index (FSI), where 0 represents a healthy plant and 5 indicates a dead plant. Root rot necrosis was also evaluated using a 0-9 root rot index (RRI). The experiment revealed a wide range of responses in both foliar and root symptoms. While most accessions exhibited high susceptibility, one of the accessions displayed very low symptomatology (FSI > 1 and RRI > 2). These results confirm the overall susceptibility of *L. sativus* to *A. euteiches*. However, the observed variability shows the possibility to identify accessions with intermediate levels of resistance, whose resistance mechanisms should be further investigated. Given the lack of effective control methods for this disease, incorporating these resistant lines into breeding programs could be a valuable strategy for developing agronomically viable, disease-resistant cultivars.

Reference:

Ellis N, Vaz Patto MC, Rubiales D, Macas J, Novák P, Kumar S, Hao X, Edwards A, Sarkar A, and Emmrich P (2022). Grasspea. In: Chapman, M.A. (eds) Underutilised crop genomes. Compendium of plant genomes. Springer, Cham. https://doi.org/10.1007/978-3-031-00848-1_12

Moussart, A, Lavaud C, Onfroy C, Leprévost T, and Le May C (2024). Pathotype characterization of *Aphanomyces euteiches* isolates collected from pea breeding nurseries. Frontiers in Plant Science, 15, [1332976]. https://doi.org/10.3389/fpls.2024.1332976

Becking T, Kiselev A, Rossi, Street-Jones D, Grandjean F, and Gaulin E (2022). Pathogenicity of animal and plant parasitic *Aphanomyces* spp and their economic impact on aquaculture and agriculture. Fungal Biology Reviews (40), [1-18] https://doi.org/10.1016/j.fbr.2021.08.001

A HOLISTIC CONCEPT ON ORGANIC PLANT BREEDING; THE PERSPECTIVE OF ECO-PB FOR THE FUTURE

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Abstract Text:

To meet the needs of the organic sector, it is essential to develop varieties and populations adapted to this production system and to diverse local contexts, whilst also maintaining accesses to a broad genetic basis for future breeding. Diversified breeding strategies are needed to achieve adaptation to a wide range of soil and climatic conditions, as well as consumers' preferences: (i) exploiting intra-crop genetic diversity of population breeding (e.g. organic heterogeneous material), (ii) improving resilience through disease resistance and enhanced plant-soil-microbiome interaction, and (iii) the further development of culinary breeding aiming at improving nutritional and sensory quality of food. These are key levers for strengthening the productivity and resilience of agricultural systems in the face of environmental and societal challenges. The organic plant breeding sector is presently offered with some new and important opportunities. Among these, there is a growing interest in agroecology and organic farming, which require organic cultivars developed for organic conditions. The European Organic Farming Regulation (EU 2018/848), which came into force in 2022, benefit organic seed and plant breeding by introducing Organic Heterogeneous Material and Organic Varieties as new cultivar types requiring simplified notification and registration procedures respectfully. Furthermore, the use of derogations for the use of non-organic certified untreated seed, will be phased out by 2036, leading to an exponential increase in demand for organic seed. At the same time, significant challenges remain. The potential deregulation of New Genomic Techniques (NGTs) in 2026 could lead to the introduction of the first NGT-derived varieties on the market as early as 2028. Additionally, increasing legal uncertainties make it more difficult for breeders to navigate the growing number of patents on plants, raising concerns about access to breeding material. The lack of clarity over which plants can still be used for further breeding could hinder the crucial work of plant breeders. Ensuring that breeders and farmers retain unrestricted access to plant genetic material is essential to safeguarding food security and food sovereignty. In this context, developing positive alternatives is a priority, as a significant number of patented NGT-based varieties are expected to enter the market from 2028 onwards. These alternatives must integrate multiple dimensions, including agronomy, market dynamics, financing, taste, and nutritional quality. Maintaining diversity in breeding approaches is crucial for preserving crop diversity at various levels. Furthermore, fostering a broad range of breeding strategies, from farmer-led initiatives to scientific breeding, strengthens both ecological and societal resilience. To ensure coherence, the systems-based breeding approach can be adopted as a framework, which provides a structured perspective on the different alternatives, highlighting

their respective advantages and limitations (Lammerts van Bueren et al., 2018).. As part of efforts to strengthen the capacities of ECO-PB's members and breeders, the following key activities must be actively pursued through the working groups established in 2024: 1. Policy support on plant reproductive material, NGTs, and other issues relevant to organic breeding and organic agriculture. 2. Education in organic plant breeding at various levels, from farmers to scientists. 3. Development and improvement of tools, methods, and approaches suited to organic breeding, ensuring both the maintenance of and access to genetic diversity at different scales (from farmer-led initiatives to scientific breeding). 4. Exploration of innovative financing approaches for organic breeding and the preservation of genetic diversity. Interconnected these key activities are envisaged not only to meet the current needs of the organic sector, but also to maintain access to crop genetic diversity for future generations.

Reference:

Lammerts van Bueren E T, Struik PC, van Eekeren N, & Nuijten E (2018). Towards resilience through systems-based plant breeding. A review. Agronomy for Sustainable Development, 38(5), [42]. https://doi.org/10.1007/s13593-018-0522-6

BREEDING FOR SUSTAINABILITY: EVALUATING ORGANIC WHEAT GENOTYPES FOR RESOURCE USE EFFICIENCY AND YIELD STABILITY

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Abstract Text:

Agroecological farming systems, such as organic farming, strongly rely on natural resources in face of the heavy use of external inputs that characterise conventional farming. Modern wheat genotypes, bred for conventional farming, efficiently utilize agrochemicals to achieve high yields and quality, but this dependence makes them poorly suited for organic farming, often resulting in lower yields and quality (Murphy, 2007). Indeed, the ability of wheat varieties to maintain stable yield and grain quality across varying growing conditions is crucial in the light of making organic farming more in line with the principles of agroecology (Stagnari, 2013). As the demand for organic products is increasingly growing, the need for high-quality genotypes that are adapted to organic systems and can withstand variable growing conditions becomes ever more critical (Wolfe, 2008). This study investigates the agronomic performance of new bread wheat lines obtained by organic breeding compared to standard organic and conventional varieties, with an emphasis on breeding methods that promote sustainability. The research was conducted by the Foundation Seminare il Futuro (SIF) over three years (2020/21; 2021/22; 2023/24) at the Centre for Agri-environmental Research "Enrico Avanzi" of the University of Pisa in San Piero a Grado (Pisa). The experiment was performed using a randomized complete block experimental design with one factor (the genotype) and three spatial replicates. Each experimental plot sized 1.5 m x 6 m. The tested genotypes included four registered wheat varieties, namely 'Bologna', an Italian modern bread-making variety, 'Wiwa,' a Swiss organic standard, 'Royal,' and 'Prim,' other Swiss organic varieties, as well as six new wheat lines under screening for organic farming suitability. The primary goal of the study was to assess the potential of the new wheat lines developed by organic breeding to adapt to low input organic farming conditions.

The experimental site was managed organically and the wheat fields were part of a 7-yr crop rotation including three years of alfalfa, followed by bread wheat, rye-vetch green manure, grain sorghum, berseem clover and durum wheat. Wheat fertilization was exclusively carried out by applying before sowing 28 kg ha-1 of N, 25 kg ha-1 of P2O5 and 30 kg ha-1 of K2O as organic fertiliser (Biorex®, Italpollina). No crop protection nor weed control operations were performed. Among key agronomic parameters measured during the study, we included grain yield, protein content, and visual symptoms of diseases. Statistical analysis was performed to test the effect of the experimental year, the genotype and their interaction by using a generalized linear mixed model. The results of the study indicate that the organic

wheat genotypes show promising potential in terms of combining good levels of yield and protein content, whereas the modern conventional variety showed opposite trends with respect to these two parameters. Among genotypes selected in bio-breeding programmes, the ARM_112_19B line showed, on average, the highest yield (4.66 t ha-1) and the highest protein content (13.4 %), outperforming some of the registered varieties in protein content in all the three years. Significant differences in grain yield among genotypes were observed only in the second year, when ANSC_2795 yielded lower than four genotypes, including Bologna and ARM_112_19B. There was significant difference in disease resistance among genotype, a critical factor for organic farming systems where chemical interventions are minimized. Bologna was the most susceptible genotype to pathogens, confirming a lower resistance to infection than the other genotypes under investigation, while SIAI14.74 showed the greatest resistance, particularly against brown rust and Septoria spp. ANSC 2795 stood out for its resistance to yellow rust and brown rust and PRIM to stem rust, while ROYAL was the most susceptible to Septoria spp.

This work supports the growing body of evidence that breeding for organic farming requires a different approach than conventional breeding, focusing on sustainable and resilient wheat varieties that can thrive under the more challenging conditions of low-input organic systems. The findings from this study need to be tested across a wider range of pedoclimatic and management conditions but look promising and can provide the foundation for specific breeding programmes aimed to produce new wheat genotypes, not only adapted to organic farming management, but also characterised by low external input needs and high stability in quantitative and qualitative production traits.

Reference:

Murphy, Kevin M., et al. "Evidence of varietal adaptation to organic farming systems." Field Crops Research 102.3 (2007): 172-177.

Stagnari, Fabio, et al. "Durum wheat varieties in N-deficient environments and organic farming: a comparison of yield, quality and stability performances." Plant Breeding 132.3 (2013): 266-275.

Wolfe, M. S., et al. "Developments in breeding cereals for organic agriculture." Euphytica 163 (2008): 323-346

IMPLEMENTING THE SYSTEMS-BASED BREEDING APPROACH: EXPERIENCES AND LESSONS LEARNED FROM THE EU-PROJECT LIVESEED

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Abstract Text:

It has become clear that agriculture needs to meet both environmental and societal challenges. Awareness about the importance of transdisciplinary approaches in meeting these challenges is increasing (Chable et al., 2020, Klerkx et al., 2012). When it comes to breeding, organic breeders must meet many requirements when developing cultivars, e.g., high yield, good quality, resource-efficiency and climate-robustness, cultural and ethical acceptability and the provision of ecosystem services. Given the current and future climatic, agronomic, economic and socio-cultural challenges, resilience can only be efficiently achieved through concerted actions. The concept of systems-based breeding integrates the strengths of different breeding orientations and provides a perspective where breeders can initiate developments towards ecologically and societally resilient crop production (Lammerts van Bueren et al. 2018). Accordingly, six sustainability targets have been identified: 1) food security, safety and quality, 2) food and seed sovereignty, 3) social justice, 4) agrobiodiversity, 5) ecosystem services, and 6) climate robustness. In this paper we present five supportive pillars for implementing the concept of systems-based breeding, based on experiences obtained during the 2017-2021 EU-project LIVESEED including results from prior related projects and literature on innovation systems and systems change. The five supportive pillars we have identified are: 1) increasing social awareness and reflection, 2) developing alternative financing approaches, 3) promoting the development of appropriate breeding methods, 4) applying integrative interdisciplinary and transdisciplinary learning in education, and 5) fostering facilitation for connecting these processes. These five supportive pillars are all necessary for fostering sustainable transformative change in complex systems, such as organic plant breeding. We argue that a multitude in breeding approaches is needed to contribute to agro-ecological and societal resilience. The workshop analyses showed that many participants, mostly organic breeders and researchers working on organic agriculture, not only looked for technological solutions, but also for solutions that address social, ethical and economic aspects. Collaboration and value chain partnerships are key elements for realising change towards ecologically and socially resilient food systems. Based on workshop outcomes we find that the main impediments to a more holistic perspective on organic breeding are the current strong focus on short-term profits and EU law and regulations. Increasing social awareness, alternative financing models, new breeding methods and multi-actor approaches are necessary for broadening breeding approaches.

Reference:

Chable, V., Nuijten, E., Costanzo, A., Goldringer, I., Bocci, R., Oehen, B., Rey, F., Fasoula, D., Feher, J., Keskitalo, M., Koller, B., Omirou, M., Mendes-Moreira, P., van Frank, G., Naino Jika, A. K., Thomas, M., Rossi, A. (2020). Embedding Cultivated Diversity in Society for Agro-Ecological Transition. Sustainability,12(3): 784. https://doi.org/10.3390/su12030784 Klerkx, L., van Mierlo, B., Leeuwis, C. (2012). Evolution of systems approaches to agricultural innovation: concepts, analysis and interventions. In: Darnhofer, I., Gibbon, D., Dedieu, B. (eds). Farming Systems Research into the 21st Century: The New Dynamic. Springer, Dordrecht. https://doi.org/10.1007/978-94-007-4503-2_20 Lammerts van Bueren, E. T., Struik, P. C., van Eekeren, N., Nuijten, E. (2018). Towards resilience through systems-based plant breeding. A review. Agronomy for Sustainable Development, 38(5), 42. https://doi.org/10.1007/s13593-018-0522-6

STRIP CROPPING-BREEDING FOR RESILIENT CROPS

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Abstract Text:

A new innovative farming practice that can limit the negative effects of monocultures whilst maintaining or even increasing yield is intercropping (Bourke, et al. 2021). Intercropping of different crops can promote ecological interactions, biodiversity, and natural pest and weed control and improve resource utilization, thereby optimizing yield, stability and quality. To benefit optimal from this cultivation system, it is not only essential to both choose the best crop combinations, but also to select the best varieties. Modern crop varieties, bred for monocropping, may not be suitable for intercropping systems. This asks for innovative methodological approaches to breed crops specifically for intercropping.

As a first step, a long term experiment was initiated at Bio-Vitalis, on an organic cultivated field, in collaboration with Crop-mix (https://cropmix.nl/en/) and Wageningen University. Aim was to test whether genotypic variation exists for being a good neighbour, expressed as optimal performance in specific crop combinations, and explore causal mechanisms. The experiment consists of six different crops (pumpkin, lettuce, leek, fennel, cauliflower and grass-clover) that are cultivated in 1.5 m strips, with five blocks. In each 140 m strip, three different genotypes are grown randomly distributed over each three plots of 15 m length. The experiment will last six seasons, combining rotation in space with rotation in time.

Preliminary results will be presented. Pumpkin was very competitive as a neighbour crop, yet the extent to which it influenced yield of neighbouring crop was strongly affected by the year and the neighbour. Cauliflower-leek was an interesting combination, as leek positively affected cauliflower yield and timing. For several crops, variation of the response to neighbours was identified that will be further explored.

Reference:

Bourke PM, Evers JB, Bijma P, van Apeldoorn DF, Smulders MJM, Kuyper TW, Mommer L and Bonnema G, 2021. Breeding Beyond Monoculture: Putting the “Intercrop” Into Crops. Frontiers in Plant Science: https://doi:10.3389/fpls2021.734167 .

TOMATO BREEDING FOR DROUGHT TOLERANCE

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Abstract Text:

Tomato (Solanum lycopersicum L.) is one of the most important crops in different parts of the world, including the Mediterranean region and one of the factors that most limits the productivity and quality of fruits is drought and several diseases, with economic consequences.

Global climate change suggests that crops will be exposed to highly stressful environmental conditions that may affect their productivity and quality, leading to a possible global food shortage. Drought is a factor in yield loss, negatively affecting several physiological, genetic, biochemical and morphological characteristics of plants. Drought also causes pollen sterility and affects flower development, resulting in reduced seed production and fruit quality. Conti et. al (2023) reviewed the contribution of specific characteristics to drought tolerance in tomato and how they vary between different cultivars, highlighting the importance for tomato biodiversity as an efficient response to drought.

In addition to the impact of biotic and abiotic factors on crop productivity, there is also difficulty in the availability of access to improved organic seeds. This limitation was also one of the factors that led us to start this open pollinated tomato breeding work with the aim of developing drought-tolerant new tomato varieties that have suitable agronomic characteristics for farmers and desirable organoleptic attributes for the market.

The breeding we are doing is segregating a F1 industrial processing tomato, due to the virus and disease resistances of these varieties in the Mediterranean area, and their holding capacity on the field. For some lines these F1s were crossed with open pollinated (OP) varieties to improve flavor and fruit characteristics for fresh consumption. The lines have been selected for tolerance to drought stress still in the nursery before planting out through a method adapted from those used by Zhang et. al (2011) and Gómez-Guillamón et. al (2021) for melon and watermelon, subjecting seedlings with 2 to 3 true leaves to submersion irrigation for a period and then leaving them without irrigation until the transplantation. The lines have been further individually selected in the field where they have been planted out in February-April, depending on the year, and irrigated once at planting and let to grow under a mediterranean climate with hot-dry summers (Koppen classification Csa).Predictably, and with the given growing conditions, natural selections occurred and plants most sensitive to heat and drought died on the field or did not produce fruits or produced poor quality fruits which were discarded.

Over the generations, pure line selection was carried out in Portugal (Idanha-a-Nova) an area with acidic soils with a well-developed structure (some clay) in which the plants were selected mainly for their vigor and plant architecture, fruit quality and flavor and also for a

presence of blossom end rot (low water availability and acid soils) and fruit cracking due to high fluctuations in water availability.

For fresh consumption, six F7 lines were stabilized for outdoor processing tomato production with adapted characteristics. In 2025 selection will be finalized and the process of trialing and registration will start.

Reference:

Veronica Conti, Luigi Parrotta, Marco Romi, Stefano Del Duca and Giampiero Cai (2023) Tomato Biodiversity and Drought Tolerance: A Multilevel Review. Int. J. Mol. Sci. 2023, 24, 10044. https://doi.org/10.3390/ijms241210044

María L Gómez-Guillamón and Rafael Fernández-Muñoz (2021) Setting up a Selection Method for Drought Tolerance in Melon Seedlings. Cucurbit Genetics Cooperative Report 44.

Haiying Zhang, Guoyi Gong, Shaogui Guo, Yi Ren, and Yong Xu (2011) Screening the USDA Watermelon Germplasm Collection for Drought Tolerance at the Seedling Stage. National Engineering Research Center for Vegetables, Beijing Academy of Agricultural and Forestry Sciences, No. 9 Shuguanghuayuan Road, Haidian District, Beijing, 100097, China Kai-Shu Ling U.S.DepartmentofAgriculture,AgriculturalResearch Service,U.S.Vegetable Laboratory, 2700 Savannah Highway, Charleston, SC 29414. HORTSCIENCE 46(9):1245–1248.

NATURAL MECHANISMS OF REGULATION OF PEA WEEVIL (BRUCHUS PISORUM L.) DAMAGE TO FIELD PEAS GROWN IN A MIXTURE WITH CEREALS.

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Abstract Text:

Field pea (Pisum sativum L.) has its own specific pest pea weevil (Bruchus pisorum L.) that has been accompanying its crops for as long as peas have been known to people. Growing winter peas in northern Germany was previously a valuable solution among other benefits for reducing the level of its damage by insects, since its flowering time is earlier than the flowering of spring peas and than the mass flight of the pea weevil and pea moth. However, climate change and weather extremes in recent years as well as the increase in the share of peas in local fields have led to colossal crop losses. In the experimental plots of Cultivari Cereal Breeding Research gGmbH in Darzau, from 60 to 98% of pea seeds, depending on the cultivar, were stocked by the pea weevil in the year 2024. Some researchers (Doss, 1995; Teshome, 2016 et al.) have so far described the property of peas to resist the pest by forming neoplastic growths on the pods (Np) under the eggs laid by the grain weevil. In response to the secretion with which the female glues the egg to the pod, the pea forms an outgrowth of dense non-meristematic tissue, “pustular outgrowths” of callus and pushes the egg away from the seed, creating an obstacle for the larva. However, this mechanism is inhibited by the presence of UV radiation, so this mechanism was observed only in greenhouses with a decrease in the UV spectrum of artificial lighting or in the field when growing peas in a mixture with sorghum or corn (Teshome, 2016).

From 2022 to 2024, Cultivari gGmbH conducted observations of the formation of Np pods on winter pea cultivars when grown in experimental fields in a mixture with hulless barley and triticale to better understand the patterns and correlations of the manifestation of this aspect. By observations and calculations, Np growths were detected on 61% of 160 winter pea cultivars and only on 1% of spring pea. Neoplasms were formed only by medium- and long-growing pea cultivars and were not found by short-growing cultivars. They were also not formed on varieties with green color of peas seeds. However, when calculating the level of damage to the yield of varieties by the pea weevil, the correlation coefficient with the presence of Np pods was only -0.21, which is insufficient to speak about the effectiveness of this natural self-defense mechanism of pea. This phenomenon requires a more thorough study with a larger number of replications over a larger number of years to better understand its potential and ways to increase its effectiveness.

The pea weevil is part of the biotic community with its own function, therefore, in sustainable agriculture, there is no goal to destroy it, but to reduce its share of pea weevil in the ecosystem. To better understand its function, the Cultivari gGmbH continues to study the interaction between pea plants and insects, including bees and bumblebees. It can be

assumed that insects that feed on pea pollen and nectar can play a similar role to bumblebees on self-pollinated lupine, which, by moving the stigma of the flower, stimulate the formation of more grains in the pod. In particular, it was investigated that pea flowers also have different aroma and sweetness. It can be assumed some cultivars seem to be more interested in attracting pollinators, although peas are a self-pollinating crop and the development of bumblebee and bee-attractive varieties may gradually fill this niche with more beneficial insects and reduce the share of pea weevil. However, this assumption requires further research, verification and scientific discussion.

Reference:

Doss Robert P., Proebsting William M., Potter Sandra W., and Clement Staphen L. (1995) Response of Np mutant of pea (Pisum sativum L.) to pea weevil (Bruchus pisorum L.) oviposition and extracts. Journal of Chemical Ecology, Vol. 21, No. 1. https://www.researchgate.net/publication/248048095_Response_of_Np_mutant_of_pea_Pisum_sativum_L_to_pea_weevil_Bruchus_pisorum_L_oviposition_and_extracts

Teshome A., Bryngelsson T., Mendesil E., Marttila S. and Geleta M. (2016) Enhancing Neoplasm Expression in Field Pea (Pisum sativum) via Intercropping and Its Significance to Pea Weevil (Bruchus pisorum) Management. Frontiers in Plant Science, May 2016, Vol. 7, Article 654. https://www.frontiersin.org/journals/plant-science/articles/10.3389/fpls.2016.00654/full

PROMOTING CROP DIVERSIFICATION IN ORGANIC AGRICULTURE THROUGH EMMER AND EINKORN LANDRACES IN HUNGARY

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Abstract Text:

Current agricultural and food systems rely predominantly on a few species and a limited number of varieties, posing challenges for biodiversity, climate adaptation and food security. Diversification is essential to increase resilience and sustainability, and two ancient cereal species, emmer (Triticum dicoccum) and einkorn (Triticum monococcum), could offer valuable alternatives due to their ability to be grown successfully under low-input and organic conditions. Despite their potential benefits and growing consumer demand, their cultivation remains limited; between 2017 to 2022, einkorn and emmer were grown on an average of only 600 hectares in Hungary. To promote their cultivation and support their re-introduction, on-farm and on-station trials coupled with seed multiplication efforts were launched in 2022 as part of the EU project DIVINFOOD (Co-constructing interactive short and mid-tier food chains to value agrobioDIVersity IN healthy plant-based FOOD). As a preparatory step, five semi-structured interviews were conducted with Hungarian farmers cultivating minor cereals to gather information on the type and source of seeds they use, such as whether they grow registered cultivars, landraces or modern varieties and if their seeds are certified or farm-saved, as well as their seed multiplication practices for einkorn and emmer. In Hungary, emmer and einkorn are classified as optionally listed varieties, meaning registration in the national variety list is not mandatory. As of 2023, only one emmer variety (Mv Hegyes, 2008) and four einkorn varieties (Mv Alkor, 2008; Mv Menket, 2011; Mv Esztena, 2017; Szarvasgedei, 2022) were registered in the plant variety database of the Hungarian National Food Chain Safety Office. This limited number of available varieties has not only hindered the spread of emmer and einkorn but also makes it difficult for farmers to select varieties suited to organic farming and to local pedoclimatic conditions. However, expanding the range of available varieties—particularly by re-introducing landraces into cultivation—could be a viable strategy for crop diversification. In addition to the number of varieties available, regulatory frameworks governing plant reproductive material production and marketing can also have a significant impact on adoption and cultivation extent of neglected and underutilised crops. According to the Hungarian Government Decree 48/2004 (IV.21), cultivars of non-listed or optionally listed species such as einkorn and emmer can be traded without certification, allowing farmers to save and exchange seeds from their own harvest, as well as to use their own saved seeds for commercial crop production. Under the current organic regulation (2018/848), organic farm-saved seed is considered certified organic without requiring derogations. However, the European Commission's proposal on the production and marketing of plant reproductive material in

the Union, published on July 5, 2023, could introduce additional bureaucratic barriers, potentially restricting farmers' ability to produce, exchange and use their own seed. Interview results indicate that farmers growing minor cereals, particularly einkorn and emmer, primarily use exchanged or farm-saved seed. Changes to existing legislation could therefore have a disproportionately negative impact, hindering the cultivation of underutilized crops with limited availability of certified seed. The reintroduction of ancient wheat varieties into organic systems presents a viable strategy for increasing biodiversity, improving resilience to climate stress, and meeting consumer demand for diverse and nutritious cereals. However, wider adoption will require supportive policies that facilitate their integration into food systems.

THE ORGANIC OUTDOOR TOMATO PROJECT AS A MODEL FOR INCREASING DOMESTIC PRODUCTION BY PARTICIPATORY ORGANIC BREEDING WITH THE VALUE CHAIN

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Abstract Text:

Tomato (Solanum Lycopersicon L.) is the most popular and consumed vegetable globally, however in Germany only 3,5% of the demand is met by domestic green house production. Processed tomato products (passata, juice, etc.) represent the largest share and are almost 100% imported. A major limiting factor to the expansion of tomato production in Germany is the difficulty of professional outdoor tomato cultivation, which is more cost-effective and has a carbon footprint about 45 times smaller than greenhouse production (Taylor 2000). Outdoor tomato crops are severely limited by late blight (Phytophthora infestans), which has become increasingly virulent since new strains of the fungus evolved in the 1990s (Rullich & Schöber-Butin 2000). An additional threat to tomato field-crops is posed by the increased frequency of extreme weather events, including draughts, caused by climate change.

To address these challenges, the Organic Outdoor Tomato Project (OOTP) was initiated after 1996, when observations on late blight field resistance were made in a few organic market gardens in Germany. It then extended, reaching up to 34 on-farm and in-garden organic participatory plant breeding (PPB) trials throughout the country since 2003. The main breeding objectives are: late blight resistance, tolerance of extreme pedoclimatic conditions and fruit quality. Selection methods have been developed to determine which resistances are effective and on how to best exploit them (Horneburg & Becker 2011). The Breeders' Sensory Test, a tool for testing a large number of fruit samples with a small team, was developed and successfully deployed to improve the flavour of tomato cultivars (Hagenguth et al. 2022). The OOTP promotes the free exchange of knowledge and seeds and has also led to the release of Sunviva, the first Open Source Seed Licenced cultivar at the global scale, by the organic seed company Culinaris (Kotschi & Horneburg 2018). The PPB activities of the OOTP have been mainly focused on indeterminate cultivars for the fresh market until 2019, when the scope expanded to determinate (bush) tomatoes. Determinate tomatoes had been grown with high chemical input outdoors at a large scale in the German Democratic Republic until the late 1980s.

In 2024 a new organic multi-actor breeding programme, involving breeders, researchers, certification bodies and transformers, started under the coordination of the Section of Organic Plant Breeding. Organic nurseries were established in Central Germany at the experimental farm Neu-Eichenberg, and in Northern Germany at LohmannsHof Gärtnerei. 198 determinate genotypes originating from Germany, Eastern Europe, Southern Europe and international genebanks were tested. 48 indeterminate advanced breeding lines were compared to internationally available outdoor cultivars. The trials followed a randomised complete block design with three replications. In addition, to simulate draught stress and assess plants' responses to reduced soil water availability, in the former location two treatments were implemented: (i) ground cover with waterproof plastic acting as a rain shelter, and (ii) ground cover with a permeable fabric mulch of the same black colour. Data on late blight and Alternaria solani susceptibility, electrical capacitance of roots, mycorrhiza, growth type, marketable and total yield and fruit quality were collected. Genome Wide Association Studies (GWAS) will be performed to provide new insights and molecular markers for key traits, relating to late blight resistance, root development, drought stress tolerance, yield and fruit quality under organic outdoor conditions.

According to the results of the first year, we expect additional options for outdoor production for fresh market and processing: In 2024 the first determinate organic open pollinated tomato cultivars with late blight resistance were released by Culinaris. The best performing indeterminate breeding lines have been selected for participatory on-farm trials and final selection in 2025. The best performing determinate genotypes are presently used as parents in diverse crosses.

Reference:

Hagenguth J, Kanski L, Kahle H, Naumann M, Pawelzik E, Becker HC and Horneburg B, (2022). Breeders' Sensory Test: A new tool for early selection in breeding for tomato (Solanum lycopersicum) flavour. Plant Breeding, 141(1), pp.96-107.

Horneburg B, Becker HC (2011) Selection for Phytophthora field resistance in the F2 generation of organic outdoor tomatoes. Euphytica 180:357-367.

Kotschi J and Horneburg B, 2018. The Open Source Seed Licence: A novel approach to safeguarding access to plant germplasm. PLoS Biology, 16(10), p.e3000023.

Rullich G, Schöber-Butin B (2000) Old and new populations of Phytophthora infestans in Germany. Fifth Workshop of an European Network for development of an Integrated Control Strategy of potato late blight. Munich, Germany, 6-10 September 2000. https://edepot.wur.nl/81132#page=233

Taylor C, 2000. Ökologische Bewertung von Ernährungsweisen Anhand ausgewählter Indikatoren. http://dx.doi.org/10.22029/jlupub-16854

APPLYING A PARTICIPATORY AGROECOLOGICAL APPROACH TO WEED CONTROL IN THE PORTUGUESE GRASS PEA LIVING LAB

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Abstract Text:

Grass pea (*Lathyrus sativus* L.) is a legume crop, traditional from Mediterranean, Asian and African countries (Dixit et al. 2016, Lambein et al. 2019). It is known for its high resistance and tolerance to some biotic and abiotic stresses and adaptation to different edaphoclimatic conditions (Campbell 1997). Adding the fact of being a low-input crop, with a high protein content, grass pea can be an interesting alternative crop especially in the context of climate change (Vaz Patto et al. 2006).

The multi-actor DIVINFOOD project aims to promote the production and consumption of underused crops, where grass pea is included. Grass pea growers have identified agroecological weed control, without the use of herbicides, as a major production constraint.

In Alvaiázere, the main grass pea production region in Portugal, a Living Lab has been established joining grass pea researchers, farmers, small processors and sellers to co-develop more agroecological solutions for grass pea production and transformation.

Four grass pea field trials were established in this region, in a participatory research approach, within farmers´ fields and using a traditional grass pea variety. The objective of these trials was to compare different interrow spacing (30 or 70 cm apart) and herbicide applications (with or without), to find more agroecological solutions for weed control. In each field, four different factors combinations were set up, with two repetitions per combination, with a total of eight plots. Plot size varied from 24 to 92.5 m2 depending on the farm, and the herbicide (when applied) was pendimethalin in pre-emergence.

During the crop lifecycle, a FieldSpec4 spectroradiometer was used to collect spectral data, later converted into different plant spectral parameters, related to plant physiological performance. At the end of the crop lifecycle, grass pea plants were harvested by plots, to assess production.

In relation to seed yield, the herbicide treatment did not show clear effects, particularly in the plots with larger interrow spacing. Nevertheless, the reduced interrow spacing, together with the herbicide treatment provided the most consistent results. Nevertheless, great variance among the different farms requests a repetition of this trial in the next season. In relation to spectral parameters, 13 indexes from FieldSpec4 data were selected: ARI (anthocyanin

reflectance), GI (greenness), GVI (green vegetation), LAI (leaf area), MCARI1 (modified chlorophyll absorption in reflectance), MSI (moisture stress), MTVI1 (modified triangular vegetation), NDII (normalized difference infrared), NDLI (normalized difference leaf), NDNI (normalized difference nitrogen), RECI (red edge chlorophyll), SRPI (simple ratio vegetation) and WI (water content). Analysis of variance showed that both the farm and the interrow spacing had significant impact on the majority of the FieldSpec4 indexes. More detailed results will be discussed.

The DIVINFOOD project is still ongoing, and a new season of the same field trials has been established to gather more data and evaluate the reproducibility of the present results, towards a more agroecological grass pea production attractive to all actors of this value chain.

Reference:

Campbell CG (1997). Grass pea, *Lathyrus sativus* L. Promoting the conservation and use of neglected and underutilized crops. IPK and IPGRI, 18.

Dixit GP, Parihar AK, Bohra A, and Singh NP (2016). Achievements and prospects of grass pea (*Lathyrus sativus* L.) improvement for sustainable food production. The Crop Journal, 4 (5), [407–416]. https://doi.org/10.1016/j.cj.2016.06.008

Lambein F, Travella S, Kuo YH, Van Montagu M, and Heijde M (2019). Grass pea (*Lathyrus sativus* L.): orphan crop, nutraceutical or just plain food? Planta, 250 (3), [821–838]. https://doi.org/10.1007/s00425-018-03084-0

Vaz Patto MC, Skiba B, Pang, ECK, Ochatt SJ, Lambein F, and Rubiales D (2006). *Lathyrus* improvement for resistance against biotic and abiotic stresses: From classical breeding to marker assisted selection. Euphytica, 147(1–2), [133–147]. https://doi.org/10.1007/s10681-006-3607-2

ENHANCING CROP DIVERSITY AND FOOD SECURITY THROUGH PARTICIPATORY PLANT BREEDING IN NAKURU KENYA

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Abstract Text:

Agricultural production and food security in Kenya are increasingly threatened by the rising frequency of drought, which has become a major and escalating concern. Irregular rainfall patterns and extended dry spells are worsening the situation, leading to climate-related crop failures and significant economic losses. As global warming continues, these challenges are expected to intensify (Odeny, 2007). Additionally, crop diversity is under serious threat, with many seeds having been lost over time. A study by the Seed Savers Network in Nakuru County found that more than 35 vital crops have been lost, and many more are at risk of extinction, leaving communities highly vulnerable to food insecurity and further loss of agrobiodiversity.

To address these challenges, Seed Savers Network, in collaboration with AGRECOL Germany, is implementing a project focused on the sustainable management of the agricultural seed system in Kenya. A key component of this project is participatory plant breeding, aimed at building a community of farmer breeders within the network. The project has two main objectives: participatory variety characterization and documentation, as well as variety selection and hybridization. It targets crops such as tomatoes, beans, Irish potatoes, sweet potatoes, sorghum, millet, and maize. Through interviews and discussions with farmers and stakeholders, the project has identified the traits most valued by the community. Surprisingly, each crop has distinct traits preferred by farmers, reflecting the diverse needs of local agricultural systems.

Farmers prioritize specific traits in different crops to ensure resilience, productivity, and food security. For beans, the key trait is adaptation to local conditions, particularly drought tolerance and disease and pest resistance. Early maturity, high yield, and seed recycling ability are also important, with an emphasis on stability in production rather than commercial factors. In the case of Irish potatoes, farmers value early maturity, high yield, and disease resistance, highlighting the importance of quick harvests and effective crop health management. Other traits such as marketability and cooking quality also play a role, balancing productivity with economic considerations. For tomatoes, farmers prioritize disease and pest resistance, drought tolerance, and high yield, while also valuing fruit quality and shelf life. In sweet potatoes, the preferred traits are high yield and drought tolerance, along with good storage properties and taste. Sorghum farmers focus on high yield, early maturity, drought tolerance, and disease resistance, with multifunctional use being particularly important. In millets, early maturity, drought tolerance, and adaptability to various soil types are highly valued. For maize, farmers prefer open-pollinated varieties

(OPVs) over hybrids, emphasizing traits like grain color, high yield, drought tolerance, and disease resistance, with additional consideration given to strong stalks, early maturity, and optimal ear placement. These findings illustrate that farmers in Kenya are seeking crop varieties that not only thrive under local environmental conditions but also meet market needs and ensure stable yields. These insights can help guide breeding programs to develop crops that are both resilient and productive, while also addressing economic and nutritional needs.

Reference:

Seed Savers Network Kenya (2023): Farmers seed practices in Nakuru Kenya. Field Survey Report. SSN Gilgil, Nakuru, Kenya.

GRAIN LEGUME CROPS: A SUSTAINABLE PROTEIN SOURCE

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Abstract Text:

Breeding grain legumes plays a crucial role in enhancing agrobiodiversity and promoting ecosystem services. By developing resilient and high-yielding varieties, breeders can improve food security while reducing environmental impacts. Grain legumes, such as chickpea, cowpea, faba bean, grasspea, lentil, and pea, contribute to sustainable agriculture by fixing atmospheric nitrogen, improving soil fertility, and reducing the need for synthetic fertilizers. Additionally, diverse legume crops support pollinators and soil microbial communities, promoting biodiversity.

INIAV is a partner in the project SPIN - Sustainable Protein (PRR-C05-i03-I-000192), coordinated by the Instituto Politécnico de Santarém (IPS/ESAS). One of the objectives of the project is to promote the value of grasspea (*Lathyrus sativus* L.) and chickpea (*Cicer arietinum* L.) varieties, reinforcing their resilience and adaptability to climate change as reliable sources of sustainable protein. An agronomic evaluation trial of chickpea varieties was established in the experimental fields of INIAV-Elvas. The trial included six varieties, three of which were developed by INIAV-Elvas and three provided by the partner Egocultum. The experimental design followed a randomized complete block scheme with three replications. The evaluation was performed on six traits: number of days to flowering and to maturity, flowering duration, plant height, 100 seed dry weight and seed yield. Additionally, the crude protein content of the chickpea seeds was determined, and the analysis also included seeds from four grasspea genotypes. Data were analysed by one-way ANOVA followed by Tukey's test.

The results highlight significant genetic variability among the evaluated varieties. Concerning the beginning of flowering, the earliest varieties reached this stage in just 97 days after sowing, while the latest ones required 112 days. Plant height ranged from 49.3 cm to 60.8 cm. Significant differences were observed in seed size, with the 100 seed dry weight ranging from 28.6 to 39.1 g. The yield of the six varieties varied between 1257 kg/ha and 2000 kg/ha. In this study, the Eldorado variety distinguished itself with the highest yield and the highest protein content in its seeds (22.7%).

With a higher protein content than chickpea seeds, grasspea emerges as a promising alternative for protein-rich diets. The analysed grasspea genotypes showed an average protein content close to 30%.

Next year, chickpea and grasspea varieties will be evaluated in more locations to analyse the genotype × environment interaction and identify the best-adapted varieties for each region.

NITRIC OXIDE-DRIVEN PROTEIN S-NITROSYLATION IN RESISTANCE RESPONSES TO POWDERY MILDEW

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Abstract Text:

Nitric oxide (NO) is a crucial signaling molecule in plants, influencing various physiological and defense-related processes. One of its key regulatory functions is through S-nitrosylation, a reversible post-translational modification that affects cysteine residues within proteins, modulating their activity. In mammals, S-nitrosylation has been extensively studied and linked to cellular processes such as redox regulation, apoptosis, ion channel modulation, and signal transduction. However, in plants, knowledge regarding NO-mediated signaling remains limited. Recent studies have demonstrated in vitro S-nitrosylation of plant proteins upon exposure to NO donors such as S-nitrosoglutathione, suggesting a significant role in plant defense responses.

Our research focuses on investigating the role of S-nitrosylation in barley (Hordeum vulgare) resistance against Blumeria graminis, a biotrophic fungal pathogen that targets epidermal cells. We previously identified a burst of NO production occurring between 12 and 16 hours post-inoculation in epidermal cells undergoing the hypersensitive response (HR), highlighting its potential role in defense signaling. In this study, we provide evidence for in vivo S-nitrosylation of proteins in response to pathogen attack, linking this modification to early defense mechanisms in barley.

To examine S-nitrosylation events, proteins were extracted from whole barley leaves and isolated epidermal cells of the resistant barley genotype P01, which carries the Mla1 gene conferring HR-based resistance. Samples were collected 15–16 hours after inoculation with B. graminis. Using the biotin-switch method, we specifically labeled S-nitrosylated proteins by reducing S-nitrosothiols with ascorbate and tagging them with a biotin moiety. Subsequent protein separation by one-dimensional (1D) acrylamide gel electrophoresis, followed by transfer to nitrocellulose membranes and probing with anti-biotin antibodies, allowed us to visualize S-nitrosylation patterns.

While no significant differences were observed in total leaf extracts, likely due to dilution effects from non-infected tissues, analysis of isolated epidermal strips revealed distinct pathogen-induced modifications in S-nitrosylated protein profiles. To further characterize these proteins, affinity purification using streptavidin-agarose beads was performed, followed by tryptic digestion and mass spectrometry analysis.

This approach enabled the identification of several key proteins undergoing S-nitrosylation during pathogen attack, including members of the peroxidase superfamily, PATATIN-like protein 5, chitinase, lipase and glutathione S-transferase family proteins. These proteins are

well known for their roles in plant defense, contributing to oxidative stress regulation, pathogen recognition, and detoxification processes. To validate the functional relevance of these modifications, we conducted enzymatic bioassays to assess changes in the activity of the identified proteins upon infection.

These findings provide new insights into the molecular mechanisms underlying NO-mediated plant immunity. This research paves the way for targeted breeding strategies and biotechnological approaches aimed at improving crop resilience while reducing reliance on chemical fungicides, contributing to more sustainable agriculture.

IDENTIFYING GENOME REGIONS ASSOCIATED WITH SPECIFIC RESISTANCE MECHANISMS TO CROWN RUST IN OAT

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Abstract Text:

Oat (Avena sativa) is an important cereal crop cultivated globally, valued for its nutritional benefits, adaptability, and versatility in food, feed, and industrial applications. In the Mediterranean region, oat production faces numerous environmental stresses, among which crown rust (Puccinia coronata f. sp. avenae) stands out as one of the most devastating diseases. This fungal pathogen significantly reduces yield and grain quality, threatening oat cultivation in regions with favorable conditions for disease development. Given the high prevalence and economic impact of crown rust, the development of resistant oat varieties is a priority. However, traditional breeding efforts often fall short due to the rapid evolution of new pathogen races that can overcome genetic resistance. To combat this challenge, the identification of new resistance sources and a deeper understanding of specific defense mechanisms at the molecular level are essential for more durable and effective breeding strategies.

Molecular marker-assisted selection (MAS) has revolutionized crop breeding by enabling the identification of genetic loci associated with disease resistance. However, most studies have focused on overall resistance rather than on the specific resistance mechanisms. The ability to identify genome regions linked to distinct defense responses, such as papilla formation or hypersensitive response would provide a significant advancement in breeding for rust resistance. Despite its importance, this approach has remained largely unexplored due to the extensive labor required for microscopic evaluation of large-scale germplasm collections. To overcome this limitation we are developing models to estimate microscopic resistance phenotypes for moderately or highly susceptible genotypes that allow us to assign values to these accessions in GWAS, while evaluating histologically resistance genotypes to ensure the highest precision in identifying resistance-associated genomic regions. The first models have shown very promising results, with an R^2 value around 0.7, demonstrating their strong fit to the data and potential for effective application in resistance assessment.

The identification of resistance loci tied to specific mechanisms could lead to the discovery of novel genes and pathways involved in plant resistance. Additionally, applying this knowledge in breeding programs will contribute to the development of more resilient oat cultivars, with durable resistance, reducing reliance on chemical fungicides and promoting sustainable agricultural practices.

DISSECTING THE ROLE OF AVENANTHRAMIDES IN RESISTANCE RESPONSES TO POWDERY MILDEW IN OATS

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Abstract Text:

Avenanthramides (AVNs) are a unique class of polyphenolic compounds found exclusively in oats, known for their antioxidant and anti-inflammatory properties, which contribute to both oat quality and human health benefits. While these bioactive compounds are well-documented for their role as antioxidant, their specific function in protecting oats against powdery mildew (Blumeria graminis f. sp. avenae) remains largely underexplored. Given the economic and agronomic importance of developing disease-resistant oat varieties, understanding the role of AVN in disease resistance responses is crucial to ensuring future food security programs.

This study aims to analyze different resistance responses at the cellular level in five oat genotypes—Orblanche, Saia, Selma, Cory, and Charming— differing in the resistance response to powdery mildew. We assessed key cellular resistance mechanisms, including papillae formation and programmed cell death, in response to pathogen invasion. Additionally, we quantified AVN production in healthy and infected plants to evaluate its contribution to resistance. Fluorescence microscopy was employed to visualize cellular responses, while high-performance liquid chromatography (HPLC) was used to determine AVN concentrations in oat leaves. By integrating these techniques, we aimed to establish a correlation between cellular resistance responses and AVN content across different oat genotypes.

The results revealed significant variation in resistance mechanisms among the five oat genotypes. Selma exhibited the highest susceptibility, allowing substantial pathogen development, whereas Saia demonstrated strong penetration resistance, primarily through papillae formation. In contrast, Cory, Charming, and Orblanche displayed both penetration resistance and the hypersensitive response (HR) respectively. The AVN analysis indicated that Saia had constitutively high levels of avenanthramide C (AVN-C), while inoculation with powdery mildew triggered an increase in AVN-A and AVN-B levels in all resistant genotypes. Further statistical analyses revealed a positive correlation between AVN levels and papillae formation.

These findings suggest that AVNs may contribute to early defense responses in resistant genotypes, potentially reinforcing cell walls and limiting pathogen penetration. The interplay between AVNs and different resistance mechanisms highlights the complexity of oat defense

strategies against powdery mildew. This research provides valuable insights into plant-pathogen interactions and the role of secondary metabolites in disease resistance, paving the way for future advancements in oat breeding and disease management.

EFFECT OF WITHIN-CROP DIVERSITY AND FARMER SELECTION ON COMMON WHEAT YIELD, YIELD STABILITY AND GRAIN PROTEIN CONTENT IN NORWAY

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Abstract Text:

There is no Norwegian cereal breeding programme specifically for organic production. Since competitiveness against weeds is not prioritized by plant breeding programs, commercial varieties may not be optimal for organic farming. The objectives of this research were to test (1) whether populations can provide better yield and yield stability than pure lines under organic conditions, and (2) whether populations resulting from two different types of "farmer's mass selection" differ for yield or protein content. Additionally, we aimed to evaluate the general performance of varieties and breeding material to generate useful information for breeders, farmers, and rural extension services.

The evaluated spring wheat material included: (a) five recent and two old Norwegian varieties, (b) four Norwegian breeding lines, (c) four Norwegian breeding populations subjected to two types of "farmer's selection" over two years, namely, selection for kernel weight using air separation, and manual selection of good-looking spikes, (d) one Swedish landrace, (e) one pure line and four organic population varieties from Denmark, all selected for high baking quality and organic conditions. We multiplied all material in two locations in 2022 and then evaluated it in organic farmers' fields at four locations in south-eastern Norway in 2023 and 2024. We measured grain yield (0 % water content) and protein content (%). We tested if there were significant differences in mean value and stability of yield and protein content between (a) populations and pure lines, (b) populations bred in Norway and Denmark, (c) new and old pure lines, and (d) populations bred using kernel weight selection and spike selection. Stability was assessed using an Additive Main effects and Multiplicative Interaction (AMMI) model and calculated as Modified AMMI Stability Value (MASV).

Two trials in 2023 were heavily infested by weeds and had very low yields (0.5 t/ha on average). The average yield in the other trials was rather low, ranging from 0.9 to 1.9 t/ha. One trial in 2024 was not harvested because of very bad conditions. Thus, seven environments (location-year combinations) were included in the analyses, including two with very low yields. Both yield and protein content were strongly affected by the environment (explaining 77% of the variation in both traits). Overall, yield was more influenced by spatial effects (7 % of the variation) and genotype-by-environment interactions (GEI) (8 %) and less by genetic effects (5 %) than protein content (3 %, 4 % and 12 % explained by spatial effects, GEI and genetic effects, respectively). Among the Norwegian-bred entries, both populations

and pure lines exhibited similar mean yield and protein content, but populations showed significantly higher yield stability across environments than pure lines. Populations bred in Norway also showed greater yield stability than populations bred in Denmark, but they had lower mean protein content. The two older pure line cultivars outperformed the newer cultivars and breeding lines on average, achieving higher average yields and yield stability and similar protein content. Among the two "farmer's selection" methods, selecting for kernel weight resulted in more stable yields and higher protein content than spike selection.

One of the populations selected for good-looking spikes displayed the highest mean yield across trials (1.52 t/ha), significantly outperforming some of the other entries. This population also displayed high yield stability (MASV = 0.69), and a relatively high yield in the trials that were heavily infested by weeds, making it a promising candidate for organic farming. The protein content of this population was among the lowest of all the entries (13.5 %) although higher than the threshold of 12% that is considered as the minimum for industrial baking in Norway. It remains to be verified, however, whether its protein content remains sufficiently high in environments that are higher yielding than the currents ones.

In conclusion, our results support the hypothesis that genetically heterogeneous spring wheat material provides better yield stability under organic conditions than pure line material. On average, the selection of populations based on kernel weight resulted in better yield stability and protein content than spike-based selection. Moreover, under organic conditions, old pure line cultivars provided both better yields and better yield stability than modern pure line cultivars bred for conventional farming practices. We have identified some material that shows promise for use in organic farming.

DEVELOPMENT OF A QUANTITATIVE PEA NECROTIC YELLOW DWARF VIRUS (PNYDV) SCREENING SYSTEM FOR THE SELECTION OF RESISTANT PEA (PISUM SATIVUM L.) ACCESSIONS

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Abstract Text:

Pea (*Pisum sativum* L.) is a widely grown grain legume in temperate regions and contributes largely to protein rich food and feed and biological nitrogen fixation in the crop rotation. However, many biotic stresses, such as fungal and viral pathogens and insect pests are crucial constraints of successful pea production. Among virus diseases, pea enation mosaic virus 1 and 2 were the most prevalent viruses detected in pea crop in Germany, followed by pea necrotic yellow dwarf virus (PNYDV) and turnip yellows virus, which was also found in the surrounding non-legume weeds (Gafaar et al. 2020). PNYDV, an obligate aphid transmitted nanovirus, emerged in Central Europe only recently during the last 16 years (Grigoras, 2010). Its genome consists of at least eight circular single stranded DNAs individually encapsidated in small isometric virions that are exclusively transmitted by various aphid species (e.g. *Acyrthosiphon pisum* and *Aphis fabae*) in a persistent, circulative, non-propagative manner. In contrast to other viral diseases of pea, PNYDV leads to substantial yield reduction or even complete loss in highly epidemic years. Control of this virus is challenging particularly in organic agriculture, where insecticidal treatment against the aphid vector is very limited or not allowed. The selection and breeding of resistant pea varieties is therefore the most promising approach. We have developed and established a screening system for the selection of resistant lines by employing a newly developed quantitative PCR (qPCR) assay based on the DNA-S encoding for the capsid protein, for the differential assessment of the virus load between pea accessions upon inoculation with aphids carrying PNYDV. This screening was also useful of detection of the virus in the vector Acyrthosiphon pisum and normalization (delta delta Cq) was done with the simultaneous quantification of host-genes. Emphasis was also given to a simple DNA extraction system that allowed the processing of several hundreds of leaf samples in an economic manner and with a minimum hands-on time required. We have also tested different plant ages for inoculation and different time points for the analysis. This quantitative assessment will allow the identification of breeding lines able to limit or suppress the virus multiplication. Breeding lines will be selected based on qPCR assay and validated in the field. This novel screening approach can be translated to other obligate aphid transmitted virus in different crops and become an important selection tool for breeding and genomic analysis.

Reference:

Gaafar Yahya Z. A. , Herz Kerstin , Hartrick Jonas , Fletcher John , Blouin Arnaud G. , MacDiarmid Robin , Ziebell Heiko. 2020. Investigating the Pea Virome in Germany—Old Friends and New Players in the Field(s). Frontiers in Microbiology 11:583242. https://doi.org/10.3389/fmicb.2020.583242.

Grigoras, I., Gronenborn, B., & Vetten, H. J. (2010). First report of a nanovirus disease of pea in Germany. Plant Disease, 94(5), 642-642. https://doi.org/10.1094/PDIS-94-5-0642C.

Hataya, T. 2021. An Improved Method for the Extraction of Nucleic Acids from Plant Tissue without Grinding to Detect Plant Viruses and Viroids. Plants 2021, 10, 2683. https://doi.org/10.3390/plants10122683

PERFORMANCE OF BIRD'S-FOOT TREFOIL (LOTUS CORNICULATUS L.) AND RED CLOVER (TRIFOLIUM PRATENSE L.) IN MULTISPECIES LEYS

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Abstract Text:

Bird's-foot trefoil (*Lotus corniculatus* L.) is a valuable legume species known for its high forage quality and tolerance to challenging environmental conditions, including drought. It thrives in poor soils and enhances protein efficiency in livestock digestion, thereby boosting overall productivity. Its inclusion in multispecies leys contributes to improved pasture stability and long-term productivity. This study aimed to assess the performance of multispecies mixtures containing bird's-foot trefoil and red clover (*Trifolium pratense* L.). The study included the following factors: (1) grazing, forage, and universal grassland types, (2) two legume species, (3) six companion grass species, and (4) ternary and quaternary mixtures. The experiment evaluated the functional group dynamics and productivity of grass-legume mixtures over two years. Each mixture contained 50% legumes, consisting of bird's-foot trefoil and red clover. Four harvests were performed per season to assess yield and compositional changes. The results indicate that both grassland management type and legume species influenced their proportion within the mixture. Although red clover initially dominated all harvests, particularly in forage-oriented leys, bird's-foot trefoil gradually increased in proportion over time, especially in forage and universal mixtures. However, seasonal drought emerged as a key factor shaping mixture dynamics, significantly reducing legume presence. While bird's-foot trefoil exhibited better initial germination than red clover, its persistence was lower during the first year due to drought stress and strong competition from Festulolium. In the first harvests of 2023, red clover showed higher initial persistence than bird's-foot trefoil ($p < 0.05$), while in the fourth cut, it exhibited higher regrowth potential. By 2024, legume proportions remained highest in forage mixtures, with bird's-foot trefoil continuing to increase in share despite earlier drought-related setbacks. The gradual rise of bird's-foot trefoil suggests that mixtures with 50% legumes naturally optimize their composition over time, highlighting its adaptability under varying environmental conditions. Adverse spring and summer conditions impacted the dry matter yield (DMY) of bird's-foot trefoil and red clover similarly in both years. In the first year, the DMY of mixtures containing both species was high (~9000 kg ha^{-1}), however, in the second year, persistent dry conditions led to a significant yield reduction. In 2024, the DMY of red clover mixtures decreased 2.6-fold, while bird's-foot trefoil mixtures declined 2.9-fold compared to the previous year. Although the difference in reduction was not substantial, bird's-foot trefoil still maintained a relatively stable yield under adverse conditions, suggesting its potential for greater resilience. Given its increasing presence, long-term persistence, and beneficial traits such as drought tolerance, bird's-foot trefoil presents a promising solution for enhancing the

stability and productivity of multispecies leys, particularly in environments prone to seasonal drought. To maximize its benefits and minimize competition, it should be incorporated into simple mixtures with non-aggressive species.

DEVELOPMENT OF AN ASCOCHYTA BLIGHT SCREENING SYSTEM FOR THE SELECTION OF RESISTANT PEA (PISUM SATIVUM L.) ACCESSIONS

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Abstract Text:

The cultivation of pea (*Pisum sativum* L.) among other leguminous crops has become more and more important in respect to biological nitrogen fixation for sustainable cropping systems and as important plant-based protein source for human nutrition. However, pea production is challenged by many biotic stresses, such as fungal and viral pathogens and insect pests. Among fungal pathogens, the root-rot pathogenic species belonging to the complex causing the soil-borne legume fatique syndrome (e.g. Fusarium, Mycosphaerella, Phoma, and Aphanomyces sp.) are very important in terms of yield loss and are limiting the cultivation of pea in short crop rotation (Fuchs et al. 2014). However, equally or even more devastating are *Ascochyta pisi*, *Didymella pinodes*, *D. pinodella*, and *Phoma koolunga* contributing to the Ascochyta blight complex infecting leaves, stems, and later also pods and seeds (Tran et al. 2015). They are causing severe or even complete yield losses in pea production, particularly in wet growing seasons which favor the epidemic spread of the pathogens. Ascochyta blight is stubble-, air-, soil- and seed-borne, hence disease control includes certified seed production and fungicide applications. However, particularly in organic agriculture the latter is not available and disease resistant varieties are needed. But the selection of resistant pea varieties is challenged by the fact that the pathogen species contributing to the disease fluctuate across time and geographic locations. Hence pea genotypes might differ in their resistance or robustness against the ascochyta blight in function of the composition of the predominant pathogen species (Boros and Marcinkowska 2010). In collaboration with an organic pea breeder, we have established reproducible screening systems for selection of resistant pea lines using artificial inoculation. Main achievements are the isolation and identification of *Ascochyta/Didymella* strains which contribute most to Ascochyta blight under local conditions, and the development and establishment of a differential scoring scales of pea leaf or tendril symptoms caused by the different *Ascochyta/Didymella* species used for inoculation. For a higher throughput this was complemented with an in vitro screening system based on the inoculation of detached leaves with spore suspension of the pathogens. Some pea varieties were shown to produce less symptoms of leaf blotch in both the in vitro detached leaf assay as well as in inoculation assays in vivo on the whole plants. These screening systems are suitable and fundamental for phenotypic selection of resistant breeding lines under controlled conditions, i.e. independent of the disease pressure in the field. Moreover, it can be employed for identification of resistance genes using genome-wide association studies or genomic prediction approaches.

Reference:

Boros, L., & Marcinkowska, J. (2010). Assessment of selected pea genotypes reaction to Ascochyta blight under field conditions and the impact of disease severity on yield components. Journal of Agricultural Science, 2(3), 84. https://doi.org/10.5539/jas.v2n3p84

Fuchs, J. G., Thuerig, B., Brandhuber, R., Bruns, C., Finckh, M. R., Fließbach, A., ... & Tamm, L. (2014). Evaluation of the causes of legume yield depression syndrome using an improved diagnostic tool. Applied Soil Ecology, 79, 26-36. https://doi.org/10.1016/j.apsoil.2014.02.013.

Tran, H. S., You, M. P., Khan, T. N., & Barbetti, M. J. (2015). Relative host resistance to black spot disease in field pea (Pisum sativum) is determined by individual pathogens. Plant Disease, 99(5), 580-587. https://doi.org/10.1094/PDIS-06-14-0655-RE

INVESTIGATING RICE ADAPTATION TO DROUGHT AND SALT STRESS THROUGH LARGE-SCALE SCREENING AND GENETIC ANALYSIS

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Abstract Text:

Rice (Oryza sativa) is one of the most important staple crops worldwide, providing food for over half of the global population. However, its cultivation is increasingly threatened by abiotic stresses such as drought and soil salinity, both of which are exacerbated by climate change. Water scarcity and soil salinization are becoming major constraints for rice cultivation, particularly in Mediterranean and coastal regions, where salinity intrusion and unpredictable rainfall patterns are severely impacting yield stability. As rice is highly sensitive to both water deficit and salt stress, identifying tolerant genotypes is crucial for ensuring food security and sustainable production.

To address these challenges, within the Pheno.gen project we are investigating the genetic and physiological mechanisms underlying rice adaptation to abiotic stresses, focusing on both drought and salinity tolerance. This study integrates high-throughput phenotypic screening with molecular analyses to identify stress-resilient genotypes and genetic loci associated with stress responses.

For drought tolerance, we are conducting a large-scale screening of the NEURICE collection, which comprises 281 japonica accessions cultivated in Mediterranean regions. Here, we present preliminary data from accessions grown in a hydroponic system using Hoagland solution, either under standard conditions or exposed to 20% polyethylene glycol (PEG-6000), which induces osmotic stress by lowering the water potential of the growth medium. After seven days of treatment, phenotypic traits such as plant height, chlorophyll content, and relative water content (RWC) were measured to evaluate their response to stress. These parameters provide key insights into plant vigor and physiological adaptation under water-limiting conditions.

Beyond the identification of specific drought-tolerant varieties, this study aims to integrate phenotypic data with genotypic information from a large number of japonica accessions to perform a genome-wide association study (GWAS). This approach will enable the identification of genetic loci associated with water stress response, providing valuable information for future breeding programs through marker-assisted selection.

In parallel, we are investigating salinity tolerance using a population of introgression lines (ILs) derived from a cross between the salt-sensitive cultivar Vialone Nano and the wild rice

O. rufipogon (PI 347745), which has shown superior salt tolerance in previous studies. A BC3F4 IL population was developed using Vialone Nano as the recurrent parent, generating a valuable genetic resource for dissecting the genetic basis of salt tolerance. Here, we present preliminary results obtained from ILs grown hydroponically under control conditions or exposed to 80 mM NaCl, a concentration known to induce salt stress in rice.

Phenotypic responses were assessed through visual scoring (SES), morphometric measurements (root and shoot fresh and dry biomass, shoot/root biomass ratio, plant height), and physiological analyses (leaf water content and photosynthetic efficiency) to determine variations in stress tolerance. Analysis of the phenotypic data with respect to SNPs generated by low pass sequencing of the ILs is currently underway for the identification of wild rice loci possibly affecting salt tolerance.

By combining phenotypic, physiological, and molecular analyses, this research aims to improve our understanding of the genetic mechanisms underlying rice adaptation to water stress and salinity. The identification of tolerant genotypes and the associated genetic loci will provide essential tools for breeding programs focused on enhancing rice resilience to abiotic stresses.

Ultimately, this work contributes to the broader goal of developing climate-resilient rice varieties that can sustain production in increasingly unpredictable environments. The findings from this study will not only benefit breeding programs but also support policy decisions aimed at mitigating the impact of climate change on global rice production.

SETTING UP A PARTICIPATORY BREEDING PROGRAMME FOR OHMS WITHIN TWO REGIONAL ORGANIC COOPERATIVES

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Abstract Text:

In France, the organic seed sector is facing a number of challenges: (i) a lack of varieties adapted to organic farming and to diverse and changing environments, (ii) difficulty in accessing quality breeding seeds, (iii) an increase in the purchase price of these seeds, despite a context of low prices for organic products and (iv) a political challenge to improve farmers' seed autonomy. The new European regulation on organic farming, which opens up the possibility of marketing heterogeneous organic materials (OHM), offers the prospect of solutions to broaden the genetic basis available. However, to date, only one wheat OHM has been notified in France, and no actor seems to be positioning itself in this sector. This opening was nevertheless seen as an opportunity for two French 100% organic regional cooperatives, Cocebi and Biocer. They have joined forces to set up a seed production station, UBS, the first to produce 100% organic seed on this scale. For the past six years, they have been conducting a participatory research approach for the development of highly diversified wheat populations in collaboration with an INRAE research team. The aim is to assess the value of the heterogeneous populations currently being developed for notification as OHMs, and to design a sustainable participatory breeding approach involving motivated farmers, cooperative research and development teams and academic research partners, while devising a viable socio-economic organisation to support it. Three highly diverse composite cross populations (CCPs) were created in 2018 and 2019, each derived from six parents mainly landraces, chosen based on the expertise of the farmers, cooperative technicians and researchers. In addition to the three CCPs made up of a balanced contribution from all biparental crosses, and in order to leave room for farmers' creativity, the development process has been open and flexible, with the creation of three other populations made up of the most productive crosses and the multiplication of certain biparental crosses separately. From 2019-20 to 2024-25, these populations were multiplied, evaluated and selected on two to four farms and at the two cooperatives' experimental stations, i.e. a total of 26 site x year environments. The participatory dimension of the research was ensured by the coordination and support of an engineer at the interface between the cooperatives and the research, and the organisation of numerous remote meetings (6 to 10 / year) to decide collectively on protocols, methods, analyses and communication activities. In addition, trial visits, information webinars and open feedback and discussion meetings were organised. From the 45 initial crosses, after five years of multiplication, evaluation and selection, more than 30 populations have been developed and are curently tested for their interest as candidates OHM. Participatory selection has provided a great deal of flexibility in terms of methods and

has made it possible to combine selection between populations, evolutionary selection, intra-population mass selection and the assembly of new populations from families that have shown interesting performance under certain conditions. Several populations showed average performances similar to some commercial varieties, while others seemed promising in terms of adaptation to particular soil and climate conditions or farming practices. However, the unbalanced design across sites and over time due to the participatory process has so far made it difficult to obtain clear results on the specific adaptations of these populations. Moreover, the processors' (millers, bakers) lack of familiarity with these populations and their particular bread-making profile together with difficulties in the multiplication at a larger scale hinder the implementation of tests and the development of outlets. Over time, the strong participatory dimension has enabled the initial farmers to appropriate the breeding knowledge and techniques and to be able to continue this process of empowerment over seed within the cooperative. This offers the prospect of a new organisation for frugal, local and 100% organic breeding, providing a wide range of diversity, within these farmers' cooperatives and their seed station. While they have a great deal of in-house expertise in the production of high-quality organic seed, the question arises as to how far they should internalise the skills required for coordination and breeding research. Finally, discussions are underway on the organisation of the actors and the economically viable model for making OHM selection sustainable and extending it to other species.

WINTER LENTIL GENETIC RESOURCES FOR MIXED CROPPING IN GERMANY

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Abstract Text:

Lentils are one of the eldest crop plants and, compared with other legumes, most suitable and preferred for human consumption as a low-fat, high-protein and high-fibre pulse crop with relatively low contents of antinutritiva. In Germany lentils are currently a neglected crop, mainly because of their low yield potential of 0.6 – 1.2 t ha-1. They are grown spring sown on a very limited acreage in hilly Southern regions of Germany, and mainly in organic farming. Breeding of autumn-sown instead of spring-sown cultivars has been an approach in several crops to achieve higher yields resulting from the extended vegetative development and making better use of winter precipitation. For lentils, this approach has been suggested as well (Barrios et al. 2016). This requires sufficient frost tolerance and resistance to biotic stresses challenging during winters. Winter lentil cultivars have been released by the USDA (Mühlbauer & McPhee 2007) and in Turkey (Aydoğan et al. 2007). In Northern France landraces and regional cultivars with high winter hardiness (Lentillon rose d’hiver) are available.

During the winter 2021/22 the JKI in Quedlinburg started to grow lentil accessions of the IPK genebank by sowing in October. 10 - 15 % of the tested accessions survived at rates higher 70 % of the emerged plants, showing a potential to find winter hardy genotypes in genebank collections. We intensified this work 2023 by acquiring the project Winter Lens Genetic Resources (WiLGeR) with four partners collaborating in North Eastern, South Eastern and South Western Germany. North Eastern sites in Quedlinburg and Gatersleben experienced black frosts of -15 °C with freezing soil up to 20 cm depth in 2022/23 and 2023/24.

Each year about 100 accessions are tested for winter-hardiness and multiplied at each partner site. Of those 30 accessions selected by performance in the previous year are grown and multiplied at all four sites. These are also tested in pots, where freezing of soil resulting in severe frost stress occurs already during milder frost conditions. The other 70 are new accessions tested for the first time only on one site. Morphological and agronomic traits, especially those determining crop architecture in mixed cropping like growth habit, plant height, phenology, ramification, height of lowest pods are observed. About ten best performing accessions each year are grown in larger plots at three sites to determine the

yield potential in mixed cropping. Results for genebank accessions from 2021 to spring 2025 in Quedlinburg and from 2023 to spring 2025 for genebank accessions, standard cultivars and breeding material from the four collaborating sites are shown.

Lentils are prone to lodging. Especially under moist conditions, this leads to difficulties in harvesting and to the infestation of pods and seeds by molds. Thus in Germany it is usual to grow lentils in mixed culture with supporting crops, mostly spring sown cereals like barley and oats or false flax (*Camelina sativa* (L.)Cranz).

Winter durum wheat (cv. Sambadur), winter spelt wheat (cv. Zollernspelz), winter Einkorn (cv. Aquino), winter barley (cv. SU Hetti), winter linseed (cv. Apalache), winter turnip rape (cv. Finito) and false flax (cv. CCE44) have been tested as supporting crops in sowing densities of 7.5 - 50% in reference to the recommended density for the mono-crop with the winter hardy lentils Lentillon and Morton. The latter were sown with 400 seeds m-2. This experiment was established at three sites from late October to the first week of November 2023. Winter linseed and turnip rape were not winter hardy enough for the late sowing and not stable enough. Einkorn as well proved to be prone to lodging. Winter barley tends to be highly competitive.

Besides the stability and competitive traits of the supporting crop separability of the harvested grains from lentils is an important feature. Lentils are very easily separated from the very small seeds of false flax and the large spelts of spelt wheat, while separation of grains of durum wheat is quite difficult with common separating machines. Altogether, winter spelt wheat was identified as the most promising supporting crop for winter lentils. It provides good stability with moderate competition, is easy to separate from the harvested lentils and would localize lentil growing as mixed culture into a more suitable (lower fertility) position of the organic crop rotation.

Reference:

Aydoğan A, Sarker A, Aydin N, Küsmenoğlu I, Karagöz A, Erskine W (2007). Registration of ‘Kafkas’ Lentil, Journal of Plant Registrations, 1, 44.

Barrios A, Aparicio T, Rodriguez MJ, Perez de la Vega M, Caminero C (2016). Winter sowing of adapted lines as a potential yield increase strategy in lentil, Spanish Journal of Agricultural Research 14, 2, https://doi.org/10.5424/sjar/2016142-8092.

Muehlbauer FJ, McPhee KE (2007) Registration of ‘Morton’ Winter-hardy Lentil, Crop Science, 47, 438.

HYPERSPECTRAL REFLECTANCE, A POTENTIAL ALTERNATIVE IN HIGH-THROUGHPUT COMMON BEAN SEED QUALITY PHENOTYPING?

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Abstract Text:

So far, suboptimal breeding initiatives have been allocated for legume species, hampering the sustainability of legume-based farming systems (Rubiales et al. 2021), and their added value remains largely underexploited.

International cooperation among legume breeding actors, is a way to leveraging on genetic progress. One of the aims of the partnership established under the BELIS European project is to develop tools and methodologies for cost-effective breeding programmes in important legume traits, prioritized by breeders and other value chain relevant actors, such as consumers.

Consumers are presently more concerned with the nutritional value and taste of foods. Nevertheless, breeding for nutritional and organoleptic quality may be cumbersome and expensive.

Hyperspectral techniques are currently used to retrieve information concerning plant biophysical traits, predominantly targeting pigments, water, and nitrogen-protein contents, structural elements, and the leaf area index (Vergara-Diaz et al. 2020). Although not traditionally used in seed quality screening as near-infrared spectra, hyperspectral data could be also exploited to overcome nutritional and organoleptic quality breeding challenges by advancing high-throughput seed quality phenotyping.

In a collaborative effort under the BELIS project, Portuguese, Italian and Serbian colleagues have gathered a common bean (*Phaseolus vulgaris* L.) germplasm collection, representative of the respective national breeding diversity, for a ring test focusing on the development of joint spectroscopic based predictive models for quality related traits.

In an innovative approach, the full-range reflectance spectra (visible (VIS)-near-infrared (NIR)-short wave infrared (SWIR)) of common bean seeds, was recorded in this collection of 99 accessions using an ASD FieldSpec 4 high-resolution spectroradiometer. A Principal Component Analysis was performed, using the full range reflectance spectra, to summarize multivariate similarities among common bean accessions, and identify the most discriminant wave bands. To visualize the potential relations between the common bean spectral variation

and common bean geographical origin, seed size or coat colour, the previously obtained PCA biplots were coded accordingly.

The two first principal components explained a total of 93.9% of the spectral variability, with PC1 mostly contributed by SWIR wavebands, and PC2 largely determined by VIS wavebands centred at 525 nm. Extensive overlap of common bean accession from different origins was observed, with Portuguese accessions showing an intermediate spectral pattern, between Serbian and Italian. Nevertheless, a group of common bean accessions from all the different geographic origins clustered together apart from the rest of the accessions. Interestingly, within each geographical origin, accessions tend to group into three non-overlapping clusters that might be related to particular seed traits.

This work has highlighted the usefulness of this screening technique to get an initial overview of the separation among common bean breeding germplasm with respect to spectral performance and, more importantly, to provide evidence of the spectral variability within common bean diversity, opening the way for future nutritional and organoleptic quality non-destructive predictions.

Reference:

Rubiales D, Annicchiarico P, Vaz Patto MC and Julier B (2021). Legume breeding for the agroecological transition of global agri-food systems: A European perspective. Frontiers in Plant Science, 12, [782574]. https://doi.org/10.3389/fpls.2021.782574

Vergara-Diaz O, Vatter T, Kefauver SC, Obata T, Fernie AR, and Araus JL (2020). Assessing durum wheat ear and leaf metabolomes in the field through hyperspectral data. Plant Journal, 102, [615-630]. https://doi.org/10.1111/tpj.14636

NATIVE HERBACEOUS PLANTS FOR ECOLOGICAL RESTORATION OF BURNED AREAS IN PORTUGAL: FIRST STEPS TOWARDS THE VALORIZATION OF UNDERUSED GENETIC RESOURCES

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Abstract Text:

The restoration and conservation of mountain regions are crucial since they are biodiversity reservoirs, freshwater sources, and providers of important ecosystem services to the global population (UNEP & FAO, 2021).

Fire has long been an ecological factor that shapes Iberian ecosystems and plays a key role in landscape dynamics. In 2022, a major wildfire burned more than 22,000 hectares in the Serra da Estrela National Park (PNSE), one of Portugal's most valuable biodiversity reservoirs, causing significant landscape changes and exacerbating environmental degradation. In this context, the recovery of burned areas involves a series of actions aimed at restoring these areas to ensure the continuity of essential goods and services. This process is fundamental to maintaining the ecological balance in the affected areas and supporting the socio-economic well-being of local communities (ICNF, 2023).

Despite the various methods available for restoring burned areas, the use of native herbaceous plants remains largely unexplored. As a Nature-based Solution (NbS), these plants can play a key role in combating ecosystem degradation by enhancing soil stability, promoting biodiversity, and facilitating ecosystem recovery, making them a promising strategy for ecological restoration (Wittenberg & Shtober-Zisu, 2023). However, in Portugal, the availability of native herbaceous plants either in genetic resource banks or the market remains scarce, limiting their large-scale application, despite their significant ecological value.

The FLoRE project (S1/2.7/F0042), funded by INTERREG-SUDOE, aims to address this gap by promoting the use of native wild herbaceous species in restoration initiatives and contributing to biodiversity conservation and sustainability. Moreover, it provides a unique opportunity to identify, characterize, and select native herbaceous plants, making them a valuable resource for ecological restoration and commercialization.

As part of FLoRE's activities, restoration actions are underway in a wildfire-degraded area of the Municipality of Manteigas within the PNSE, one of the most severely affected regions by August 2022's wildfires. A pilot zone will be established to test the effectiveness of this NbS, in facilitating ecosystem restoration. To support this work, a floristic survey will be conducted in a selected area of the PNSE that hosts native herbaceous flora, identifying suitable species

for restoration, including harvesting, storage, and testing, as well as nursery practices promoting natural regeneration.

In addition to ecological restoration, the project offers a chance to stimulate the Portuguese native herbaceous plant market, which currently lacks both in supply and demand. By demonstrating their ecological and economic value, and encouraging local participation, FLoRE aims to improve biodiversity conservation and promote sustainable ecological restoration practices. Ultimately, this work will constitute the basis for breeding approaches towards the identification and selection of plant materials with potential to establish a sustainable framework for incorporating native herbaceous plants into ecological and economic systems, reinforcing their role in landscape restoration and biodiversity preservation.

Reference:

ICNF (2023). Complexo de incêndios do Parque Natural da Serra da Estrela e Regiões Limítrofes - Relatório de danos e recuperação pós-incêndio | Versão final. https://www.icnf.pt/api/file/doc/e3ca7020c4ecf9fb

UNEP, & FAO (2021). UN Ecosystem Restoration Playbook: a practical guide to healing the planet. Https://Www.Decadeonrestoration.Org/Publications/Ecosystem-Restoration-Playbook-Practical-Guide-Healing-Planet

Wittenberg, L., & Shtober-Zisu, N. (2023). Restoring fire-affected soils: The potential of nature-based solutions. Current Opinion in Environmental Science & Health, 36, 100520. https://doi.org/https://doi.org/10.1016/j.coesh.2023.100520

SUSTAINABLE AGROECOLOGICAL STRATEGIES FOR ORGANIC FARMING IN VEGETABLE GARDENS: SMALL SCALE COMPOSTING

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Abstract Text:

The HARVEST project is funded under the Recovery and Resilience Plan (PRR), which gathers 14 partners from whole country. Launched in early 2023, the project aims to Valorize the Family Gardens to Educate for a Healthy and Sustainable Mediterranean Diet. Under its implementation, HARVEST is promoting several actions to promote and strengthen low input and organic farming, agroecological methods and practices, with a particular focus on enrolment of local farmers, plant producers and population in multi-actor approach. These approaches seek mutual benefits for consumers, farmers, and the environment while fostering sustainable agricultural systems.

Small-scale family farming, which accounts for over 90% of agricultural holdings, supports many Portuguese families today (Candeias, 2021). A consumption model focusing on revitalizing local landraces, healthy food production systems, and short value chains will safeguard biodiversity, the environment, while safeguarding cultural heritage. To support the adoption of organic farming, composting agricultural waste (solid organic waste from the garden) to produce organic fertilizer represents an accessible and practical solution that small-scale growers can benefit from.

The research focuses on the assessment of the efficiency of the composting process for a small family farming, two compost bins (1000 L), made of alternating layers of goat manure and horticultural waste (1:2) retrieved from each garden, were installed in the Polytechnic Institute of Bragança (IPB) community gardens in Bragança, northeastern Portugal. The primary objective is to develop and optimize a composting process within urban gardens that produce organic fertilizer, enabling farmers to improve the health of their garden by utilizing waste and by-products at the end of their useful life cycle. This solution promotes the reduction of environmental inputs in agricultural operations, lowers associated activity costs, and enables the efficient reuse of agricultural waste.

Since their assembly on November 19, 2024, the composting bins have been monitored through sampling and physicochemical analysis. Sampling was conducted weekly for the first month and biweekly for the second month. In the third month, one sampling was performed, followed by bimonthly samplings until the end of the process. The physicochemical properties measured included temperature, humidity, density, pH, electric conductivity (EC), organic matter (OM), weight loss, ash content, carbon-to-nitrogen ratio (C/N), and germination index (GI) to evaluate biological activity, the evolution of organic compounds, and the reduction of phytotoxicity in the compost. While the process is progressing, we

expect that compost produced under the scope of the HARVEST project will be used by the farmers of IPB's community farming. Also, we will provide a manual of good practices for implementing composting. The conclusions drawn from this research will also be shared with the horticultural community through a training session, enabling each participant to correctly carry out the process and independently promote this agro-sustainable practice.

Reference:

Candeias S (2021). Jornadas da Agricultura Familiar. AFAVEL – Agricultura Familiar e Valorização Territorial Sustentável em Contexto de Alterações Climáticas. Estado da arte Estatuto da Agricultura Familiar. Direção-Geral de Agricultura e Desenvolvimento Rural. https://www.dgadr.gov.pt/images/af/minutas/Estado_arte_EAF_Jornadas_AFAVEL_18.02.2021.pdf.

AGRONOMIC PERFORMANCE OF SPRING BARLEY COMPOSITE CROSS POPULATIONS IN ORGANIC FARMING SYSTEMS IN POLAND.

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Abstract Text:

There are various methods to increase genetic diversity in cereals that can stabilize the crop performance and buffer against environmental fluctuations, especially in organic or low input cropping systems.

One way to increase genetic diversity of the crop is to use segregating composite cross populations (CCPs). To do so, seven high-performing spring barley commercial cultivars were crossed together in a complete half-diallel. As a result, seven CCPs were produced by bulking F2 seeds from the individual crosses and multiplied them for 5-6 consecutive years in diverse sites. In the years 2016, 2017, 2018 and 2019, all CCPs and their parental cultivars were multiplied and observed in few sites all over the country. In each year, CCP seed that had been harvested in the preceding cropping year, was used to set-up next multiplications, thereby allowing for potential evolutionary adaptation of the genetically heterogeneous materials to site-specific cropping conditions.

In the growing seasons 2022 and 2023, all developed CCPs and their parents were tested under organic growing conditions, using RCBD block design at Plant Breeding and Accclimatization Institute, Radzików. Plot size used was 15 - 16 m2.

Assessements of main morphological and agronomic parameters and grain quality parameters were carried out on a plot basis on each (CCPs and their parental cultivars). In addition to grain yield level (t *ha−1, at 15% moisture content), other agronomic characters and yield components were assed. Spring barley CCPs, and their parental cultivars were compared for various attributes such as grain yield together with important agronomic and quality parameters. Different statistical indices were used for experimental data processing. .

Where spring barley disease pressure was high, the disease infestation of the parental lines was generally greater than that in the populations. Especially, under organic conditions, when no fungicides were applied, the spring barley CCPs were always considerably healthier, presumably due to their inherited diversity in disease resistance.

We can therefore conclude, that introducing higher diversity of crops in the form of CCP is an appropriate way to improve overall adaptation and stability of spring barley in organic and low-input systems in diverse environmental conditions.

Summarizing, crop diversification by growing mixtures or CCPs may be considered as an alternative or supplementary way to achieve higher and more stable crop productivity, especially in the face of climate change.

PRINCIPLES AND PRACTICES OF ORGANIC ONION BREEDING AND SEED PRODUCTION, TOOLS FOR A MULTIACTOR APPROACH

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Abstract Text:

Onion production in Portugal decreased 23% in area from 1979 ha (2021) to 1518 ha (2023) and 8,9% in yield from 66 148 Mg (2021) to 60 261 Mg (2023) (INE, 2024). Onion is the third vegetable more consumed with 13 kg per capita per year (Rodrigues et al, 2011). Research has been done in the impact of weather conditions and post-harvest conditions on the quality characteristics of local varieties in Portugal, and concluded that a great variability in chemical composition in mainly due to genetic factors (Rodrigues et al 2003) and that the latitude seems to be an important factor for the chemical profile, which can contribute to geographical protection of food and simultaneously benefiting both consumers and farmers (Fernandes et al, 2020). Therefore, the promotion of plant breeding tools are of paramount importance to boost the production of the crop at national level, stressing the importance of traditional varieties where Participatory Plant Breeding can have a play to role. The 2024 National catalogue indicates 30 varieties from which 18 were hybrids and three of them were traditional varieties (Vermelha de Povairão, Setúbal Portuguesa, and Garrafal). Of these 30 varieties, 13 are ‘short day ‘varieties because their bulbs need 12 hours of light a day to grow. 4 varieties are instead ‘intermediate day’ that need 12-14 hours of light a day to grow. And finally, 13 are late varieties or also called ‘long day’ because they need 14-16 hours of light a day to grow. For this reason, while the former are preferably sown in autumn, for the others it is better to wait until early spring, when the hours of light increase considerably. The characteristics that are most sought after in onions for their improvement concern various aspects such as adaptability to the cultivation area, shelf life, size, improvement of the dormancy level of the bulbs and resistance to diseases (especially downy mildew caused by the fungus Peronospora destructor) which would allow a lower use of pesticides for better protection of the environment and health.

The aims of this work intended to both translate into Portuguese, a tool for onion breeding produced by Organic Seed Alliance (Organic Seed Alliance, 2018) and organize a technical itinerary for onion breeding and seed production for Portugal. The translation of “Onion Seed Production: Quick Reference” (Organic Seed Alliance, 2018), published by the Organic Seed Alliance were followed by the search of academic references plus other sources (e.g., GRIN, ECPGR, FAO/IPGRI, DGAV and INE, onion descriptors, statistics, internet, national varieties’ catalogue). The translation and the researched sources allowed the production of a

technical onion itinerary of breeding and seed production that will be a contribution to farmers, students and technicians from Portuguese speaking countries.

Reference:

Instituto Nacional de Estatística - Estatísticas Agrícolas : 2023. Lisboa : INE, 2024. available at www: . ISSN 0079-4139. ISBN 978-989-25-0680-7

Fernandes S., Gois A, Mendes F, Perestrelo R, Medina S, Câmara JS. (2020). Typicality Assessment of Onions (Allium cepa) from Different Geographical Regions Based on the Volatile Signature and Chemometric Tools. Foods. 9(3):375. https://doi.org/10.3390/foods9030375

Peters, S., Foster, P. (2017). California Organic Onion Variety Trials 2015-2016. Organic Seed Alliance, Port Townsend, WA. https://seedalliance.org/publications/california-organic-onion-variety-trial-2015-2016/

Organic Seed Alliance (2018). Onion Seed Production: Quick Reference. available at https://seedalliance.org/publications/onion-seed-production-quick-reference/.

Rodrigues, A., Fogliano V., Graziani G., Mendes S., Vale A., Goncalves, C. (2003). Nutritional value of onion regional varieties in Northwest Portugal. Electron J Environ Agric Food Chem. 2., https://www.researchgate.net/publication/256402471_Nutritional_value_of_onion_regional_varieties_in_Northwest_Portugal

Rodrigues A.S., Pérez-Gregorio M.R., García-Falcón M.S., Simal-Gándara J., Almeida D.P.F. (2011). Effect of meteorological conditions on antioxidant flavonoids in Portuguese cultivars of white and red onions,Food Chemistry,Volume 124, Issue 1, Pages 303-308, ISSN 0308-8146, https://doi.org/10.1016/j.foodchem.2010.06.037.

HOW TO BREED TOMATOES AND CARROTS FOR ORGANIC AGRICULTURE AND THE CURRENT PORTUGUESE BREEDING INITIATIVES

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Abstract Text:

The articles take into account the importance of the breeding work for diversity conservation on tomatoes (Solanum lycopersicum) and carrots (Daucus carota), going into detail about setting breeding goals, explaining the reproductive biology of the species, detailing plant breeding methods and timelines, and suggesting techniques that may be used for each species. Tomato production in Portugal accounted for 1 640 781 Mg in 2024, a number that has been moderately steady for the last decade (IFAP, 2024). As for carrots, data from 2021-2023 shows a spike in production in 2021 (140 873 Mg), with a drop in production (100 057 Mg) in 2022, followed by a significant recovery in production in 2023 (126 175 Mg (INE, 2024). In 2023, industrial tomatoes and carrots figured as two out of five crops with the biggest production increase in Portugal, registering a 37% and 26% increase, respectively (INE, 2024). Therefore, since both tomatoes and carrots are staple foods in the human diet, showing a strong presence as fresh market produce and being important for the preserving industry, the need to understand how to breed new varieties well suited to different needs emerges as essential. Tomatoes are a great species for breeding, not only because they are a self-pollinated crop species that produces a prolific amount of seeds, but also because there are many varieties for the breeder to work with. As it is, tomatoes are presently bred for specific markets and the OSA's approach ensures the incorporation of a great degree of genetic diversity in one's breeding work. The article gathers a plethora of essential information for the breeder, such as detailed agronomic traits, defensive traits, and fruit quality, descriptions of how to source germplasm, the species' reproductive biology, pollination techniques and two breeding methods (OSA method and Pedigree method) with a breeding timeline. Carrots are a relevant market crop worldwide and nutritionally important vegetable as an everyday staple of the human diet. There are dozens of market types of carrots, and even though it was mostly used for cooking in the past, nowadays it is popular as a fresh market crop sold with the tops intact. OSA's article explains simple methods for developing an open-pollination carrot variety suited to serve farmer breeders and independent seed companies, thus helping select a variety for different climates and cultural needs. The article describes useful information for the breeder such as breeding goals, carrots' reproductive biology, plant breeding techniques (like strain cross), desired traits, and how to source germplasm. Since the production of carrot seeds on the farm is usually done across two seasons, the article's provided timeline via two approaches (mass selection and family selection) emerges as a helpful tool for the breeder. Since carrots and

tomatoes are key ingredients in the Mediterranean diet, the breeding and production of seeds from these species in Portugal arise as a potentially lucrative market for the country. It is possible to identify some varieties of each crop in Portuguese markets, curated for different finalities and/or produced under different conditions, thus creating space for different breeding programs for tomatoes and carrots. Innovative breeding initiatives, such as those developed by farmers and educational institutions, aim to preserve these species' diversity. Hence, the translation of OSA's articles (Navazio, 2014; McKenzie, 2014) to Portuguese complemented by academic sources, data from GRIN Global, ECPGR, FAO/IPGRI, DGAV and INE, will enable the creation of a technical tomatoes and carrots breeding and seed production itinerary. This could potentially influence breeders, farmers, and students to whom the information can become easily available and understandable, thus spreading organic breeding knowledge and hopefully entrusting the conservation of diversity to Portuguese-speaking countries.

Reference:

John Navazio (2014). How to breed carrots for organic agriculture. Organic Seed Alliance. www.seedalliance.org

Laurie McKenzie (2014). How to Breed Tomatoes for Organic Agriculture. www.seedalliance.org

IFAP (2024). Setor do Tomate. https://www.ifap.pt/portal/estatisticas-setor-do-tomate

INE - Statistics Portugal (2024). Estatísticas Agrícolas - 2023 https://www.ine.pt/xportal/xmain?xpid=INE&xpgid=ine_publicacoes&PUBLICACOESpub_boui=439500127&PUBLICACOESmodo=2

EVALUATING PLANT GROWTH-PROMOTING BACTERIA (PGPB) ASSOCIATION IN ANCIENT AND MODERN RICE VARIETIES

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Abstract Text:

Rice (Oryza sativa) is still one of the most important cereals that accounts for more than 50% of the world's need in food supplies. Its cultivation is currently demanding in terms of chemicals to deal with the biotic and abiotic environmental stressing conditions. Rice domestication and the selection of new high-yielding varieties led to a continuous loss of biodiversity which impacted the rice ability to adapt to several abiotic stress factors, and to exploit the potential benefits coming from a positive association with soil microbiota.

Our research project aims to evaluate the characteristics of different old and modern rice varieties selected within a germplasm collection which includes about 300 genotyped varieties of Oryza sativa L. ssp. japonica released in 100 years of rice breeding in order to investigate the impact of historical rice breeding on the ability to associate with selected root endophytic bacteria (plant growth - promoting bacteria or PGPB).

The selected strains have been shown to improve rice growth, promoting nitrogen fixation and producing phytohormones that sustain plant development, and hence could represent an opportunity for a more sustainable agriculture, hinting at a reduction in the use of phytochemicals and fertilizers.

To verify the possible effects that recent breeding had on the rice aptitude to associate with PGPB, a pool of 40 traditional and recent rice varieties was selected and we screened them for their ability to associate with strains of PGPB, known to promote and sustain rice growth. We tested rice association with the combination of two different endophytic PGPB strains, RCA25 - Kosakonia sacchari and RCA24 - Herbaspirillum huttiense by applying a specific protocol. Phenotypic results were obtained by counting the number of colony forming units (CFUs) per grams of treated roots.

Both the four ancient and recent varieties that showed the best aptitude in establishing a positive association with RCA25 and RCA24 were then inoculated and grown in soil pots to measure and evaluate the differences in morpho - physiological characteristics and yield parameters, comparing the results obtained to those of the same non inoculated plants.

Finally, seeds were evaluated for their metabolomic composition, to assess the effect of PGPB on rice nutritional composition.

EVALUATING GREEK TOMATO LANDRACES AND HYBRIDS IN LOW-INPUT FARMING SYSTEM FOR PRODUCTIVITY AND NUTRITIONAL VALUE

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Abstract Text:

Nowadays, the cultivation of tomato (*Solanum lycopersicum*) predominantly depends on F_1 hybrids, which are developed and widely utilized in high-input agricultural systems. These systems feature intensive irrigation, widespread use of fertilizers and different crop protection strategies to promote optimal growth and productivity. It is widely recognized that F_1 hybrids serve as superior genetic materials with high yield, consistent fruit quality and uniformity. However, there is an urgent need to identify and develop genetic material capable of performing efficiently in low-input systems, helping to reduce both the environmental footprint of agriculture and cost of production. A valuable tool to achieve this goal could be the utilization of traditional cultivars. More specifically, tomato landraces are characterized by adaptability to low-input conditions, a fact that makes them an ideal genetic resource for the implementation of sustainable management systems and a potential solution to the challenges posed by climate change.

This work is part of a broader breeding program focused on identifying and developing genetic materials that can thrive under low-input conditions, particularly regarding yield potential and nutritional value. For this reason, we selected three out of a selection of forty-five landraces, which serve as a valuable source of genes well-adapted to low-input conditions through natural selection, to develop pure lines or F_1 hybrids derived from these traditional cultivars. More specifically, in the present work, three tomato landraces (Kardia vodiou, Pantaroza-pink, Lemonati), two hybrids created after the combination of these landraces (Kardia vodiou x Pantaroza-pink F_1, Kardia vodiou x Lemonati F_1) and one commercial hybrid (control: Formula F_1) were evaluated in a greenhouse under a low-input farming system. The first trait that was examined was the yield, as it is a crucial characteristic in tomato cultivation, because it is the second most consumed vegetable crop after potato, a fact that highlights its global significance. In terms of productive potential, the evaluated components were the yield in g/plant, the number of fruits/plant, and the average fruit weight. In addition, tomatoes are a rich source of essential nutrients, including vitamin C and antioxidants like lycopene and minerals, that contribute to a healthy diet, so in terms of

nutritional value, pH, total soluble solids and carotenoids were evaluated with the help of pH meter, refractometer and HPLC, respectively. Finally, the remarkable quality of landrace “Kardia vodiou” fruits (e.g. lycopene content: 24.14 mg/100 g fresh plant material) and the high production of the hybrid “Kardia vodiou x Pantaroza-pink F_1” (3143.06 g/plant) under a low-input system confirm the proposal that local tomato varieties can be crucial to sustainable agriculture. These findings highlight the potential of traditional tomato cultivars as valuable genetic resources, from which pure lines can be developed through mild intra-varietal breeding, along with F_1 hybrids that can be used in breeding programs, offering a sustainable alternative to conventional hybrids while maintaining high productivity and superior fruit quality in low-input systems.

EXPLOITATION THE ROOT PHENOTYPING TO SELECT COWPEA DROUGHT TOLERANT ACCESSIONS

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Abstract Text:

Climate change has significantly increased plant stress levels, with drought being one of the most critical abiotic stresses limiting crop productivity. Different mechanisms have been developed by plants for adaption and survival to drought periods. Root system architecture (RSA) plays a crucial role in drought adaptation; however, it remains an understudied trait. Phenotyping studies can help our understanding of crops ecophysiology and abiotic stress resilience by establishing synergisms between root architecture and drought resilience. Cowpea (*Vigna unguiculata* L. Walp.) has emerged as a promising short-cycle, warm-season multipurpose crop with a high capacity to fix atmospheric nitrogen, contributing to soil health. Additionally, its high protein content and drought resilience make it a valuable grain legume crop.

Our objective was to develop and implement a simple and cost-effective root phenotyping methodology to select cowpea accessions with resilience to drought stress. Furthermore, this study aimed the identification of drought-responsive genes.

A total of 24 cowpea accessions were grown semi-hydroponically in germination paper pouches under control (water) and drought stress (PEG; -1,5 bars) conditions for eight days under a 16h/8h (25 ± 1°C). Drought stress condition was assessed through lipid peroxidation by malondialdehyde (MDA) content at the eighth day of stress and root images were acquired, pre-processed and analysed using the RootNav to extract key parameters, including total length of the root system, average length of all roots, average length of lateral roots, lateral root number and the length of primary root.

Statistical analysis revealed significant differences among accessions for all the parameters, except average of root length and lateral root length. Drought stress significantly affected all the root growth parameters, while accession × treatment interactions were significant only for average root length. MDA determination allowed to prove that genotypes were in stress, showing differences between the accessions suggesting several levels of drought tolerance. The integrate analysis from the root and MDA parameters allowed the selection of six accessions (Vu_4, Vu_6, Vu_15, Vu_17, Bambey 21 and IT93K-503-1), with different levels of drought resilience. These accessions were used for gene expression studies. A total of ten drought-related genes were studied, with three (*VuCPRD12*, *VuDREB2*, and *VuHsp17.7*)

showing significant differential expression under drought stress and were used to qPCR analysis. These genes were positively regulated under drought stress conditions.

This study allowed to integrate innovative technology (digital imaging), biochemical and molecular techniques contributing for the identification of cowpea accessions resilient to drought stress. These results can supply data to breeding programs focused on improving drought resilience in grain legumes.

BIOCHEMICAL CHARACTERIZATION OF 12 GRAPEVINE VARIETIES IN THE UPPER DOURO REGION

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Abstract Text:

Vitis vinifera (grapevine) is one of the most cultivated crops in Portugal and worldwide, playing a pivotal role in the Mediterranean countries' economies. However, this region has increasingly face extreme weather events, such as heat waves, water scarcity, and soil degradation, driven by climate change. These abiotic stresses negatively impact plant growth, lead to poor development, reduce yield, and lower crops quality.

Exploring grapevine varietal diversity can address these challenges by identifying the most promising genotypes to cope with both biotic and abiotic stresses in different environments. This strategy will allow the use of traditional varieties that can guarantee a historical mark and add value to top quality wines. Our study's main objective was to characterize the lipid peroxidation, polyphenolic content and antioxidant capacity of different grapevines varieties at different phenological stages.

To achieve this goal, we examined 12 different varieties ('Alicante Bouschet', 'Aragonez', 'Donzelinho Tinto', 'Malvasia Preta', 'Mourisco de Semente', 'Tinta Barroca', 'Tinto Cão', 'Touriga Fêmea', 'Touriga Franca', 'Touriga Nacional', 'Trincadeira' and 'Vinhão') grown in the Upper Douro sub-region from Douro Demarcated Region. Well-developed leaves were collected in two different phenological stages (veraison and maturity) throughout the 2023 growing season. Polyphenolic contents were determined through the evaluation of total phenolic, flavonoids and ortho-diphenols contents, as well as the in vitro antioxidant capacity using DPPH (2,2-diphenyl-1-picrylhydrazyl), ABTS (2,2'-azino-bis(3-ethylbenzothiazoline-6-sulfonic acid)) and FRAP (ferric ion reducing antioxidant potential) assays. Additionally, lipid peroxidation was measured using thiobarbituric acid reactive substances (TBARS) content.

In general, significant differences ($p < 0.05$) were observed between varieties and phenological stages for all the evaluated parameters. Polyphenolic contents and antioxidant capacity assays and lipidic peroxidation decreased in the maturation stage comparatively to veraison, except for the varieties 'Donzelinho Tinto' and 'Touriga Fêmea' that presented an increase for polyphenolic content and antioxidant capacity parameters. In general, in both

phenological stages, the variety 'Mourisco de Semente' revealed the highest values for polyphenolic content parameters and DPPH and FRAP assays, while the varieties 'Alicante Bouschet' and 'Tinta Roriz' presented the highest values for ABTS assay. In conclusion, our study showed significant differences between varieties revealing some with high adaptability to the Upper Douro climatic conditions.

PRINCIPLES AND PRATICES OF ORGANIC BEET BREEDING AND SEED PRODUCTION TOOLS FOR A MULTIACTOR APPROACH

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Abstract Text:

Beta vulgaris L., better known as beet, is a root vegetable member of Chenopodiaceae family and is among the 10 most powerful antioxidant vegetables. Both the roots and leaves of the plant are edible and, due to their high nutrient content, mineral salts, vitamins and carbohydrates, they offer valuable medicinal properties such as analgesic, antioxidant, antimicrobial, anti-inflammatory, antiviral, anti-migraine, antihypertensive and antihyperglycemic. In Portugal, beet is typically used in salads or soups and is a fundamental element in a healthy diet. Plant breeding, when diversity exist, can increase quality, productivity as well as making the crop more resilient to climate change and to pests and diseases, contributing for highest nutritional quality of products and to climate change (Rehman et al, 2024). This work aims to both translate into Portuguese, a tool for beet breeding by Organic Seed Alliance and conduct a technical itinerary for beet breeding and seed production in Portugal The translation and adaptation of the papers related with the Beet Seed production (Navazio et al, 2010, OSA 2018) published by Organic Seed Alliance will be complemented by academic sources and data from GRIN Global, ECPGR, FAO/IPGRI, DGAV and INE. This will enable the creation of a technical beet breeding and seed production itinerary that will be useful to farmers, students, and technicians from Portuguese-speaking nations who wish to begin their breeding efforts on beet. Recognizing the importance of beet in our country and in our diet.

Reference:

Navazio, J., Colley, M., Zyskowski, J. (2010). Principles and Pratices of Organic Beet Seed Production in the Pacific Northwest https://seedalliance.org/publications/principles-practices-organic-beet-seed-production-pacific-northwest/

Rehman, S., Mufti, I.U., Ain, Q.U., Ijaz, B. (2024). Bioactive Compounds and Biological Activities of Red Beet (Beta vulgaris L.). https://doi.org/10.1007/978-3-031-44746-4_42

Skyros Congressos (2024). VI EUCARPIA Conference on breeding to meet environmental and societal challenges. https://skyros-congressos.pt/eucarpia2025/index.html

PARTICIPATORY DEVELOPMENT OF ORGANIC HETEROGENEOUS MATERIALS IN TOMATO IN SPAIN AND PORTUGAL: SPECIFIC ADAPTATIONS AND OPPORTUNITIES FOR WIDE ADAPTATION

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Abstract Text:

Climate change is forcing tomato producers, technicians and breeders to face agroclimatic risks, working towards a more diverse and resilient farming sector. To this regard, organic heterogeneous materials or OHMs are plant populations bred for organic farming, quite homogeneous for appearance in many traits, but also preserving certain underlying genetic at the same time, including genes that might offer adaptative response to a changing climate. OHMs are usually obtained by crossing several varieties, followed by mass selection under cross pollination conditions. In this study, a composite cross population obtained by crossing 4 tomato landraces (COMAV-UPV seedbank), was first evaluated and mass selected in 2023 spring-summer season open field, under Mediterranean organic farming conditions (Valencia). Then, seed lots of the offspring were shared for double evaluation in 2024 in two different organic conditions: i) Valencia (again spring-summer 2024 open field Mediterranean) and ii) Coimbra (Portugal, under agroforestry conditions). Yield per plant and fruit weight were the main traits evaluated.

Yield in Valencia open field were considerably higher on average than in Coimbra under agroforestry (1.15 kg/plant vs. 0.25 kg/plant), although the variation still present at this stage enabled the identification of plants which reached 500-600 g/plant. Fruit weight averages were not so different among both conditions (75 g), and a high degree of variation was observed in both conditions, with several individuals reaching >150 g/fruit. The high variation found enabled the selection of specifically adapted individuals to each growing condition, showing satisfactory combinations of yield and fruit size. Despite Mediterranean open field conditions differ considerably from agroforestry conditions, the occurrence of individuals with satisfactory yield and fruit size in the latter system (despite coming from a preliminar selection in 2023 in Mediterranean conditions), suggest there are opportunities to develop OHM with a satisfactory adaptation to both conditions. Therefore, the seeds from the best individuals on each location will be used further for developing OHM adapted to each condition in 2025. But also part of the seeds from selected individuals in

Portugal/agroforestry will be also evaluated under 2025 in Mediterranean conditions of Valencia . Following a shuttle breeding procedure, to assess the opportunities to develop OHMs with wide adaptation/stability to extreme different conditions. Further implications and breeding parameters are discussed in the work

EVALUATION OF THE GERMINATION RATE OF PEPPER TRADITIONAL VARIETIES (CAPSICUM ANNUUM L.) AFTER THERMOTHERAPY DISINFECTION TREATMENTS

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Abstract Text:

Peppers are, with tomatoes and eggplant, one of the most crucial crops of the Solanaceae family. The presence of pathogens affecting this crop and the phytosanitary requirements for the movement of seeds within the EU make it necessary to subject seeds to disinfection treatments against these pathogens. These treatments can often be aggressive and affect the viability of the seeds and this knowledge is of special interest in seedbanks, like the COMAV-UPV. Moreover, not all treatments are accepted in organic farming. In this regard, thermotherapy is among the treatments accepted by organic farming and the more aggressive the treatment the higher effectiveness is expected against pathogens. However, the limits of temperatures and/or time of exposure for seed surveillance and germination have been not studied in detail in peppers.

In the present study, based on three pepper traditional cultivars from the COMAV-UPV seedbank, representing different typologies, their germination rates were evaluated after two blocks of thermotherapy and different temperatures: i) dry heat and ii) hot water. Dry heat treatments included four main temperatures-time treatments: i) 72ºC for 72 h (control), ii) 78ºc for 24h, iii) 85ºC for 24 h and iv) 85ºC for 12 h. Hot water treatments were: i) soaking seeds in 51,6 ºC for 30 minutes (control), ii) 70 ºC for 5 min, iii) 80ºC for 5 min, iv) 90 ºC for 5 min (Skelton et al., 2023). After the treatments, 50 seeds per combination variety x treatment were sowed in Petri dishes. Seed germination was evaluated with two parameters: standard germination test and time to germination that represents the speed of germination (Samarah et al., 2020). The Petri dishes were covered with lids and incubated at 25ºC in 12 hours of light per day. For the standard germination rate seeds with the cotyledons out were counted at 1, 2, 3, 4 weeks after sowing. On the other hand, for recording the speed of germination, seeds with radicle protrusion were counted at 3, 5, 7, 9 and 11 days after sowing.

Our results showed that extreme temperature treatments may decrease germination parameters, although it highly depended on the genotype and the temperature and time of exposure. Thus, regarding dry heat, germination decreased with 85ºC treatments, but

relatively low in comparison to < 80ºC treatments. In the case of hot water treatments, 90ºC treatment decreased considerably the germination parameters, while 80ºC rates were higher and did not differ significantly from 70ºC. These results suggest that we can use hard thermal treatments to eliminate a higher number of pathogens, although still further experiments are necessary to fit temperature and time of exposure without compromising largely the viability of the seeds.

Reference:

• Díez, M. J., De la Rosa, L., Martín, I. et al, 2018. Plant gene banks: present situation and proposals for their improvement. The case of the Spanish Network. Front. Plant Sci. Sec. Plant Breeding 9, e01794. https://doi.org/10.3389/fpls.2018.01794

• FAO. 2014. Genebank Standards for Plant Genetic Resources for Food and Agriculture. Rev, ed. Rome. https://www.fao.org/4/i3704e/i3704e.pdf

• FAO & ISTA. 2023. Guidelines for the establishment and management of seed testing laboratories – Joint FAO and ISTA Handbook. Rome. https://doi.org/10.4060/cc6103en

• Samarah, N., Sulaiman, A., Salem N. M,. et al, 2020. Disinfection treatments eliminated tomato brown rugose fruit virus in tomato seeds. Eur J Plant Pathol (20219 159: 153-162. https://doi.org/10.007/s.10658-020-02151-1

• Skelton, A., Frew, L., Ward, R., et al., 2023. Tomato Brown Rugose Fruit Virus: Survival and Disinfection efficacy on common glasshouses surfaces. Viruses 2023, 15, 2076. https://doi.org/10.3390/v15102076

PRINCIPLES AND PRACTICES OF ORGANIC BROCCOLI BREEDING AND SEED PRODUCTION, TOOLS FOR A MULTIACTOR APPROACH

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Abstract Text:

Broccoli (Brassica oleracea var. italica) production in Portugal has slightly decreased, 0.86% in area from 3014 ha (2021) to 2988 ha (2023) and 13.74% in yield from 39526 Mg (2021) to 34093 Mg (2023) (INE, 2024). Broccoli production faces several challenges, including climate change impacts and reduced genetic diversity. The 2024 National catalogue has only 3 registered varieties, all of them being hybrid (Atacama, Greenbow and Sonora). Modern hybrid broccoli varieties have experienced a significant reduction in allelic diversity compared to traditional landraces. This reduction in genetic diversity can limit the adaptability and resilience of broccoli crops to environmental changes and diseases (Zachary Stansell et al.2020). Therefore, the promotion of plant breeding tools is of utmost importance to boost the production of crop at national level, stressing the importance of traditional varieties where Participatory Plant Breeding can have a play to the role. This work aims to both translate into Portuguese, a tool for broccoli breeding by Organic Seed Alliance and conduct a technical itinerary for broccoli breeding and seed production in Portugal.

The translation of the papers “California Organic Broccoli Variety Trial 2013- 2014” (Coke, C et all 2015) and “Broccoli Seed Production: Quick Reference”, published by Organic Seed Alliance will be complemented by academic sources and data from GRIN Global, ECPGR, FAO/IPGRI, DGAV and INE. This will enable the creation of a technical broccoli breeding and seed production itinerary that will be useful to farmers, students, and technicians from Portuguese-speaking nations who wish to begin their breeding efforts on broccoli.

Reference:

Ahirwar, C., & Nath, R. (2020). Organic Broccoli Farming: A Step Towards Doubling Farmers’ Income. , 2, 47-50.

Ciancaleoni, S., Onofri, A., Torricelli, R., & Negri, V. (2016). Broccoli yield response to environmental factors in sustainable agriculture. European Journal of Agronomy, 72, 1-9. https://doi.org/10.1016/J.EJA.2015.09.009.

Valverde, J., Reilly, K., Villacreces, S., Gaffney, M., Grant, J., & Brunton, N. (2015). Variation in bioactive content in broccoli (Brassica oleracea var. italica) grown under conventional and organic production systems.. Journal of the science of food and agriculture, 95 6, 1163-71 . https://doi.org/10.1002/jsfa.6804.

EXPLORING THE LOCAL GENETIC DIVERSITY OF BIRD'S FOOT TREFOIL FOR IMPROVED FORAGE AND ECOSYSTEM SERVICES

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Abstract Text:

Legume crops play a crucial role in diversifying Europe's simplified crop rotations, improving sustainability, and addressing the increasing demand for protein-rich forage (Rubiales et al. 2021). Among minor legumes, bird's foot trefoil *Lotus corniculatus* L., (BFT) has garnered renewed interest due to its adaptability, resilience, and agronomic benefits, particularly in low-input livestock systems under unfavorable pedo-climatic conditions. Despite its ecological and agronomic significance, research on local BFT accessions, their genetic diversity, and agrobiological traits remains limited in Lithuania.The natural populations of the species serve as significant gene pools to produce improved varieties, therefore this knowledge is crucial for the *in situ* conservation of genetic diversity, which forms the basis for genetic breeding (Abraham et al. 2015). BFT is widespread across Lithuania, occurring in a range of habitats from semi-natural grasslands to roadside verges. Due to its adaptability, BFT exhibits significant morphological and agronomic variability, leading to the formation of distinct ecotypes. This variability presents opportunities for breeding superior cultivars with enhanced productivity and resilience. However, habitat degradation and biodiversity loss threaten the conservation of native genetic resources. To support conservation and breeding efforts, the seeds of 39 wild populations of BFT were collected from semi-natural grasslands representing diverse phytogeographical regions across Lithuania in 2023. These wild populations were compared with five commercial cultivars grown at LAMMC experimental fields. Seed morphometric analysis revealed significant ($P < 0.05$) differences between wild ecotypes and cultivated varieties, with wild seeds having 11.8% lower weight. Wild ecotypes from nutrient-poor habitats showed significantly ($P < 0.05$) lower values compared to populations from other habitats. The ecotypes from habitats 6210*, typically found on poorly developed, calcium-rich, and low-organic-matter soils, and habitats 6230, characterized by nutrient-poor, acidic soils, exhibited the lowest 1000-seed weight values, with weights 21.1% and 0.93% lower, respectively, compared to populations from other habitats. Conversely, ecotypes from anthropogenic environments displayed larger seed sizes ($P < 0.05$), likely due to selective pressures associated with disturbed habitats. These findings highlight the impact of environmental conditions on seed traits and suggest potential breeding strategies for improving seed quality and germination success.

Since genetic resources are vital not only for breeding but also for enhancing the productivity of grass-legume mixtures, assessing the competitive ability of BFT in mixed

stands is crucial for optimizing forage production. Two years field study was conducted to evaluate the performance of an old Lithuanian cultivar, 'Gelsvis' in mixes with ×*Festulolium* Asch. & Graebn., *Arrhenatherum elatius* (L.) P.Beauv. ex J.Presl & C.Presl, and *Festuca arundinacea* Schreb. The objective was to assess biomass production and species interactions in mixes with varying levels of grass competitiveness. Results indicated that ×*Festulolium* exhibited a more aggressive growth pattern compared to *F. arundinacea*. The biomass proportion of BFT in mixes with ×*Festulolium* and *A. elatius* was 14.25 % lower than in those with *F. arundinacea* and *A. elatius*, although the differences were not statistically significant ($P > 0.05$).

Currently, Lithuania lacks a locally developed BFT cultivar derived from native genotypes. Old cultivar 'Gelsvis,' was developed through interspecific hybridization with Caucasian-origin and other varieties. Cultivar trials at LAMMC show that the annual dry matter yield of 'Gelsvis' (7,740.1 kg/ha) does not differ statistically from other commercial cultivars in Lithuania, which yield between 1.87% less and 4.40% more dry matter. However, genetic resource exploration may provide greater variation, facilitating the development of higher-yielding, locally adapted cultivars.

Reference:

Rubiales D, Annicchiarico P, Vaz Patto MC, & Julier B (2021). Legume breeding for the agroecological transition of global agri-food systems: A European perspective. Frontiers in Plant Science, 12, [782574]. doi: 10.3389/fpls.2021.782574

Abraham EM, Ganopoulos I, Giagourta P, Osathanunkul M, Bosmali I, Tsaftaris A, ... & Madesis P (2015). Genetic diversity of Lotus corniculatus in relation to habitat type, species composition and species diversity. Biochemical Systematics and Ecology, 63, [59-67]. https://doi.org/10.1016/j.bse.2015.09.026

ASSESSING TRADITIONAL RYE VARIETIES FOR ORGANIC AGRICULTURE. TRIADIC VERSUS AGRONOMIC CHARACTERIZATION

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Abstract Text:

Rye cultivation in Portugal declined by 94,000 hectares (1989–2019), reducing cereal area by 14% (CNA, 2019). Yet, its resilience in poor soils and low-input systems highlights its potential for organic farming.

This study aims to identify traditional rye varieties suited for organic farming based on their agronomic performance and to compare it with stakeholder-based triadic evaluations.

The experimental design comprised eleven traditional rye accessions collected through a collaborative effort with Portuguese farmers across diverse agroecological regions. This initiative was supported by institutional partnerships with the Instituto Politécnico de Bragança (IPB), Confederação Nacional da Agricultura (CNA), Instituto Nacional de Investigação Agrária e Veterinária (INIAV), New Organic Planet (NOP), and Cascais Ambiente. These collaborations facilitated not only the acquisition of germplasm but also the integration of traditional agricultural knowledge, ensuring a comprehensive representation of regional genetic diversity and cultivation practices. A commercial variety was included as control.

Field trials were conducted in a certified organic plot at the Escola Superior Agrária de Coimbra (ESAC-IPC) in 2024, with stakeholder evaluations on June 5, engaging 33 multidisciplinary stakeholders representing farmers, processors, academics, and end-users.

A dual analytical approach was implemented combining yield and plant height measurements with stakeholder-based evaluations of yield, plant height, disease resistance, lodging tolerance, and phenotypic uniformity, captured through the SeedLinked digital platform. This mixed-methods approach enabled the identification of rye varieties suited for organic farming while allowing parallel comparisons of agronomic parameters and qualitative stakeholder evaluations of analogous traits.

ANOVA and Tukey tests were used to assess significant yield differences among the rye varieties, while Principal Component Analysis (PCA) and boxplot comparisons were performed to elucidate trait relationships and contrast agronomic measurements with stakeholder evaluations.

Yield analysis showed that most traditional varieties performed similarly to the control, with one exhibiting significantly higher yield and another significantly lower yield ($p < 0.05$).

Highlighting their potential for organic cultivation. PCA revealed that the first two principal components explained approximately 80% of the total variability among the varieties, with the biplot showing an almost 90° angle between measured yield and evaluated yield, indicating a weak correlation between the two variables. The varieties showed differing patterns when comparing agronomic measurements with the stakeholder evaluations, with the top-ranked variety in the agronomic measurements corresponding to the fifth rank in the stakeholder evaluations. These results highlight discrepancies between quantitative yield measurements and stakeholder perceptions, contrasting with findings from previous studies on maize and pepper. (Mendes-Moreira et al. 2024 & Pereira et al. 2024). This divergence of results among species could be drived by 1) the number of participants; 2) the instruction of participants about their role in the evaluation; 3) the familiarity of the group with the crop. Nevertheless, the results observed both agronomic measures and stakeholder evaluations can indicate to us some important traits for selection.

Reference:

Confederação Nacional da Agricultura (CNA). (2019). A produção de cereais em Portugal: Trajetória e horizonte de um pilar fundamental para a Soberania Alimentar. https://inforcna.pt/Media/Files/20211223_ArtigoTecnicoVt106.pdf

Mendes-Moreira, P., Pereira, A., Penincheiro, A., Matos, A., Dinis, I., & Santos, D. (2024). Combining local knowledge and data: a collaborative effort to evaluate traditional maize landraces for sustainable farming [Conference abstract]. Eucarpia General Congress Leipzig 2024.

Mendes-Moreira, P., Pereira, A., Penincheiro, A., Matos, A., Rosa & G., Burruezo, A. (2024). Comparative evaluation of pepper landrace performance and stakeholder perception in organic and agroforestry systems [Conference poster]. Eucarpia General Congress Leipzig 2024.

PRINCIPLES AND PRACTICES OF ORGANIC LETTUCE SEED PRODUCTION, TOOLS FOR A MULTIACTOR APPROACH.

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Abstract Text:

Lettuce (Lactuca sativa L.) is a self-pollinating annual plant belonging to the Asteraceae family. Lettuce varieties can have smooth or moderately curly leaves, with color gradations between light green and intense green, and can have "head" or their absence. In Portugal, lettuce is generally grown in greenhouses from November to April, while the rest of the year is grown outdoors. Lettuce represented Portugal in 2023, with 2672 ha and 71600 Mg of total production (INE, 2024). The optimum conditions for lettuce production in Portugal are a soil pH between 6.5 and 7.5 and a temperature range between 15 to 20ºC. The growth of lettuce seeds is influenced by several factors such as the climate, the soil and its fertility, field preparation, and watering. For genetic breeding/maintenance, the size of the lettuce population must be considered to maintain genetic diversity (Zyskowski, 2010). The aims of this work intended to translate into Portuguese and adapt the 2010 publication "Principles and Practices of Organic Lettuce Seed Production in the Pacific Northwest" (Jared Zyskowski, 2010) by Organic Seed Alliance (OSA) and organize a technical itinerary for lettuce breeding and seed production in Portugal. The paper translation on Organic Lettuce Seed Production (Zyskowski, 2010) was followed by the research in sources in scientific papers but also in GRIN, ECPGR, FAO/IPGRI, DGAV and INE, Lettuce descriptors, Statistics, Internet, National Varieties Catalogue and Organic Seed Database) research. The organic seed database indicates 27 available varieties (Organic Seed DataBase). In addition, some traditional varieties are on farmers' hands and adapted to the locations and uses. 228 entries are referred to BPGV (Portuguese Germplasm Bank) however their access is not available (BPGV, 2024), which emphasizes the need for a dynamic management of these genetic resources.

The translation and the research sources allowed the production of a technical lettuce itinerary of breeding and seed production that will contribute to farmers, students, and technicians from Portuguese-speaking countries who will start their breeding initiatives on lettuce.

Reference:

Banco Português de Germoplasma Vegetal. BPGV16511, Lactuca sativa L., Alface tradicional de Verão. Available at: http://bpgv.iniav.pt/gringlobal/accessiondetail?id=15774

Base de Dados de Material de Reprodução Vegetal. Plant Reproductive Material Database. Available at: https://app.dgadr.gov.pt/sementes/entrada/

Instituto Nacional de Estatística - Boletim Mensal da Agricultura e Pescas : julho de 2024. Lisboa : INE, 2024. Disponível na www: . ISSN 1647-1040

Zyskowky, J., Navazio, J., Morton, F., & Colley, M. (2010). Principles and practices of organic lettuce seed production in the Pacific Northwest. Organic Seed Alliance, Port Townsend, WA.

PORTUGUESE TRADITIONAL RYE POPULATIONS - GENETIC DIVERSITY

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Abstract Text:

The CERTRA Project - Development of Traditional Cereal Value Chains for Sustainable Food in Portugal, intends to help the production of traditional cereals (maize, wheat and rye) and to promote its derivative products. This project emphasizes the importance of autochthonous genetics resources and the need to manage agrobiodiversity adapted to local conditions.
Rye (*Secale cereale*) grown primarily for grain production in areas where the climate and soil are unfavorable to other cereals or as a winter crop where temperatures are too low for winter wheat. As a minor crop, rye is well positioned as an interesting alternative to produce cereals intended for food or feed, in a scenario of climate change. Rye is a relevant in the northern region of Portugal where local farmers cultivated the same rye seed populations for generations under a subsistence agricultural system. Traditional rye bread baking is an important cultural heritage that CERTRA wants to continue and innovate. As genetic diversity of populations evolves along changing environments, estimation of current genetic diversity of traditional rye accessions will look at an eventual potential genetic adaptation.

In this study we present the preliminary results obtained by the genetic molecular characterization of 13 traditional rye populations collected in northern regions of the country at small and familiar farms. These populations were DNA extracted and genotyped using nine microssatellite loci using PCR based techniques. PCR generated products were separated by capillary electrophoresis and visually analyzed to determine the molecular size of the amplified alleles.

Population differentiation showed a medium value of F_{st} of 1.5 ±0,2 suggesting a low to moderate differentiation between the 13 populations. Molecular variance analysis showed a percentage of 6% of variance among populations.

Population structure analysis reveals no substructure of studied Portuguese populations meaning that we are probably dealing with a unique population with a common ancestry. Results are according to previous work performed with European rye [(Targońska et al, 2015; Monteiro et al, 2016). In fact, it was demonstrated that rye populations from South Europe

showed mainly one unique population from a potential two populations of Europe. Our study confirms this hypothesis.

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References

Targońska M, Bolibok-Brągoszewska H, Rakoczy-Trojanowska M. Assessment of Genetic Diversity in *Secale cereale* Based on SSR Markers. Plant Mol Biol Report. 2016; 34:37-51. doi: 10.1007/s11105-015-0896-4. Epub 2015 Jun 6. PMID: 26843779; PMCID: PMC4722074.

Monteiro F, Vidigal P, Barros AB, Monteiro A, Oliveira HR, Viegas W. Genetic Distinctiveness of Rye In situ Accessions from Portugal Unveils a New Hotspot of Unexplored Genetic Resources. Front Plant Sci. 2016 Aug 31; 7:1334. doi: 10.3389/fpls.2016.01334. PMID: 27630658; PMCID: PMC5006150.

CHARACTERIZATION OF PORTUGUESE TRADITIONAL MAIZE POPULATIONS

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Abstract Text:

The CERTRA Project - Development of Traditional Cereal Value Chains for Sustainable Food in Portugal, intends to help the production of traditional cereals (maize, wheat and rye) and to promote its derivative products. This project emphasizes the importance of autochthonous genetics resources and the need to preserve agrobiodiversity adapted to local conditions. Traditional maize populations are important due to their better technological characteristics highly valued for the production of *broa* (a traditional Portuguese maize bread) (Vaz Patto et al, 2009) and their better resilience to pests, diseases and abiotic stresses (Vaz Patto et al, 2013).

In this study we present the preliminary results obtained by the characterization of 30 traditional maize populations, originating from VASO participatory maize breeding program (Vaz Patto et al, 2013) or collected in several regions of the country from small farms. These populations were previously genotyped using 21 microssatellite loci. The PCR products were separated by capillary electrophoresis and visually analyzed to determine the molecular size of the amplified alleles.

These maize populations were also sown together in a common-field experiment with three replications in Coruche region, during 2024, to be characterized concerning to several agronomic parameters (plant height, number of ears, hundred kernel weight, specific weight, grain yield) and nutritional composition (protein, fat, starch, ash).

Results from genetic analysis indicates that there is some allele fixation in all populations studied. The population differentiation determined by PCA (principal component analysis) can explain the molecular variation in axes 1 and 2, with an accumulated percentage of 33,8 %. Differentiation between populations was determined by the F statistic between pairs of populations and the values varied between 0,096 and 0,378. ANOVA analysis demonstrates that the main source of molecular variation in the maize populations is the variation between individuals within the same population.

The statistical analysis of agronomic parameters indicates that *Fandango* and *Santana Branco* were the highest maize plants, *Broa 187* presented the biggest number of ears/plot and *GB Amarelo* presented the biggest value of grain yield (7588 kg/ha). Genetically, *Broa 187* and *GB Amarelo* share the same ancestry after population structure analysis.

Concerning to nutritional profiles, almost all maize populations presented similar starch content (medium value 67,4 %) excluding three: *Broa 70* (63.9 %), *Freiras* (63,3 %) and *Gafanhão Vermelho Torrado* (62,8 %). Genetically, the more similar are *Freiras and Gafanhão Vermelho Torrado.* More variable protein and fat contents were obtained, but the population *Viseu Branco* stood out by present simultaneously the highest values of protein (14,1 %) and fat (5,0 %). Correlation of genetic and agronomic data is under study.

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References

Vaz Patto, M.C.; Alves, N.F.; Almeida, C.S.; Mendes, P.; Satovic, Z. Is the Bread MakingTechnological Ability of Portuguese Traditional Maize Landraces Associated with Their Genetic Diversity? Maydica 2009, 54, 297–311.

Vaz Patto, M.C.; Mendes-Moreira, P.M.; Alves, M.L.; Mecha, E.; Brites, C.; do Rosário Bronze, M.; Pego, S. Participatory Plant Quality Breeding: An Ancient Art Revisited by Knowledge Sharing. The Portuguese Experience. In Plant breeding from laboratories to fields; InTechOpen: London, UK, 2013, pp. 255–288.

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