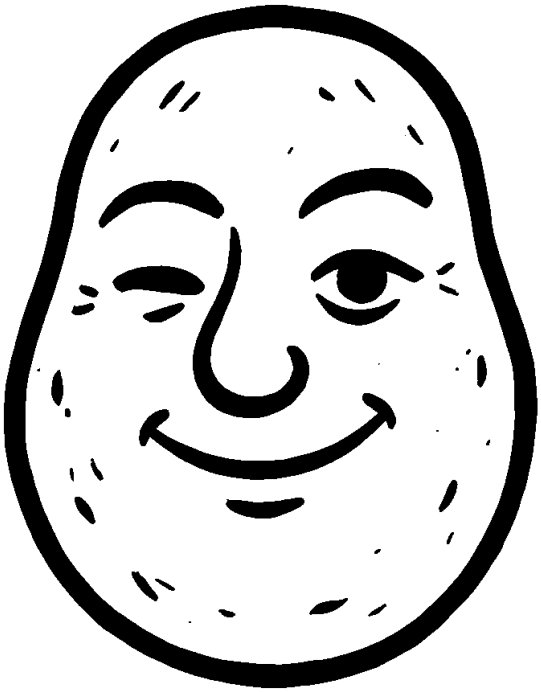
Meeting of joint EAPR sections Agronomy & Physiology and Post Harvest



Warsaw, 16-19.06.2026

IHAR
Plant Breeding and Acclimatization Institute
- National Research Institute

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Conference program in electronic version - scan QR code below:

CONFERENCE PROGRAM

Day I Tuesday 16.06.2026			
18:00 – 20:30	Registration		
18:30 – 20:30	Welcome cocktail at Hotel Gromada		
Day II Wednesday 17.06.2026			
8:15 – 8:45	Registration		
8:45 – 9:00	Official opening of the conference		
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10:10 – 10:30	Sprout control and stimulation of seed potatoes	Andreas Meyer	17
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Session II Physiology and Fertilization Chairs: Kürt Demeulemeester & Pia Heltoft Thomsen			
11:00 – 11:20	Use of pre-treatments for improved control of the tuber-set process, tuber number and tuber size	Pia Heltoft Thomsen	18
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	plant development, and yield of potatoes in Northern Germany		
12:20 – 12:40	Preharvest nitrogen reduction delays endodormancy break through genotype specific sugar responses in potato	Fabian Villamil	22
12:40 – 13:20	**EAPR section meeting** Chairs: Dominika Boguszewska-Mańkowska, Mari Carmen Alamar & Andreas Meyer		
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15:30 – 15:50	Potato late blight pathogen population dynamics in Northern Baltics: impact of potato cultivars and pathogen reproductive mode	Krystallia Komninaki	27
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9:30 – 9:50	Potato breeding development under climate change conditions	Michał Broda	31
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POSTERS

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7	Optimizing nitrogen use in potato cultivation: insights from multi-site field trials	Kürt Demeulemeester	45	Agronomy/ Fertilization

8	Preliminary in vivo evaluation of a granular fertilizer derived from potato starch processing by-products as a potential nitrogen substitute in potato	Ilze Dimante	46	Agronomy/ Fertilization
9	Assessment of potato resistance to a small-spored Alternaria strain and the antifungal potential of four essential oils for its control	Riane Syrine Fergani	47	Diseases
10	Broad host range and host-dependent pathogenicity of Algerian Pectobacterium isolates associated with potato soft rot	Imane Zaid	48	Diseases
11	Mechanical phenotyping of diploid potato genotypes differing in PVY resistance using micro-extensometry	Katarzyna Szajko	49	Diseases
12	Smart farming in potato cultivation: AI/ML-designed nanobioreceptors for PLRV detection and safe peptide-based crop protection	Beata Gromadzka	50	Diseases
13	Population structure of *Phytophthora infestans* in Poland	Marta Janiszewska	51	Diseases
14	Potato – *Globodera pallida* interaction during the resistance reaction in the roots of potato plants attacked by larvae of the white cyst nematode at the di- and tetraploid level	Dorota Milczarek	52	Diseases
15	The StBBX22 protein is involved in cultivated potato reproduction	Klaudia Grądzka	53	Physiology
16	Evaluating potato regeneration ability through cell cycle parameters	Paulina Smyda-Dajmund	54	Physiology

17	Wound-induced transcriptional dynamics reveal bulk-dependent differences in potato tuber wound-response programmes	Anna Grupa-Urbańska	55	Physiology
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19	Metabolomic and biochemical analysis of four potato cultivars (*Solanum tuberosum* L.) from an organic farm	Beata Tatarowska	57	Post Harvest
20	Phenolic compounds and antioxidant potential of coloured-flesh potato tubers under temperate climate conditions of Poland	Barbara Krochmal-Marczak	58	Post Harvest

*Full lists of authors and affiliations can be found in the abstract pages.

Excursion Program

Day III Thursday 18.06.2026	
08:00	Departure from Hotel Gromada Warszawa Centrum
09:00 – 9:45	Visit to the Białuty Sp. z o.o company, producer and distributor in the agri-food industry, supplying both the domestic and international markets. *Main areas of activity:* • Agricultural production: growing, confectioning, and distributing vegetables (including packing potatoes) • Fruit and vegetable processing: production of concentrated juices, purees, and concentrates • Food processing for the catering industry

9:45 -10:30	Visiting potato field
11:00-12:30	Visit to Plant Breeding and Acclimatization Institute – National Research Institute (IHAR–PIB) in Radzików The program includes visits to selected scientific departments and research facilities: • National Centre for Plant Genetic Resources • The Genetically Modified Organisms Controlling Laboratory
12:30 -14:00	Lunch at the IHAR Training Centre in Radzików located next to the institute
14:00	Departure from Radzików to Warsaw
15:00 – 17:00	Guided walking tour in Warsaw Old Town, starting from Royal Castle in Warsaw

Excursion hosts:

Białuty sp. z o.o. has been operating since 1976 in Białuty near Błonie, 30 km west of Warsaw. Our production activities include food processing and a farming area of 500 ha. The food processing department's main products include:

- apple juice concentrate, colored fruit concentrates and fruit flavors
- mayonnaise and sauces - available on our regional market.

On our farm we specialize in the production of table potatoes and onions.
Thanks to professional cultivation, storage and selected varieties of potatoes, we are a valued supplier.
We guarantee:

- large, uniform batches of products and continuity of supply throughout the year
- great taste, premium quality, clean label,
- openness to new needs and expectations of our customers.

The Plant Breeding and Acclimatization Institute—National Research Institute (IHAR-PIB) is the biggest research center in Poland focused on improving crops, biotechnology, and conserving and enhancing plant genetic material. It was founded in 1951 for research on the breeding and seed production of major field crops.

IHAR-PIB has significant achievements in research on genetics and mapping of genetic factors underlying important agronomic and quality traits in field crops such as wheat, barley, rye, triticale, maize, potato, rapeseed, sugar beet, various grasses, and energy plants.

It employs 272 employees, of which over 80 are scientists (2025). IHAR-PIB runs and manages the National Centre for Plant Genetic Resources: Polish Genebank, which has a collection of more than 1500 potato types (including cultivars, breeding lines, and wild species). The Genetically Modified Organisms Controlling Laboratory for Poland is also located within IHAR-PIB.

Many research projects are implemented at IHAR-PIB, funded by EU Horizon programs, the Polish National Science Centre, the National Centre for Research and Development, the Ministry of Agriculture and Rural Development, and others.

Next to the scientific part, IHAR-PIB holdings include six closely collaborating experimental stations and five companies focusing mostly on commercial plant breeding that ensure the efficient implementation and commercialization of the results of IHAR-PIB's research.

Abstracts

Oral presentations

Advanced genetic and genomic approaches to understanding tuber dormancy in potato

Sanjeev Kumar Sharma

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Tuber dormancy is a key agronomic trait in potato, underpinning the long-term storage required for year-round supply. Premature dormancy release and subsequent sprout growth during storage are associated with substantial quality deterioration and present challenges for postharvest management. The recent withdrawal of the chemical sprout suppressant chlorpropham further emphasises the need for alternative strategies, including the development of cultivars with modified dormancy characteristics.

This study investigated the genetic architecture of tuber dormancy and assessed the potential for genomics-assisted breeding. Phenotypic data for dormancy break, previously reported from a genome-wide association study of ~300 tetraploid cultivars, were re-analysed in conjunction with dense genotyping generated using a recently developed, gene-targeted Single-Primer Enrichment Technology (SPET; SPUD-SPET) platform. This platform was designed to capture functional variation across the potato gene space while representing genetic diversity from the wider cultivated gene pool, and targets ~90,000 high-impact single-nucleotide polymorphisms distributed across the annotated potato gene space.

Genome-wide association analyses, performed using models accounting for autotetraploid inheritance, identified significant marker-trait associations across multiple chromosomes. Several loci were consistent with previously reported QTL, but were resolved with greater precision, and additional signals were detected, including a strong-effect locus on chromosome 12 that has been only sporadically reported. The gene-based design and marker density of the SPUD-SPET platform enabled improved resolution of association signals and facilitated interrogation of genic regions underlying trait variation. Integration of current and prior findings indicates that tuber dormancy is governed by a complex genetic architecture involving all 12 chromosomes and loci spanning a range of effect sizes, from small to large. These observations indicate that both marker-assisted selection and genomic prediction warrant further evaluation for this trait.

Ongoing work is focused on the development of allele-specific assays and the evaluation of genomic prediction models for dormancy-related traits. The results provide a basis for refining selection strategies and support the development of potato cultivars with tailored dormancy characteristics.

Enhancing potato dormancy to reduce postharvest losses

M. Carmen Alamar[1], Edwin van der Vossen[2], Gemma Chope[3]

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[2)] Solynta, Wageningen, The Netherlands; [3)] PepsiCo International Limited, Leicester, United Kingdom
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Potato, (*Solanum tuberosum*), is the UK's most important fresh produce commodity, delivering ~50% of dietary carbohydrate intake and supporting over 20,000 jobs across farming, transport, and manufacturing. To maintain year-round supply, ~1.5 million tonnes of potatoes are stored for up to eight months under cold conditions with sprout suppression treatments. Since the withdrawal of chlorpropham (CIPC) in 2020, previously used on 85% of stored crops, sprouting losses can increase by 5–10% and storage duration reduce to four months or less. This has created an urgent need for alternative strategies to limit waste and reduce reliance on imports. Furthermore, cold storage contributes ~25% of greenhouse gas emissions in the potato supply chain, necessitating approaches that enable higher storage temperatures without compromising dormancy.

This research addresses the biological and environmental regulation of tuber dormancy with the aim of extending storage life while reducing chemical inputs and energy demand. Novel potato diploid germplasm is used to identify genomic regions controlling variation in dormancy, ultimately enabling the development of varieties with extended dormancy and stability at elevated temperatures alongside key agronomic traits. Complementary transcriptomic analyses will characterise gene expression changes in tuber meristems during potato dormancy transition, providing mechanistic insight into dormancy regulation.

To support these studies, innovative phenotyping methods will be developed to detect dormancy break, including high-resolution imaging, image analysis, and measurement of electrical signals associated with physiological changes. In parallel, the influence of pre- and postharvest environmental conditions on dormancy behaviour will be evaluated through controlled storage experiments, linking field conditions to storage performance.

Together, this work will generate new knowledge and practical solutions to extend tuber dormancy, reduce postharvest losses, and lower energy use in potato storage systems. These outcomes will support a more sustainable and resilient potato supply chain under changing regulatory and environmental constraints.

This study was funded by Biotechnology and Biological Sciences Research Council (BBSRC) (United Kingdom), PepsiCo Inc. and Solynta. The views expressed in this abstract are those of the authors and do not necessarily reflect the position or policy of PepsiCo Inc.

Volatile metabolomic fingerprints reveal early diagnostic signatures of storage diseases in *Solanum tuberosum*

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Postharvest storage diseases greatly diminish potato quality and lead to significant economic losses worldwide. Early detection of infection is difficult because visible symptoms usually only appear after extensive pathogen colonization. Plant–pathogen interactions provoke dynamic metabolic responses, often reflected in the emission of volatile organic compounds (VOCs), implying that volatile metabolomic signatures could offer an early, non-destructive method for disease detection in stored tubers. Here, we investigated pathogen-induced volatile metabolomic responses associated with two major potato storage diseases—bacterial soft rot and fungal dry rot—using headspace solid-phase microextraction coupled with gas chromatography–mass spectrometry (HS-SPME-GC–MS). Comparative volatile metabolomic profiling across infection stages revealed pathogen-specific emission patterns and infection-stage-dependent metabolic reprogramming that emerged during early asymptomatic stages, before visible symptom development. Soft rot infection generated a distinct volatile fingerprint dominated by 1-octen-3-ol, 3-octanone, 2-methylisoborneol, 1,4-dimethyladamantane and 2-methyl-2-bornene, which clearly discriminated infected tubers from healthy controls. In contrast, fungal dry rot was characterized by a different suite of VOCs, including linalool tetrahydride, γ-muurolene, alloaromadendrene and α-isomethyl ionone, highlighting pathogen-specific volatile metabolomic fingerprints associated with disease progression. Comparative interpretation further suggests that early pathogen invasion triggers oxidative signaling and phytohormone-mediated defense responses, resulting in metabolic reprogramming and emission of diagnostic VOCs during asymptomatic infection stages. Together, these findings reveal pathogen-specific volatile metabolomic fingerprints that underpin early detection of potato storage diseases. The identified VOC signatures provide a foundation for developing rapid, non-destructive monitoring tools, including sensor-based detection systems, for surveillance and management of diseases in potato postharvest storage environments.

Sprout control and stimulation of seed potatoes

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In practice seed potatoes are stored at approximately 4°C to prevent sprouting and minimize storage losses. At the same time, storage at higher temperatures, or targeted aging of the tubers, would be desirable to stimulate more eyes to start sprouting, when potatoes are planted in the field. Particularly in the propagation of processing potatoes with weak seed formation, methods for increasing the number of tubers set are being sought.

In 2023/24 Versuchsstation Dethlingen carried out a pre-trial with 10 varieties of potatoes stored in a conventional cold store, in ethylene atmosphere and treated with DMN. After storage potatoes were planted out in the field, were number of stems and number of tubers set were documented. The main trial started in 2024/25 with about 30 varieties from seven breeding companies and is designed for tree storage/vegetation periods. Potatoes are stored in climate-controlled storage units where three different treatments were carried out: (A) Cold storage at 4°C, (B) Ethylene treatment
8/4°C and (C) DNM treatment 6°C. Storage losses, dry and soft rot, number of sprouts per tuber and length of longest sprout per tuber were recorded. After storage potatoes were planted in the field were emergence, number of stems, yield, size and number of tubers were recorded.
Preliminary results indicate that it is possibly advantageous to store seed potatoes under warmer conditions with use of seed treatment during storage. Storage losses and sprouting were affected by the treatments. Emergence of potatoes was not negatively affected by treatments. Compared to cold storage (A), both storing regimes (B and C) led to higher number of stems and tubers.

Use of pre-treatments for improved control of the tuber-set process, tuber number and tuber size

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Green-sprouting at elevated temperature combined with light advances the physiological age of seed tubers and may be used to shorten the field growth period and modify tuber number and size distribution. In addition, selected growth regulators applied to seed potatoes may increase tuber number, reduce mean tuber size, and improve uniformity within defined size classes.
This study investigated seed potato pre-treatments at slightly elevated temperature to promote physiological ageing towards increased tuber set and shift production towards smaller, more uniform tubers. Specifically, we studied (i) the use of growth regulators (1,4SIGHT) and (ii) the potential effects of low intensity red or far-red light.

Controlled experiments were conducted over two winter storage seasons (2023–2024 and 2024–2025) to evaluate growth regulator pre-treatments for sprouting control and subsequent tuber-set outcomes in table potato production. Four cultivars differing in sprouting potential (Folva, Anouk, Colomba and Celandine) were included. Treatments included 1,4SIGHT applied at 10–15 ml t−1 as either one or two applications, alongside an untreated control. One storage season (2024-25) were used to evaluate low intensity light pre-treatment for cultivars (Solist, Asterix and Mandel), alongside an untreated control, all with a subsequent 300 daydegree green-sprouting period in greenhouse daylight. Tuber set and quality aspects were assessed using in-season underground evaluations and post-harvest yield and size grading analyses.

Two applications of 1,4SIGHT increased total tuber number in Folva in both seasons. In Anouk and Celandine, an increase in total tuber number was observed after one and/or two applications, but only in the first season. In Colomba, both 1,4SIGHT treatments increased total tuber number only in the second season. Across all cultivars and both seasons, 1,4SIGHT increased the number of tubers in the 25–40 mm size fraction. There were no significant effects of low-intensity pre-sprouting light on stem numbers. However, Solist responded with higher tuber number and lower tuber size under far-red light, whereas Mandel showed higher tuber numbers under red light.

The results demonstrate cultivar- and year-dependent effects of elevated temperature and 1,4SIGHT on total tuber number. These preliminary findings support the development of cultivar-specific pre-treatment recommendations.

Rebalancing the nitrogen cycle

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Modern potato production depends on high nitrogen (N) inputs, yet a substantial fraction of this nitrogen is lost to the environment rather than captured in yield. Nitrogen in soil is continuously shared and competed for between plants and microbial communities, with nitrate (NO_3^-) leaching and nitrous oxide (N_2O) greenhouse gas emissions representing the dominant loss pathways. Together, these losses reveal a system that is not only inefficient, but fundamentally out of balance.

This presentation explores how soil physicochemical conditions, particularly pH, interact with microbial communities to regulate key nitrogen transformation pathways. Special emphasis is placed on the final step of denitrification, where the activity of N_2O reductase is highly sensitive to environmental constraints. In acidic soils, this sensitivity limits the reduction of N_2O to dinitrogen (N_2), leading to elevated emissions. The result is a functionally "decoupled" nitrogen cycle, in which microbial processes proceed, but fail to deliver agronomic efficiency or environmental stability.

Rather than treating these losses as inevitable, this talk reframes the nitrogen cycle as a biologically regulated system that can be steered. Drawing on recent advances in soil microbiology and biogeochemistry, it examines opportunities to improve nitrogen cycling through targeted interventions, including pH management, microbial-based strategies, and the use of agricultural side-streams to enhance microbial function.

By linking microbial mechanisms with field-scale outcomes, this talk will highlight practical pathways to restore balance in the nitrogen cycle and to advance more resilient, climate-smart production systems.

Living mulch for weed management and soil health in potato production

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Potato cultivation is a key agricultural sector in Europe, and maintaining soil health is essential for ensuring long term sustainability. Within the EU Horizon innovation project MultiSoil (Multifunctional Soil Biodiversity: Unlocking Potential for Healthy Cropping Systems), we investigate the use of living mulches as both weed suppressors and soil health enhancers in potato production systems. Our core concept builds on the potential of winter rye (Secale cereale) as an effective living mulch due to its strong competitive ability, shading capacity, and allelopathic properties. Root exudates—bioactive compounds released into the rhizosphere—play a central role in plant–soil interactions by influencing nutrient dynamics, plant growth, and soil microbial communities.

Field experiments are conducted at the Centre of Estonian Rural Research and Knowledge in Jõgeva, Estonia, where five high biomass winter rye varieties are sown in spring between potato furrows. In the project we use Estonian and Polish open-pollinated winter rye varieties, e.g. ´Elvi´, ´Kanter´, ´Granat´. The potato trials include both Estonian early and late season cultivars, ´Maret´ and ´Tiina´ respectively. Additionally, mixed winter rye–legume living mulch systems are tested. Weed pressure is monitored throughout the growing period using both visual assessments and drone based imaging. Soil microbiome analyses are performed during the season to better understand plant–plant and plant–soil interactions, alongside comprehensive evaluations of yield and its quality.

Complementary greenhouse experiments help determine the allelopathic potential and competitive performance of the selected winter rye varieties. The combined greenhouse and field results will identify the most effective winter rye variety for weed management in potato cultivation. Following the experimental phase, the optimized living mulch strategies will be implemented on commercial farms. The first research outcomes are expected in the fall 2026.

Influence of N fertilization levels and fertilizer placement on N uptake, plant development, and yield of potatoes in Northern Germany

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Nitrogen (N) losses in potato production systems are particularly pronounced on sandy soils, making improvements in nitrogen use efficiency (NUE) essential. Fertilizer placement has been proposed as a strategy to enhance spatial and temporal N availability, yet its effectiveness under field conditions remains insufficiently quantified.

A factorial field experiment was conducted in 2025 at Trauen in Northern Germany on sandy soil using the potato cultivar Belana. Three N rates (0, 87, and 121 kg N ha-1) were combined with two fertilizer placement strategies (broadcast vs. band placement). Plant and soil samples were collected at five growth stages to assess N uptake dynamics as well as interactions with phosphorus (P) and potassium (K) nutrition.

Band placement at the recommended N rate resulted in the highest tuber yield (64600 kg ha-1) and consistently showed higher yield levels compared with broadcast application, suggesting improved N availability and uptake. In contrast, omission of N fertilization led to reduced tuber set (18 tubers per plant), lower biomass accumulation (1.67 t ha-1), and altered C/N ratios (41) at early growth stages, underlining the importance of adequate N supply during tuber initiation. Notably, the lowest foliar P concentrations (1.82 g kg-1) were observed in the absence of N fertilization despite full PK supply.
This highlights the strong dependency of P uptake on adequate N supply.

These results highlight that both N rate and fertilizer placement are critical factors for improving NUE in potato systems. In particular, optimizing early-season N availability appears essential for efficient nutrient uptake and crop development under sandy soil conditions.

Preharvest nitrogen reduction delays endodormancy break through genotype specific sugar responses in potato

Fabian Villamil, Sofia Kourmpetli, Katherine Cools, Edwin van der Vossen, Gemma Chope, M. Carmen Alamar

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Potato (*Solanum tuberosum*), the world's third most consumed food crop, remains a breeding priority for improved pathogen resistance, climate resilience, and tuber quality. Postharvest traits are also important because they influence tuber quality from store. Of these traits, timing of endodormancy break is especially significant, as it initiates a series of metabolic and physiological changes that may decrease quality and cause food losses. Therefore, understanding the impact of genotype per environment interaction (e.g. effect of nitrogen on different genotypes) on endodormancy is essential for the sustainability of the potato industry.

Nitrogen (N) fertilisation has been reported to affect dormancy duration. To assess the role of N in dormancy, two potato genotypes were grown under standard N application and a 30% reduced N application in the UK. After harvest, tubers were stored at 15 ºC and dormancy status was monitored weekly for eight weeks. Tubers were classified into six developmental stages based on their apical buds: dormant; pre eye movement; dormancy break; sprout < 1 mm; 1–2 mm sprout; sprout > 2 mm. Concentrations of sugars (sucrose, fructose, and glucose) in the tuber flesh were also quantified.

Repeated-measures ANOVA indicated that reduced N application was associated with a delayed dormancy break without affecting field yield. In both genotypes, the 30% reduced-N application consistently showed a lower proportion of tubers that had broken dormancy compared with the standard N application between 13 and 27 days after harvest (DAH). Meanwhile, yield did not differ significantly between genotypes or N applications.

The general trend showed that concentrations of all measured sugars decreased at each sampling point in both genotypes. However, statistically significant differences in sugar accumulation were detected only in one genotype, specifically for fructose and glucose, where the standard N application resulted in lower concentrations of both sugars. This could suggest that genotype-specific metabolic responses may modulate how N availability influences the transition from dormancy to sprouting.

These findings emphasize the need for a broader understanding of how genotype by environment interactions regulate postharvest traits such as dormancy. Integrating these components represents a key step toward improving endodormancy control and reducing postharvest losses in potato.

Soil microbiota differences in potato fields with contrasting soft rot and blackleg incidence

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Soft rot Pectobacteriaceae (SRP), including *Dickeya* spp. and *Pectobacterium* spp., are major bacterial pathogens responsible for blackleg and soft rot diseases of potato, leading to substantial global yield losses. Increasing evidence suggests that soil microbiota may contribute to disease suppression regardless of its physicochemical properties. In this study, we investigated potato fields differing in long-term incidence rates of SRP-associated diseases to identify factors potentially associated with reduced disease occurrence.

Comparative physicochemical analyses revealed that most soil parameters were similar between the analysed fields. Culture-based methods combined with molecular identification confirmed the presence of *Pectobacterium* spp. exclusively in the high-disease-incidence field. Amplicon sequencing of the 16S rRNA gene performed for the initial two-field comparison showed comparable alpha-diversity but distinct beta-diversity between the fields. Notably, genera such as *Bacillus*, *Rummeliibacillus*, Acidobacterium and *Gaiella* were more abundant in soils with low disease incidence, suggesting a potential role in disease suppression. To further investigate the significance of the observed phenomena, complementary studies were conducted using soil samples from multiple fields with varying degrees of soft rot. Survival tests of Dickeya solani IFB0099 and *Pectobacterium atrosepticum* IFB5399 in these collected soils revealed a gradual decline in the pathogen population over time, with no correlation between pathogen survival dynamics and disease incidence. Isolation and characterization of soil bacteria, however, allowed for the development of a set of soil bacteria, among which selected *Paenibacillus* spp. isolates demonstrated antagonistic activity against the tested SRP, as well as other economically important plant pathogens. Additionally, soil-derived microbiome and metabolite extracts were prepared to investigate their role in pathogen suppression. Although sterile soil extracts did not display direct antibacterial

activity, microbiome-derived fractions demonstrated an effect on pathogen behaviour and disease development under laboratory conditions.

Taken together, these results suggest that differences in soil microbiota composition may contribute to variation in disease incidence. Identifying antagonistic bacteria and microbiome-related effects opens new perspectives for microbiome-based strategies in sustainable control of potato diseases.

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Genetic mapping of resistance to potato dry rot caused by *Fusarium sambucinum* and finding some new tuber rots in Poland

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Potato, the fourth most important crop species in the world, is attacked by many pests and diseases and due to climate change the importance and geographic ranges of particular pathogens change dynamically, challenging the potato industry. Pathogens causing potato tuber rots benefit from increased temperatures and sub-optimal harvest conditions (too warm and/or wet weather) and emerge as causal agents of severe storage losses. Tuber dry rot is an important disease of potato caused by soil and seed-borne pathogens of the *Fusarium* genus leading to losses that may reach 60% of the yield. We have investigated the inheritance of the dry rot resistance in two diploid potato hybrid populations (11–36 and 12–3) with complex pedigrees, including several wild *Solanum* spp. We used an aggressive isolate of *F. sambucinum* for phenotyping both progenies, parents, and standard potato cultivars in laboratory tuber tests, in three subsequent years. The QTL for dry rot resistance were mapped by interval mapping on existing genetic maps of both mapping populations. The most important and reproducible QTL for this trait was mapped on chromosome I and additional year-and population-specific QTL were mapped on chromosomes II, VII, XI, and XII, confirming polygenic control of this resistance.

Other storage diseases that gain importance are pink rot is usually caused by a homothallic funguslike organism *Phytophthora erythroseptica* (Oomycetes) and water rot (aka Pythium leak) is in majority caused by also homothallic *Globisporangium ultimum* (formerly *Pythium ultimum*, Oomycetes). We have isolated *P. erythroseptica* and *G. ultimum* strains from symptomatic potato tubers, identified by specific markers and sequencing of ITS. Selected strains were tested in laboratory tests on whole tubers of several potato cultivars and very strong, characteristic symptoms were observed, regardless of potato genotype. A new disease, yellow tuber rot has been described in 2022 in Russia (Belosokhov et al. 2022 Fungi 8, 1160) and our preliminary results indicate the presence of the causal agent, fungus *Trichocladium solani* also in Poland. Identification and population studies of pathogens causing tuber rots enable future studies on improvement of potato resistance to these diseases and reducing the storage losses.

Distribution and shared pathogenicity of small-spored *Alternaria* on Solanaceous crops in Europe

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Alternaria spp. are cosmopolitan, ubiquitous necrotrophic pathogens responsible for early blight and leaf spot diseases, causing substantial harvest losses in solanaceous crops. To investigate their diversity, spread, and adaptive potential, we collected Alternaria-infected leaves from potato, tomato, and wild solanaceous hosts across three climate zones and multiple farm types in Estonia, Poland, Serbia, and Germany. Molecular identification using the markers Alt a1 and RPB2 revealed that infections were dominated by small-spored species of section Alternaria, primarily *A. alternata*, findings further confirmed by morphological examination.

Sequencing of the two markers revealed five widespread haplotypes with similar frequencies across host plants, farm types, and climate zones. Comparative diversity analyses (π, Tajima's D) likewise showed no significant genetic differentiation among isolates from different hosts. These results suggest that, based on these markers, small-spored *Alternaria* populations exhibit considerable genetic heterogeneity at the continental scale and a remarkable ability to colonise and infect across diverse environments.

However, phenotyping using detached-leaf assays revealed significantly higher virulence in isolates originating from wild host plants, highlighting the importance of wild hosts as reservoirs that may contribute to pathogen spread.

To further characterise population structure, admixture, and adaptive potential, we generated whole-genome sequences for 320 *A. alternata* isolates, enabling high-resolution analyses of gene flow and recombination. In addition, we are assessing fungicide resistance profiles, with a particular focus on the emergence and spread of resistance in wild host populations.

Together, our results provide an integrative view of the ecology, population biology, and adaptive capacity of small-spored *Alternaria*, with direct implications for disease monitoring and sustainable management strategies in Europe.

Potato late blight pathogen population dynamics in Northern Baltics: impact of potato cultivars and pathogen reproductive mode

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The market share of global/large potato seed producers is continuously increasing, raising a critical question of whether shared potato cultivars and geographic isolation (contiguous land vs. islands) shape the *Phytophthora infestans* population structure and temporal dynamics in the northern potato cultivation range. A collection of 735 *P. infestans* isolates were sampled from 45 potato cultivars from the Estonian mainland (542 isolates) and islands (193) over five years, with 326 of these genotyped using SSR markers. Both A1 and A2 mating types were detected in all years and areas, with nearly equal frequencies. Across *P. infestans* isolates, 62.0% (202) were multi-locus genotypes (MLGs), whereas 67.8% (137) of MLGs were unique. The genetic diversity of the isolates was high in both the island (0.978) and mainland (0.995) populations, suggesting that the pathogen population is dynamic and adaptable across regions, and not limited by geographic isolation. The share of pathogen genetic variation within the host (95.79%) was much greater than among the host genotypes, indicating that cultivar choice alone has limited influence on pathogen population structure. Each annual sample was characterized by distinct genotypes with high genetic flow among mainland and island populations. Genetic parameters support sexual mode of reproduction and highlights the role of oospores in driving late blight epidemics. Agronomically, these findings emphasize the need for integrated disease management strategies, including deployment of quantitatively resistant cultivars, optimized fungicide programs, extended crop rotations to reduce oospore survival, strict seed tuber certification, the use of disease-free planting materials, using cultivar or species mixtures, and regionally coordinated disease monitoring.

Alternative ways of weed control in potatoes

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Limitation of using herbicides in several potato production regions requires alternative procedures of weed control. Mechanical cultivation could be a possible strategy. Working bodies were constructed for weed control to be used under conditions of de-stoning technology. The bodies were mounted onto the potato cultivator Varior 500. The machine was constructed for the technology of potato growing in de-stoned ridges, where usual mechanical cultivation is not done. In developing of working bodies for weed control the emphasis was put onto gentle soil loosening to prevent subsequent support of soil mineralization processes, an increase of CO2 emissions and loss of water from the soil after more intensive soil aeration.

Field trials were performed in the potato production region of the Czech Republic in 2021 and 2022. Three options of weed control were compared. The basis was the conventional weed control using a pre-emergent herbicide containing active ingredients metribuzin and flufenacet. Mechanical cultivation using bodies for mechanical weed destruction was compared to the conventional variant.

This operation was done twice prior to potato emergence. The third variant (only in 2021) involved mechanical weed destruction on two dates prior to emergence (similarly as the second variant) supplemented with the post-emergent application of a rimsulfuron-containing herbicide.

In 2021, mean weed control efficacy of the conventional variant using a pre-emergent herbicide achieved 81%. Compared to this variant, double mechanical treatment using innovated working bodies had mean weed control efficacy of 75 %. The most effective was the variant of the same mechanical treatment supplemented with the post-emergent application of a rimsulfuron-containing herbicide. The variant achieved 85 % of mean weed control efficacy. In 2022, mean weed control efficacy of mechanical destruction was 88 %, mean efficacy of the herbicide application was 91%.

Similar results were also obtained for potato yield.

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Artificial intelligence in crop smart farming: molecular design for biosensing and sustainable plant protection

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The global food supply faces a silent yet devastating crisis: plant viruses. Responsible for crop losses equivalent to the caloric needs of one billion people annually, these pathogens remain largely untreatable once infection takes hold. Particularly challenging are the "naked" viruses - those lacking a lipid envelope—which act as highly efficient molecular destruction machines. Traditionally, detection relies on visual symptoms, which often appear too late to prevent systemic spread.

This lecture presents a paradigm shift from reactive "blind chemistry" to Molecular Precision Agriculture. We explore how the intersection of AI-driven protein engineering and advanced biosensing is creating a "peptide firewall" for the modern farm. Key focus areas include:

- AI as the Virologist: Utilizing diffusion models and AlphaFold 3 to bypass years of laboratory trial-and-error, designing bio-nanoreceptors and antiviral peptides with atomic precision in under 48 hours.
- The Pocket Laboratory: The integration of optical and electrochemical biosensors with micro-filtration systems, enabling real-time, in-field viral diagnostics within minutes.
- Smart Farming Integration: Closing the loop between data and action. We discuss how 60-second biosensor results instantly update risk maps, triggering autonomous bio-control drone deployments rather than indiscriminate chemical spraying.

The session concludes by demonstrating how leveraging the structural vulnerabilities of plant viruses - specifically their lack of an envelope - allows us to engineer targeted peptide solutions that protect crops sustainably. Attendees will gain insight into a future where every hectare is monitored by an intelligent, molecular-scale defense system.

Monitoring of potato varietal response to drought based on vegetation indices derived from UAV imagery

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In years with water shortages and uneven rainfall distribution, the average national potato yield in Poland decreases significantly. This is because potato possesses a sparse, shallow, and weak soil-penetrating root system, and most potato fields have been unirrigated. A closed potato canopy during the bulking period intercepts most of the light used for dry matter production, and soil water evaporation is reduced. Remote sensing methods, which are indirect measures of crop canopy and yield, could be useful as proxies for detecting drought onset and ranking potato varietal responses to this abiotic stress. For this purpose, vegetation indices (VIs) derived from imagery are used. Among these are images obtained from unmanned aerial vehicles (UAVs), which enable their high spatial resolution and image collection even in cloudy conditions. The aim of this research was to determine VIs useful for detecting drought onset and varieties that exhibit an extreme yet stable response to this stress across growth stages and years. A field experiment was conducted from 2023 to 2025 with 18 potato varieties bred by the Zamarte Potato Breeding Ltd. The experimental setup was a split-block design. Irrigation treatments were established as the main plots, and varieties as the subplots. At harvest, tuber yield and its quality were assessed. Aerial data was collected during UAV lights, which were conducted four times in 2023 and five times in 2024 and 2025, with 2-week intervals, starting from formation of basal side shoots below and above soil surface. The following Vis were derived from UAV imagery: NDVI, NDRE, GOSAVI, CI1, and MSR. In 2023, 2024, and 2025, yield reductions due to water stress were 54.6%, 21.1%, and insignificant, respectively. Accordingly, across all varieties tested, the earliest and strongest reduction in VIs was observed in 2023, and the weakest in 2025. Due to the ease of interpretation, NDVI was used to rank varieties based on their reaction to water limitations. Varieties Lawenda and, to a lesser extent, Gwiazda could be considered as those with the lowest NDVI and yield reduction, under no irrigation. Variety Astana did not reduce the canopy on unirrigated plots, but this was not reflected by higher yields. In contrast, Lenka might be regarded as a variety with the highest reduction in NDVI under water deficit, which also resulted in the highest yield decrease. Piwonia showed a slightly lower than Lenka, negative response to the deficit of water.

Potato breeding development under climate change conditions

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Progressive climate change constitutes one of the major challenges for contemporary potato production in Poland and across Europe. Increasing air temperatures, intensifying drought stress, and increasing variability in meteorological conditions negatively affect yield stability as well as the technological and processing quality traits of potato tubers. Therefore, breeding programs focused on developing cultivars with improved adaptability to environmental stresses and stable productivity under changing climatic conditions are becoming increasingly important.

One of the main objectives of potato breeding is enhancing tolerance to drought stress. Studies indicate that the response of potato genotypes to water deficit is complex and includes both physiological and morphological adaptations related to root system architecture, water-use efficiency, and recovery capacity after stress conditions. Drought tolerance is considered a polygenic trait requiring the integration of conventional breeding methods with modern molecular biology and functional genomics tools.

Another important breeding objective is increasing resistance to diseases, particularly late blight caused by *Phytophthora infestans*. Climate change may intensify pathogen pressure and reduce the effectiveness of genetic resistance. Consequently, breeding programs should focus on developing durable polygenic resistance, allowing a reduction in the use of chemical plant protection products.

An additional direction of breeding improvement is the shortening of the growing period of potato cultivars. Early-maturing genotypes are better able to avoid the negative effects of thermal stress and water deficit during the final stages of the growing season and are less susceptible to pathogen infection, especially *Phytophthora infestans*.

Studies also indicate that drought stress significantly affects tuber quality parameters, including starch content, reducing sugar levels, and metabolic activity during storage. These changes directly influence the technological and storage value of potato tubers and highlight the need for breeding selection focused not only on yield potential but also on the stability of quality traits under abiotic stress conditions.

The future of potato breeding requires the integration of conventional breeding approaches with modern phenotyping technologies, genomics, and molecular biology tools. The development of cultivars with enhanced drought tolerance, improved pathogen resistance, and shortened growing periods will be essential for adapting potato production to ongoing climate change and increasing environmental pressure.

Gene expression responses to drought and high temperature in potato: from robust normalization to markers of tolerance

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Climate change increasingly exposes potato production to concurrent drought and heat stress. We investigated transcript and protein responses in two contrasting cultivars—Gwiazda (tolerant) and Oberon (sensitive)—to identify robust reference genes and stress-responsive markers for the selection of resilient breeding lines. Using growth-chamber experiments across four treatments (control 21°C; drought 21°C; heat 38°C; and combined drought/heat), we identified EF1α as the most stable reference gene for RT-qPCR normalization across all conditions. To evaluate stress-signaling dynamics, we analyzed RAB18 and CUL3A. Both genes were significantly induced by drought, with expression peaking approximately three days after stress onset. Notably, the response in the sensitive cultivar (Oberon) was stronger and more delayed than in the tolerant one (Gwiazda). While high temperature attenuated the RAB18 induction ratio, CUL3A expression remained highly informative, suggesting its utility as a temperature-resilient indicator of drought response. Furthermore, we profiled the expression of selected aquaporins - Plasma membrane Intrinsic Proteins (PIP). In Oberon, drought repressed PIP transcripts at 21°C, a trend further exacerbated at 38°C. Conversely, Gwiazda maintained stable or slightly elevated expression across all stress treatments. Western blot analysis using commercial anti-PIP antibodies largely mirrored these transcriptional patterns: Oberon exhibited significant protein-level fluctuations and suppression under combined stress, whereas Gwiazda remained comparatively stable. Despite limited antibody specificity for individual potato PIP isoforms, the convergence of mRNA and protein trends identifies aquaporin regulation as a key discriminator of tolerance. Together, our results provide: (i) validated reference gene (EF1α) for reliable normalization under multi-stress conditions; (ii) RAB18/CUL3A dynamics that reflect genotype-specific stress intensity; and (iii) a PIP expression/protein signature that distinguishes tolerant from sensitive cultivars. These findings offer a practical molecular framework for screening breeding lines and linking water transport regulation with agronomic performance under a changing climate.

Epigenetic imprints of drought priming in potato cultivars

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Drought significantly limits potato production worldwide. In this study, we explored whether a single drought "priming" event can induce a stress memory that influences tuber yield and DNA methylation across subsequent generations. The cultivar Katahdin and five related cultivars were exposed to one period of drought and then cultivated under optimal conditions for two successive tuber generations.

Tuber yield was recorded and genome-wide DNA methylation patterns were analyzed. Plants previously exposed to drought produced markedly lower yields in the first generation, with only partial recovery observed in the second. Methylation analysis showed extensive, cultivar-specific alterations in the first progeny, with each cultivar displaying distinct differentially methylated regions (DMRs) as a result of priming.

These epigenetic modifications were inherited by the first generation but were largely reset by the second. Overall, our results demonstrate the presence of transgenerational drought stress memory mediated by DNA methylation in potato, with responses varying among cultivars. Insights into this epigenetic mechanism may contribute to the development of potato varieties with improved drought tolerance.

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Chlorophyll fluorescence as an indicator of environmental stress in potato plants: insights from physiological and morphological studies

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Potato (*Solanum tuberosum* L.) is a plant particularly sensitive to water deficits, due to its relatively shallow root system and large leaf transpiration surface. In the face of global climate change, understanding potato adaptation mechanisms to abiotic stress—especially drought—is becoming a priority for breeders and producers. Traditional methods for assessing resistance, based on biometric measurements and final yield, are time- and labor-intensive. Therefore, rapid, non-invasive diagnostic methods are sought. Chlorophyll a fluorescence, as an indicator of photosynthetic efficiency, has emerged as a powerful tool for detecting early stress signals, often before morphological symptoms (wilting, chlorosis) become visible to the naked eye.

The aim of this study is to analyze the usefulness of chlorophyll a fluorescence parameters as indicators of environmental stress in potatoes, with particular emphasis on drought stress, high temperature, and nutrient deficiencies, and to assess their correlation with final tuber yield.

The research is based on the analysis of measurements of photosystem II (PSII) quantum efficiency parameters. Key measured metrics include: – PSII maximum quantum yield, commonly considered an indicator of photoinhibition. – Performance Index, a sensitive parameter integrating energy flow through PSII. – Leaf Greenness Index (SPAD) and Leaf Area Index (LAI).

Studies show that chlorophyll fluorescence parameters precisely differentiate potato varieties in terms of their tolerance to unfavorable conditions. Drought stress leads to a significant drop in values. High temperature has been shown to exacerbate the negative impact of drought, leading to profound disruptions in electron transport during the light-sensitive phase of photosynthesis. Tolerant varieties maintain higher stability of fluorescence parameters compared to sensitive varieties. When grown in various systems (with limited fertilization), a strong positive correlation was found between photosynthetic parameters and tuber mass. Particularly high correlation coefficients were observed for the LAI index and photosynthetic efficiency parameters measured during the potato flowering phase.

The effect of drip irrigation on yield and dry matter content in potato varieties with colored flesh

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Irrigation of field crops has recently emerged as a critical factor in successful cultivation amid climate change and frequent water shortages during the growing season. Potatoes are highly sensitive to water shortages, particularly during tuber formation and later in the growing season. According to Akkamis et al., Badr et al., Crosby et al., and da Silva et al., whether using subsurface or surface methods. Varieties with colored flesh contain a range of health-promoting substances, such as anthocyanins, antioxidants, etc. Their cultivation carries a number of risks; these are mostly low-yielding varieties, and their drought resistance is lower than that of conventional varieties (Reyes- Cabrera et al., Rolbiecki et al., Wenzel et al.). Therefore, they were included in a field experiment with subsurface drip irrigation.

From 2023 to 2025, the field trial with drip irrigation evaluated the red-fleshed varieties Val Blue, Val Red, and Cibared in comparison with the yellow-fleshed variety Antonie. The field experiment at the VÚB Havlíčkův Brod research station was set up in two variants: non-irrigated and irrigated using drip irrigation. In each year, 300 mm (2023), 234.6 mm (2024), and 134.2 mm (2025) of irrigation water were supplied, depending on weather conditions. The data collected were subjected to analysis of
variance (ANOVA).

In 2023, the average yield for non-irrigated varieties was 30.82 t/ha, and for irrigated varieties, 53.14 t/ha. In this case, irrigation increased the tuber yield by 72%. With irrigation, the lowest yield was recorded for the Val Blue variety at 28.34 t/ha, and the highest for the Cibared variety at 74.69 t/ha. In 2024, for the non-irrigated variant, tuber yield ranged from 19.3 t/ha for the Val Blue variety to 43.7 t/ha for the Cibared variety. For irrigated varieties, yield ranged from 38.9 t/ha for the control variety to 89.5 t/ha for the Val Red variety. In 2025, tuber yield in the control non-irrigated variant ranged from 14.34 t/ha for the Val Blue variety to 42.06 t/ha for the Antonie reference variety. Significantly higher tuber yields were achieved by varieties in the irrigated variant (20.40 t/ha for the Val Blue variety). For most varieties of potatoes with colored flesh, drip irrigation increased tuber yield. In this case, the use of drip irrigation can act as a significant stabilizing factor in their cultivation, in accordance with the conclusions of Makani et al. and Gonzales et al.

Culinary evaluation of potato breeding lines in the fifth field generation as a tool for selection

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Culinary evaluation of potatoes is an integral part of the breeding program aimed at determining the suitability of lines for specific uses. In the breeding program conducted in Zamarte, culinary assessment begins in the second field generation and continues until a variety is released to the market, which takes approximately 8 years. Clones are either steamed or fried depending on the crossing combination. In the case of table-type lines, taste, culinary type, and flesh darkening after 10 and 24 hours from cooking are evaluated. Lines intended for French fries and chips are subjected to frying.

Based on culinary tests, clones characterized by undesirable taste or excessive flesh darkening after cooking are eliminated from further breeding. For French fries and chips, colour is the decisive parameter. In the case of internal defects occurring at early stages of breeding, lines are strictly eliminated. In more advanced breeding stages, a larger sample is taken to assess internal defects.

The study summarizes the results of lines evaluated three times, currently representing the fifth field generation. A total of 111 lines were assessed over three years (2023–2025). Among the tested clones, there were 53 table-type lines, 22 French fry-type lines, 5 chip-type lines, and 20 starch-type lines from which chips were prepared. Additionally, for 11 lines, both steaming and frying (French fries and chips) were performed.

The collected data illustrate the direction of the breeding program in Zamarte. It is likely that one or more of the evaluated clones will be released as new varieties within the next 5–6 years.

Creating bruise resistant cv. Maris Piper potatoes

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Mechanical damage during harvesting, handling and storage frequently causes internal bruising in potato (*Solanum tuberosum* L.) tubers, reducing quality and marketability, and hence resulting in food waste. Bruising results from cellular disruption and enzymatic browning reactions within damaged tissues. This study aims to characterise the spatial and temporal progression of bruise development in the commercially important cultivar Maris Piper under controlled impact and compression conditions. Tubers were subjected to impact and compression bruising treatments to simulate mechanical damage experienced during postharvest handling and storage. Impact bruising was induced using a drop-ball impactor (simulating a drop height of 70cm during processing), while compression bruising was applied using a weight-based apparatus to simulate a mechanical loading force of 32-40kPa. Bruised tissue was sampled from stolon and equatorial tuber regions across a 48-hour time course for post-impact treatments, with monthly sampling for pressure bruising treatments. Discolouration was quantified using digital image analysis to derive lightness, chroma and hue angle values describing bruise development. Statistical analyses assessed temporal and spatial differences in bruise progression. Additional samples from the same regions were collected for dry matter content (DMC) quantification. Bruise development showed strong region-, time- and storage-dependent responses. DMC was consistently higher in stolon than equatorial tissue during impact treatments, while temporal changes in DMC were limited overall. In contrast, colorimetric analyses indicated clear post-damage progression. Lightness, chroma and hue angle all changed significantly over time, with stolon tissue exhibiting earlier and more severe discolouration than equatorial tissue. These findings demonstrate clear spatial and temporal variation in bruise development and indicate the influence of storage duration on bruise susceptibility in cv. Maris Piper tubers. These findings provide a foundation for future transcriptomic analysis to identify genes involved in bruise response pathways, with subsequent CRISPR-based gene editing used to evaluate their role in improving tuber bruise resilience.

Abstracts

Posters

Impact of drought and high temperature on the expression of aquaporin-encoding genes

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Drought and high temperature increasingly threaten agricultural productivity, making it essential to understand plant responses to these stresses. Potato, although highly sensitive to temporary water deficits, displays significant genetic variability, offering opportunities to breed cultivars with improved tolerance. Developing a rapid marker-based test for selecting stress-tolerant breeding lines would accelerate the creation of improved cultivars.

This study examined the expression of genes encoding aquaporins—membrane proteins forming water channels that regulate cellular water transport. Aquaporins play crucial roles in photosynthesis, seed germination, root development, and maintain cellular homeostasis under stress. Their regulation is complex and understanding it may provide practical insights for crop improvement.

Two potato cultivars with contrasting drought tolerance were analyzed: Gwiazda (tolerant) and Oberon (susceptible). Plants were subjected to drought stress and high temperature (38°C). Samples from stressed and well-watered plants were used for real-time RT-qPCR to quantify expression of selected plasma membrane aquaporins (PIP2-8, PIP1-4, PIP2-6).

In Gwiazda, drought stress caused an approximately twofold increase in aquaporin expression relative to controls. This increase was not observed in the susceptible cultivar Oberon. Under high temperature, both cultivars exhibited decreased aquaporin transcript levels, indicating that heat and drought trigger distinct regulatory pathways.

Previous findings show that reduced StPIP1 expression leads to impaired seed germination, abnormal leaf elongation, faster wilting, and reduced growth (Wang et al., 2017). These observations are consistent with morphological traits in our study: Oberon showed strong wilting under water deficit.

The drought-induced upregulation of aquaporins in the tolerant cultivar suggests that aquaporin expression may serve as a molecular marker of drought tolerance in potato. Conversely, the consistent decrease in expression under high temperature indicates that these genes may reflect drought tolerance specifically, but not heat tolerance.

Development of an IPM assessment tool for comparing crop protection scenarios taking into account potato cultivation

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Pesticides play a central role in modern agriculture by protecting yields and reducing crop losses. However, their intensive use poses significant risks to human health, biodiversity, and the environment. Achieving sustainable agri-food systems, as envisioned in the EU Farm to Fork Strategy, requires reducing reliance on high-risk pesticides and promoting Integrated Pest Management (IPM). Despite policy support, IPM adoption remains limited due to structural barriers, economic constraints, and the lack of practical tools that allow farmers to assess and compare crop-protection strategies at field level.

To address this gap, the EU-funded project SUPPORT (Supporting Uptake of Integrated Pest Management and Low-Risk Pesticide Use) developed the IPM Monitoring (SIM) tool. SIM is a web-based, scenario-driven self-assessment tool that evaluates crop protection strategies using environmental, economic, and health indicators. It integrates operational costs, greenhouse gas (GHG) emissions, and a newly developed Pesticide Load Indicator harmonised for Europe (PLEU).

The SIM tool was validated using real-world data from ten European countries, covering eight crops and 112 active ingredients. For each crop, at least two management scenarios were analysed, including conventional practices and improved IPM strategies. This validation demonstrates the scalability of the tool and its ability to capture diverse crop-protection practices across Europe.

SIM allows farmers and advisors to construct detailed management scenarios, including tillage systems, mechanical and chemical interventions, machinery use, costs, and expected yields. The tool calculates pesticide-related risks, GHG emissions, and operational costs, presenting results via dashboards and downloadable reports. Users can compare strategies, identify high-risk practices and active ingredients, and evaluate trade-offs between environmental, economic, and health impacts.

The aim of the study is comparing two potato production scenarios in Poland conventional management with IPM scenarios. By linking field-level decisions to sustainability objectives, SIM demonstrates how scenario-based monitoring tools can support informed decision-making, advisory services, and the wider adoption of low-risk crop protection strategies.

The effectiveness of mechanical and chemical haulm destruction in potatoes

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Destroying potato haulms is important for controlling tuber size, improving skin set and managing diseases, as well as making harvesting easier. In seed potato production, it is particularly important for limiting virus infections, which have a significant impact on the quality of seed tubers. The ban on diquat, which came into force in 2019, has substantially restricted the range of chemical options available for effectively destroying potato haulm. This study therefore focused on evaluating the effectiveness of various strategies for destroying potato haulms in terms of reducing biomass and preventing regrowth. In 2025, a block experiment was set up in Slovenia at Spodnji Brnik, involving three different methods of destroying the potato haulm and ten late-maturing cultivars of potato. In the first treatment, mulching was the only method applied, on 25 August 2025, using a specialised, two-row potato flail mower (Grimme). The second treatment involved mulching followed by chemical desiccation using carfentrazone-ethyl (60 g/ha) the next day. The third approach, which was non-chemical, combined mulching with additional thermal haulm destruction using the HOAF KB 1.5 Twin machine two days later. This system integrates a conventional flame weeder with a closed chamber that provides supplementary infrared radiation. Visual assessments of the proportion of destroyed haulm and the number of regrowing plants were conducted on 4 September 2025. The results showed that mulching alone was ineffective, as regrowth was observed in all cultivars evaluated, with an average regrowth of 47.1%, ranging from 7.4% for the Cartagena variety to 100% for the Lucinda variety. While the combination of mulching and flaming did not completely eliminate regrowth, it substantially reduced it to 13.7%, ranging from 0% in the KIS Sora variety to 38.9% in the Lucinda variety. The combination of mulching and carfentrazone-ethyl application provided the highest level of control, with regrowth detected only in the Alverstone Russet (1.9%) and Peter Pan (16.7%) cultivars. Our findings indicate substantial differences in cultivar sensitivity to the evaluated haulm destruction methods, highlighting the need for further research into non-chemical approaches to potato haulm destruction.

Comparison of NDVI from Sentinel-2 and drone imagery for estimating potato tuber yield in commercial fields

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Potato tuber yield is of key economic importance and depends on the course of the growing season as well as on diverse environmental and agronomic conditions. Consequently, remote sensing methods are becoming increasingly important because they enable monitoring of crop condition during the growing season and assessment of yield potential. The normalized difference vegetation index (NDVI) is a useful tool for evaluating various aspects of crop condition, reflecting photosynthetic activity and overall plant vigor.

The aim of the study was to assess the relationship between NDVI and potato tuber yield in 11 production fields in Poland during 2020-2022. Drone flights using a Phantom 4 Multispectral were carried out at two-week intervals. Orthorectified reflectance maps were prepared in Pix4Dfields (Pix4D S.A., Prilly, Switzerland), and NDVI was calculated in QGIS 3.16. Several sampling areas (3 m^2 each) were designated within each field, and potato tubers were harvested manually from these areas at the end of the growing season.

NDVI values derived from Sentinel-2 imagery showed significant correlations with potato tuber yield more frequently than NDVI values derived from drone imagery. Moreover, the dates on which significant NDVI-yield relationships were observed differed between satellite and drone data. In some fields, no significant correlations were found between drone-derived NDVI and potato tuber yield, whereas significant relationships were identified using Sentinel-2 imagery. The relationship between NDVI and potato tuber yield was strongly dependent on location, year, observation date, and data acquisition method. The higher temporal frequency of satellite observations allowed more precise identification of the periods when NDVI was significantly related to tuber yield. Furthermore, despite the higher spatial resolution of drone imagery and the use of the same sampling areas for NDVI assessment and tuber yield measurements, satellite-based NDVI appeared to provide a more stable signal at the field scale. In contrast, drone-based assessment may have been more sensitive to local small-scale variability, especially under highly heterogeneous field conditions.

Alternatives to crop rotation in long-term potato monoculture

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Long-term continuous potato cropping is usually associated with reduced tuber yield, deterioration in crop structure, and a lower share of marketable tubers. A long-term field experiment conducted at the Production–Experimental Station in Bałcyny near Ostróda, belonging to the University of Warmia and Mazury in Olsztyn, evaluated the possibility of compensating for the lack of crop rotation through intercropping, cultivar selection, and chemical plant protection. Potatoes in monoculture have been grown at this site continuously since 1973, while a six-course crop rotation system has been conducted in parallel within the experiment.

In 2015–2018, both cropping systems (crop rotation and monoculture) included, in accordance with the original experimental design, two potato cultivars—Catania and Red Sonia—grown under three plant protection variants: without plant protection products, with herbicides, and with herbicides combined with fungicides. In the second experimental period (2019–2023), an additional intercrop of oilseed radish (*Raphanus sativus* L.) cv. Rolterra was introduced in both cropping systems. The results obtained in 2015–2023 (43rd–51st year of continuous monoculture) were compared with a six-course crop rotation system including potato, oat, flax, winter rye, faba bean, and winter triticale.

The introduction of intercropping significantly reduced the negative effects of long-term potato monoculture and proved more effective than cultivar selection or chemical plant protection. In the Catania cultivar, the yield difference between crop rotation and monoculture decreased from 50.4% in the first experimental period to 22.3% after the introduction of intercropping. In the Red Sonia cultivar, the corresponding values were 45.5% and 12.9%. Intercropping also increased the share of marketable yield in monoculture from 35.1% to 51.9% for Catania and from 23.6% to 35.8% for Red Sonia. The effect of increasing the intensity of chemical plant protection was relatively limited, reducing yield losses by only 6.6%.

The results indicate that oilseed radish as an intercrop can effectively mitigate the negative consequences of long-term continuous potato cropping, improving total yield, yield stability, and the proportion of marketable tubers, while reducing dependence on chemical plant protection.

Less fertilizer, same yield: Improving nitrogen efficiency in starch potato production

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Improving nitrogen use efficiency in starch potato production is essential to reduce environmental impacts and comply with increasingly strict fertilization regulations in nitrate-vulnerable zones, yet maintaining yield and quality under reduced fertilization remains a key agronomic challenge.

However, despite previous research, it remains unclear whether fertilization below recommended nitrogen rates can reliably maintain yield, starch content and improve nitrogen efficiency in modern cultivars under present-day production conditions.

To address this, multi-site field experiments were conducted across four years in northern Germany within the PotenzioN project ('Potentials for increasing nutrient efficiency and reducing nitrogen emissions in starch potatoes') to evaluate reduced nitrogen inputs under practical conditions.

Experiments (2021–2024) were carried out at four sites using a randomized block design with multiple cultivars, an unfertilized control, and mineral and organic fertilization at 80% (144 kg N ha-1) and 100% (180 kg N ha-1) of the recommended rate, reflecting current fertilization practice.

Across sites and years, the recommended fertilization rate (100%) showed no significant advantage over the reduced rate (80%) for fresh matter or starch yield. The unfertilized control generally produced lower yields, although differences were not consistently significant. Slightly higher fresh
matter yields at 100% were offset by increased starch contents at 80%, resulting in equal or higher starch yields under reduced fertilization. Organic fertilization tended to result in higher yields than mineral fertilization, but maximum starch yields were frequently achieved at 80% in both systems.

Higher nitrogen uptake at 100%, particularly in aboveground biomass, did not translate into yield gains, indicating improved nitrogen use efficiency at reduced fertilization. These patterns were consistent across cultivars, although one cultivar consistently showed the highest performance across experiments, while overall yield levels were mainly driven by site and year rather than fertilization level.

Reducing nitrogen fertilization to 80% of the recommended rate can maintain yield and starch content while improving nitrogen use efficiency. This may reduce input costs and environmental risks such as nitrate leaching and N_2O emissions, and allow nitrogen savings to be allocated to crops with higher demand.

Optimizing nitrogen use in potato cultivation: insights from multi-site field trials

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Introduction
Nitrogen (N) fertilization is a key determinant of potato yield and quality. However, current fertilization guidelines often overlook cultivar-specific N requirements. With increasing regulatory pressure on nutrient inputs, optimizing N use efficiency is essential for sustainable potato production.
Methods
In 2025, a multi-site field trial was conducted at three Belgian locations (sandy loam, loam, and clay soils) to evaluate four potato cultivars (Alegria, Challenger, Fontane, Markies) under four N application levels (0, 75, 150, 225 kg N ha^{-1}), split-applied at planting and tuber initiation. Parameters assessed included crop growth, canopy senescence, N uptake in shoots and tubers, final yield, and post-harvest soil nitrate.
Results
Unfertilized plots showed reduced early growth, faster senescence, and significantly lower yields. Alegria, an early-maturing cultivar with low N demand, reached near-maximum yield and N uptake at 75 kg N ha^{-1}. In contrast, the later-maturing cultivars required higher N inputs (150–225 kg N ha^{-1}) to achieve optimal yields, though yield gains between 150 and 225 kg were modest and often not significant. Residual soil nitrate increased sharply at 225 kg N ha^{-1}, indicating reduced N use efficiency. Nitrogen uptake patterns reflected cultivar-specific traits such as canopy duration and N translocation dynamics.
Discussion
These findings highlight the inadequacy of uniform N recommendations based solely on maturity class. Tailoring N fertilization to cultivar-specific needs and site conditions can enhance yield and N efficiency while minimizing environmental impact. This approach gains relevance as more cultivars with significantly lower N requirements enter the market, offering new opportunities for sustainable intensification in potato systems.

Preliminary in vivo evaluation of a granular fertilizer derived from potato starch processing by-products as a potential nitrogen substitute in potato

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Circular valorisation of potato starch processing by-products creates opportunities to develop value-added fertilisers for potato production. In this study, a granular organic fertiliser was produced from potato cell juice retentate obtained after ultrafiltration. The technology combines membrane-based processing of potato cell juice by-products with subsequent concentration and granulation steps. Laboratory- and pilot-scale filtration work included microfiltration testing in the 0.2 µm range (with 1.1 µm planned for further evaluation), while pilot processing with a dynamic cross-flow filter enabled concentration of potato cell juice solids to 15-20%; in one 2 m3 batch, approximately 80 L concentrate was obtained, corresponding to about 24-fold concentration. The retentate was then heated at 60-70 °C with continuous stirring, dried in a thin layer at 35-45 °C, mechanically granulated using a screw extruder, and dried to a moisture content below 7%.

The resulting product is a plant-derived organic material corresponding to PFC 1(A) organic fertiliser. Granule analysis showed 6.6% moisture, 93.8% dry matter, 94.61% organic matter in dry matter, 5.39% ash, and 10.8% total nitrogen.

An in vivo experiment under controlled conditions was conducted to evaluate the suitability of the new product as a nitrogen source for potatoes. Plants are grown in a peat-based substrate amended with perlite. The study includes two potato cultivars and four fertilisation treatments: mineral fertilisation without N, mineral fertilisation with mineral N, mineral fertilisation with the new organic product as a substitute for mineral N, and mineral fertilisation with the new product as a substitute for mineral N combined with Trichoderma viride. Nitrogen was supplied at 1.0 g N per 10 L of substrate in the mineral N treatment and at 1.5 g N per 10 L of substrate in the organic fertilizer treatments, considering the slower expected nitrogen availability from the organic product.

At this stage, the experiment is in the early phase, and the available data are limited to plant emergence. Emergence observations confirmed the successful establishment of potato plants and provided the basis for further assessment of treatment effects on plant physiological status, growth, and yield parameters. Subsequent evaluations will include SPAD and additional growth- and yield related traits.

This research is being conducted within the project No. 1.1.1.3/1/24/A/155 (BioFromPot).

Assessment of potato resistance to a small-spored alternaria strain and the antifungal potential of four essential oils for its control

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Worldwide, potato (*Solanum tuberosum* L.) ranks as the fourth most important food crop after the major cereals: wheat, and rice. In Algeria, potato represents the leading agricultural crop, even surpassing wheat, with a production exceeding 4.6 million tons cultivated over approximately 150,000 hectares. The aim of this study was to evaluate the resistance of potato to a virulent small-spored Alternaria strain and to investigate the antifungal activity of four essential oils (lemon, orange, mandarin, and bitter orange) in its control. To achieve this, a detached leaf assay was conducted on the potato cultivar Spunta and four resistance parameters were measured: incubation period, latency period, lesion size, and sporulation intensity. For the control strategy, three different concentrations of each essential oil were incorporated into the PDA culture medium, onto which mycelial fragments were placed, and the inhibition zones were measured after 7 days of incubation. The results indicate that mandarin essential oil appears to be the most effective (68%), followed by lemon (58%). Bitter orange essential oil showed limited efficacy (18%) but remained slightly more effective than orange essential oil, which proved to be ineffective.

Broad host range and host-dependent pathogenicity of Algerian *Pectobacterium* isolates associated with potato soft rot

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Potato soft rot and blackleg caused by soft-rot *Pectobacteriaceae* are major constraints to potato production in Algeria, yet the pathogenic diversity of local *Pectobacterium* populations remains poorly documented. This study presents the first comprehensive quantitative assessment in Algeria of the host range and host-dependent pathogenicity of 12 representative Pectobacterium isolates recovered from symptomatic potato stems and tubers collected in five major potato-producing regions between 2018 and 2023; six reference strains were included for comparison. Isolates were characterized by phenotypic and biochemical tests and confirmed by PCR using the genus-specific Y1/Y2 primers. Pathogenicity was evaluated under greenhouse conditions on nine cultivated host species representing five botanical families, and disease severity was assessed 21 days after inoculation using a disease index (DI). Data were analyzed by two-way ANOVA, Tukey's HSD test, hierarchical clustering, and principal component analysis. All isolates showed typical pectinolytic activity, yielded the expected PCR amplicon, and induced soft rot on potato tuber slices. Whole-plant assays revealed a broad host range, but disease expression was strongly host dependent. Potato was the most susceptible host, with most isolates inducing maximal tissue maceration (DI = 100%), while tomato and sunflower also developed severe symptoms. In contrast, maize, turnip, pepper, and cardoon showed lower or more variable susceptibility. Disease severity was significantly affected by isolate, host species, and their interaction ($P < 0.001$). These findings demonstrate substantial pathogenic diversity within Algerian *Pectobacterium* populations and provide a basis for seed health surveillance, crop rotation planning, and integrated soft rot management in potato-based cropping systems.

Mechanical phenotyping of diploid potato genotypes differing in PVY resistance using micro-extensometry

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Plant growth depends on coordinated genetic regulation, cellular signaling, and the mechanical properties of the cell wall. Because irreversible wall extension under sustained stress is a key component of growth, measurements of tissue extensibility and creep may provide useful phenotypic markers of plant responses to biotic stress.

In this study, selected diploid potato genotypes differing in genetic resistance to Potato virus Y (PVY) were inoculated with PVY and analyzed three days after inoculation. Leaf mechanical behavior was assessed using a micro-extensometer with optical tracking operated through MorphoRobotX software.

The aim was to evaluate whether PVY resistance status is associated with differences in leaf mechanical properties after infection and to test the usefulness of this interdisciplinary phenotyping approach for potato research. This approach integrates plant virology, genetics, and biomechanics and may support the development of new tools for biophysical characterization in crop improvement.

Smart farming in potato cultivation: AI/ML-designed nanobioreceptors for PLRV detection and safe peptide-based crop protection

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Potato leafroll virus (PLRV) remains one of the most destructive viral pathogens of potato, causing severe yield losses and compromising tuber quality worldwide. To address this challenge, we applied an integrated AI/ML-driven pipeline to design nano-scale peptide bioreceptors targeting the PLRV capsid (PDB ID: 6SCO) for both sensitive detection and peptide-based interference with virus propagation.

In the first stage, the virtual phage display platform called – PeptAIm, generated large combinatorial libraries of short peptides (4–7 amino acids), which were subsequently screened by high-throughput docking against structurally defined binding pockets of the capsid, including inter-subunit interfaces and the RNA-packaging region. Docked complexes were refined by molecular mechanics and solvent-explicit energy minimization, enabling quantitative evaluation of non-bonded interaction energies (electrostatic and van der Waals) and identification of favourable binding motifs. This *in silico* workflow revealed two functionally distinct classes of peptides: (i) destabilizing binders that occupy key assembly interfaces or perturb RNA-packaging sites, thereby predicted to hinder capsid formation and limit systemic infection, and (ii) stabilizing binders that reinforce inter-subunit contacts, suitable for engineering virus-like particles as standardized antigenic and diagnostic materials. Selected peptide sequences can be either immobilized on electrochemical or use in optical sensors as nanobioreceptors for PLRV detection in field-relevant samples. In parallel these AI/ML generated peptides can be evaluated as safe crop-protection candidates that do not rely on conventional pesticides. The presented approach demonstrates how AI/ML-assisted peptide design, combined with rigorous structure-based simulations, can accelerate development of smart farming tools that simultaneously enhance phytosanitary monitoring and support environmentally friendly control of viral diseases in potato cultivation.

Population structure of *Phytophthora infestans* in Poland

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Phytophthora infestans (Mont.) de Bary, Oomycetes, is the most destructive potato (*Solanum tuberosum* L.) pathogen worldwide. Late blight caused by *P. infestans* is an airborne disease, but seed potatoes are another source of inoculum and may contribute to the dissemination of pathogen strains. This pathogen is heterothallic, with asexual and sexual life cycles. The goal of this work was to analyse the genetic structure of the population of *P. infestans* in Poland, focusing on a role of seed tubers in pathogen migration and on the role of sexual recombination in generating diversity. Every year, potato seed tubers came from the same sources in all experiments, which provided a unique opportunity to study the migration of *P. infestans*. An additional goal was to monitor *P. infestans* population for the presence of the isolates from European clonal lineages.

Potato leaflets with single late blight lesions were collected from unprotected fields in 11 different locations in Poland, in years 2016-2021 and 2024. The total number of obtained *P. infestans* isolates was 996. Mating type, mitochondrial haplotype and diversity of 12 microsatellite markers were determined. Resistance to metalaxyl was tested on rye A agar media. For virulence scoring, a subset of *P. infestans* isolates were tested in detached leaflet assays on 11 Black`s differentials and new resistance sources.

Phytophthora infestans isolates of both mating types (A1 - 482, A2 - 373), two mitochondrial haplotypes (Ia - 588, IIa - 268), sensitive (467), intermediate (120), resistant (244) to metalaxyl were detected. While virulence against all resistance genes was observed the frequency at which each occurred varied markedly. Among 858 *P. infestans* isolates from years 2016-2021, 309 multi locus genotypes (MLGs) were identified. 204 isolates belonging to five European *P. infestans* genotypes were described: EU13 (113), EU34 (30), EU41 (23), EU36 (23) and EU37 (15). The remaining, 654 isolates of *P. infestans*, belonged to MLGs unique to Poland which strongly suggests sexual recombination. In 2024, we identified *P. infestans* isolates of the genotype EU43, which is resistant to active substance of fungicides, mandipropamid, but also genotype EU45. Our study emphasizes the sexual recombination and seed potato-related migrations as factors affecting the *P. infestans* population structure in Poland, increasing the pathogen's genetic adaptability.

Potato – *Globodera pallida* interaction during the resistance reaction in the roots of potato plants attacked by larvae of the white cyst nematode at the di- and tetraploid level

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Potato cyst nematodes are sedentary parasitic nematodes that attack potato plants. The most effective and the most environmentally safe method of their control is based on the cultivation of resistant potato varieties. However, the cultivation of varieties resistant to the golden potato cyst nematode (*Globodera rostochiensis*) leads to an uncontrolled increase in populations of the pale potato cyst nematode (*G. pallida*). This constitutes a major problem because there are no highly resistant forms to this pest species available in the potato breeding pool in Poland. Moreover, the latest reports indicate a breakdown of resistance introduced into cultivated potato germplasm from the source *Solanum vernei*. Therefore, the search for new sources of resistance to this quarantine pest is well justified.

As part of previous studies, resistance to the Pa2 and Pa3 pathotypes of *G. pallida* was characterized in a new source – the wild species *S. gourlayi*. This resistance is pathotype-specific and may be controlled by different genes. Genomic regions involved in the resistance response occurring in potato plants under attack by *G. pallida* larvae were identified.

QTLs responsible for nematode resistance were identified on potato chromosomes II, IV, V, VI, VII, X, XI, and XII, explaining from 10.1 to 21.5% of the observed variation. The most significant QTL responsible for resistance to the Pa2 pathotype of *G. pallida* was identified on chromosome XII, explaining 20.9% of the observed variation. The most significant QTL for resistance to the Pa3 pathotype of *G. pallida* was identified on chromosome VI, with the CAPS marker Exp928 at its peak, explaining 21.5% of the observed variation. In the reference region of the potato genome on chromosome VI, corresponding to the location of our strongest QTL for cyst nematode resistance, four genes encoding expansins are located, which may represent candidate genes underlying the resistance conferred by this QTL.

The resistance identified in *S. gourlayi* was introduced into diploid interspecific potato hybrids and into the tetraploid cultivated form. At both the diploid and tetraploid levels, potato plants attacked by larvae of the pale potato cyst nematode exhibit a resistance response based on restricting the formation of proper syncytia. However, the resistance response occurring at the tetraploid level is clearly stronger.

The StBBX22 protein is involved in cultivated potato reproduction

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B-box (BBX) proteins are a diverse group of zinc finger transcription factors and regulators found in many plant species. They are defined by unique, highly conserved B-box domains, though some also possess a CCT domain and VP motif. Family members differ widely in structure and play distinct roles in plant growth and development. These roles include regulating seed germination, photomorphogenesis, thermomorphogenesis, floral transition, tuberization, senescence, hormonal pathways, and responses to biotic and abiotic stimuli.

In this work, we dissect the physiological role of the StBBX22 protein in potato reproduction that localizes to both the cytosol and nucleus. We revealed that *Solanum tuberosum* stbbx22 knockout mutants produced significantly fewer tubers than wild-type (WT) and StBBX22-overexpressing lines. Overexpressing plants also had markedly more flowers than stbbx22 and WT plants. Additionally, we found that StBBX22 protein interacts with StSP6A and StFTL1, key FT-like family members, which are crucial regulators of tuberization and flowering. Altogether, our data show that StBBX22 advances potato reproduction, enhancing flowering and tuber yield.

Evaluating potato regeneration ability through cell cycle parameters

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Efficient plant regeneration in vitro is essential for the application of modern genomic techniques and bacterial vector–mediated transformation, yet potato often exhibits slow and inefficient shoot regeneration. Plant growth and development rely on key cell cycle processes—mitosis, endoreplication, and meiosis—with mitosis playing a central role in organ formation. The cell cycle is composed of four phases (G0/G1, S, G2, and M), regulated by cyclins (CYC) and cyclin-dependent kinases (CDKs).

In this study, we evaluated the regenerative capacity of 20 potato genotypes, including 18 diploid interspecific hybrids and 2 cultivars maintained under in vitro conditions. Cell cycle progression was assessed at 9, 12, 15, and 28 days following explant transfer. We analyzed the proportion of cells in G1, S, and G2 phases, as well as the endoreduplication index (SCV) and the ratio of nuclei with DNA content greater than 2C to 2C nuclei (Σ>2C/2C). In parallel, phenotypic traits were recorded, including the number and length of roots and shoots, leaf number and size, and the percentage of regenerated plants.

Our results revealed clear differences between genotypes with high and low regeneration capacity, reflected in cell cycle dynamics, morphological characteristics, and the expression of genes associated with cell cycle regulation. These findings highlight the importance of cell cycle parameters as indicators of regenerative potential in potato tissue culture.

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Wound-induced transcriptional dynamics reveal bulk-dependent differences in potato tuber wound-response programmes

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Mechanical injury to potato tubers during harvest and post-harvest handling reduces quality by increasing water loss and creating entry points for microorganisms. The early transcriptional dynamics of tuber wound responses and their variation within breeding material are not fully characterised. We analysed RNA-seq data from two phenotypically contrasting tuber bulks of the DS-13 diploid potato mapping population, derived from parents differing in response to soft-rot bacteria. Motivated by observations that resistant genotypes tend to show faster wound suberisation, we focused here exclusively on the transcriptional response to mechanical wounding. Wounded tuber tissue was compared with non-treated tissue (W vs NT) in the two bulks, designated R and S, at 8, 24 and 48 h after wounding; wounded tubers were incubated at 27 °C. Differential expression was defined as FDR ≤ 0.01 and |log2 fold change| ≥ 2. Wounding induced broad transcriptional activation in both bulks. At 8 h, 665 genes were upregulated in both bulks, with 300 R-bulk-specific and 309 S-bulk-specific genes. At 24 h, the response remained extensive but became more bulk-specific: 548 genes were shared, whereas 737 and 709 genes were specific to the R and S bulks, respectively. By 48 h, the wound-induced gene set was larger in the R bulk than in the S bulk (392 vs 110 genes), including 320 R-bulk-specific and 38 S-bulk-specific genes. KEGG enrichment analysis of wound-upregulated genes revealed recurrent enrichment of phenylpropanoid biosynthesis, together with phenylalanine metabolism, glutathione metabolism, MAPK signalling, ABC transporters, and cutin, suberin and wax biosynthesis in selected bulk-time combinations. These categories are consistent with transcriptional activation of processes linked to wound periderm formation, oxidative metabolism, signalling and barrier-associated functions, but they should not be interpreted as direct evidence of completed suberin deposition. The results suggest that the two tuber bulks initiate a broadly comparable wound-induced transcriptional programme, but differ in its persistence and pathway composition over time. This wound-only analysis identifies candidate pathways for future validation in relation to tuber wound-healing capacity and post-harvest resilience.

Variation of amylose/amylopectin ratio in potato starch across varieties, growing systems and years

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Starch is the main component of potato tubers, accounting for roughly three-quarters of tuber dry matter, and it strongly influences storability, processing performance, and nutritional properties. Potato starch is composed primarily of amylose and amylopectin, and their ratio is a main factor determining the physicochemical and functional properties of starch. Although potato starch typically contains about 20–30% amylose and 70–80% amylopectin, these proportions vary with genotype and environmental conditions. Higher amylose content is often associated with increased resistant starch formation, whereas amylopectin-rich starch tends to be linked with a higher glycaemic response. Previous research indicates that genotype is a major driver of starch quality traits (including total starch, amylose content and granule size), while growing conditions and year-to-year weather variation, soil characteristics and tubers maturity can also have significant effects. However, comparatively less attention has been paid to how environmentally friendly farming systems, particularly low-input and organic systems with reduced or no mineral fertiliser, affect starch composition across multiple seasons. This study will evaluate the influence of genotype, growing system (low-input and organic), and several year weather conditions on the amylose/amylopectin ratio in potato starch. Ten potato varieties will be assessed in different growing systems over several growing seasons, enabling identification of the most significant factors shaping starch composition and their interactions.

Research was carried out with the support of the National FLPP Projects lzp-2019/1-0371 (Potato breeding for low input and organic farming systems: nitrogen use efficiency and quality aspects of potato protein) and lzp-2025/1-0559 (Linking genotype, farming system, and processing: nutritional and biochemical profiling of freeze-dried potatoes).

Metabolomic and biochemical analysis of four potato cultivars (*Solanum tuberosum* L.) from an organic farm

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According to the Food and Agriculture Organization of the United Nations (FAO), the potato ranks fourth in terms of food production, behind rice, wheat, and corn, and first among tuber and root crops. The importance of the potato cannot be overstated. It is a valuable source of carbohydrates, antioxidants, and vitamins. Many studies focus on the metabolic processes occurring in the potato plant to elucidate the mechanisms responsible for yield, the accumulation of compounds determining flavor and nutritional value, the maintenance of tuber quality during storage, the plant's resistance to pathogens, etc. The sum of metabolites produced as a result of metabolic network activity is defined as the metabolome. Comprehensive studies of metabolic diversity using state-of-the-art chromatographic methods and highly precise detection of individual compounds have revealed the specificity of metabolic profiles from the subcellular to the organismal level, as well as their remarkable plasticity under the influence of various internal and external stimuli. Metabolomic approaches are already being used to phenotype available cultivars, assess the resistance of potato plants to environmental challenges, and detect changes occurring in tubers during cultivation in various production systems.

The aim of the study was to investigate the metabolomic changes occurring in the tubers of the potato *Solanum tuberosum* L. grown under organic conditions, with particular emphasis on the synthesis and distribution of health-promoting compounds, including those with high antioxidant potential. The global metabolite profile of potato genotypes was determined using mass spectrometry (MS) combined with high-resolution separation techniques, such as liquid chromatography (LC) and gas chromatography (GC). The study was conducted on four potato cultivars: Finezja, Oberon, Meluzyna, and Tajfun. To identify the nutrients with the greatest impact on the antioxidant potential of potato tubers, their total antioxidant activity was assessed by using the FRAP (Ferric Reducing Antioxidant Power) method. Another objective of the study was to determine the extent to which organic farming affects metabolic pathways in potato tubers. Mass spectrometry provided important information regarding the qualitative and quantitative specificity of the potato metabolome.

Phenolic compounds and antioxidant potential of coloured-flesh potato tubers under temperate climate conditions of Poland

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The increasing demand for functional foods creates a need to identify raw materials with enhanced nutritional value. The aim of this study was to comparatively evaluate the profile of phenolic compounds and antioxidant activity of eight potato cultivars differing in tuber flesh colour. The study included five coloured-flesh cultivars (“Rote Emma”, “Blue Salad”, “Vitelotte”, “Red Emmalie”, “Blue Congo”) and three light-flesh cultivars (“Bella Rosa”, “Lord”, “Tajfun”), cultivated in south-eastern Poland in the years 2023–2025. Phenolic acids and anthocyanins were analysed using highperformance liquid chromatography (HPLC), while antioxidant capacity was determined using DPPH and FRAP assays.

Chlorogenic acid was the dominant phenolic compound in all analysed cultivars (62.37–116.88 mg·100 g^{-1} FM). Coloured-flesh cultivars exhibited significantly higher total phenolic content and the presence of specific anthocyanins, including derivatives of pelargonidin, peonidin and petunidin. The “Vitelotte” cultivar showed the highest antioxidant capacity, exceeding that of the “Lord” cultivar by more than twofold.

A clear relationship between tuber flesh colour and biological activity was observed, indicating the high potential of coloured-flesh potato cultivars for the development of functional foods and applications in the pharmaceutical industry. These findings may also support breeding strategies aimed at developing potato cultivars with enhanced health-promoting properties.

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For 30 years, EUROPLANT Polska Sp. z o.o. has been developing potato breeding and the production of certified seed potatoes in Poland. The company offers a wide portfolio of table potato varieties, including Vineta, Corinna, Bernina, and Otolia, as well as varieties for processing, such as starch varieties including Zuzanna and Euroresa, chip varieties such as Omega and Sorentina, and French fry varieties such as Donata and Etana. Production is carried out on two seed farms in northern Poland, with an emphasis on high plant health and quality. As the Polish market leader, Europlant sets the direction for the development of individual potato production sectors, seeking the best solutions in variety selection and agronomy to meet the demands of the market and consumers.

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PMHZ Ltd. is a Polish breeding and seed company specializing in potato breeding and the production of seed potatoes. For more than 70 years, the company has been developing potato breeding programs and providing farmers with modern varieties adapted to market needs.

PMHZ operates through four branches located in northern Poland, conducting breeding activities and producing certified seed potatoes.

Our portfolio includes both table and starch potato varieties. The company is particularly recognized as one of the leading domestic breeders of starch potato varieties in Poland.

PMHZ combines the tradition of Polish plant breeding with modern seed production, focusing on quality, production safety, and the development of varieties that meets the challenges of contemporary agriculture.