eapr
2024

22nd EAPR Triennial conference
Oslo, Norway, July 7-12, 2024

Book of abstracts

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22nd EAPR Triennial conference
Oslo, Norway, July 7-12, 2024

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Content

Detailed program per day	4
Keynote abstracts	8
Session 1 – Breeding robust cultivars	24
Session 2 – Improved potato health	49
Session 3 – Integrated pest management	56
Session 4 – Improved soil health	72
Session 5 – Agronomy and tuber physiology	76
Session 6 – Precision technology in potato cultivation	92
Session 7 – Sustainability in a changing climate	99
Session 8 – Post harvest	109
Poster list	120
Poster abstracts	124

Monday July 8

Conference hall Atlantis 1 + 2

9.00	Opening ceremony and plenary session Chair: Arne Hermansen and Ian Toth
9.30	Keynote: Food security. Potato: the smart crop for food security. Monica Parker, International Potato Center, Vancouver, Canada
10.00	Coffe break
10.30	Keynote 2: Insects as vectors of pathogens. May Bente Brurberg, NIBIO and NMBU, Ås, Norway
11.00	Keynote 5: New insight in seed tuber physiology. Paul Struik, Wageningen University and Research, The Netherlands
11.30	Keynote 6a: Towards data-driven precision crop management of potato. Corné Kempenaar, Wageningen University & Reserach, The Netherlands
12.00	Lunch

	Atlantis 1	Atlantis 2	Atlantis 3	Nautilus
13.00	Session 1: Breeding robust cultivars Chair: Mehmet Çalişkan	Session 2: Improved potato health Chair: Carl Spetz	Session 5: Agronomy and tuber physiology Chair: Dominika Boguszewska-Mańkowska	Session 6: Precision technology in potato cultivation Chair: Corné Kempenaar
	102 - Phenotypic and genotypic screening for nitrogen and phosphorus efficiencies in potato genetic resources. Klaus J. Dehmer, Germany	201 - Aggressiveness and behavior of different pectinolytic bacteria species involved in potato blackleg disease. Jérémy Cigna, France	501 - Is plant maturity a reliable indicator of bruise susceptibility? Michael Thornton, USA	601 - Risk maps in VIPS deliver late blight warnings at high spatial resolution. Berit Nordskog, Norway
	103 - Innovative potato breeding through fixation and restitution – the happy medium between conventional tetraploid and diploid F1 hybrid breeding. Corentin Clot, The Netherlands	202 - A microscopic examination of potato root infection by *Pectobacterium atrosepticum*. Ian Toth, United Kingdom	502 - Environmentally triggered russeting – an overview. Idit Ginzberg, Israel	602 - Potassium management strategy in starch potatoes. Malte Nybo Andersen, Denmark
	104 - Development of new potato varieties for north of Norway. Hans Arne Krogsti, Norway	203 - Bacterial wilt of potato: a threat to food security in sub-saharan Africa. Kalpana Sharma, Kenya	503 - Quantifying differences in source-sink relations between hybrid potato plants grown from two types of propagules. Jiahui Gu, The Netherlands	603 - Using drone-retrieved multispectral data for phenomic selection in potato breeding. Alessio Maggiorelli, Germany
14.00	105- Transcriptomic dynamics and biochemical insights into anthocyanin-enhanced tolerance to *Rhizoctonia solani* in potato. Vincenzo D'Amelia, Italy	204 - Pepper ringspot virus (PepRSV), the latest threat to the South African potato industry. Lindy Esterhuizen, South Africa	504 - Agronomy of field transplanted hybrid potato crops. Olivia Kacheyo, The Netherlands	604 - Screening a breeding program for nitrogen use efficiency using drone imagery. Laura M. Shannon, USA
	106 - Predictability of breeding further improved by doubled haploid technology. Wessel Holtman, The Netherlands	205 - Losses from seedborne Potato Virus Y infection dependent on strain and variety. Mark Pavek, USA	505 - Promoting international collaboration in potato breeding to transfer frost tolerance from *Solanum commersonii* into native potato cultivars from the Andean region and the Altiplano. Alfonso H. del Rio, USA	605 - In-season potato crop nitrogen status assessment from satellite and meteorological data. Jean-Pierre Goffart, Belgium
	101 - The role of Yip1 proteins in membrane trafficking and potatoes' resistance to stress. Zainab M. Almutairi, Saudi Arabia	206 - Operator influence on roguing efficacy for controlling potato virus Y in seed potato fields. Brice Dupuis, Switzerland	506 - Revolutionizing Seed Potato Production System in Africa and Asia. Kalpana Sharma, Kenya	606 - Combining remote sensing and crop growth model for better decision support on water and nitrogen management in potato. Fedde D. Sijbrandij, The Netherlands

15.00	Poster presentations in sessions
15.15	Coffe break
15.45	Poster session
17.00	Reception /Boat trip

Tuesday July 9

Conference hall Atlantis 1 + 2
Plenary session – Chair: Paul Struik

9.00	Keynote 6b: Next generation of more efficient fertilizers. Søren Husted, University of Copenhagen, Denmark
9.30	Keynote 7: The impact of climatic change on potato production: a focus on water management. Anne Gobin, K University of Leuven, Belgium
10.00	Keynote 1: Renseq: a fast-track method for development of potato pests and disease resistance markers from genome sequences. Ingo Hein, The James Hutton Institute and the University of Dundee, United Kingdom
10.30	Coffe break
11.00	Section meetings, rooms, see page 4
12.00	Lunch

	Atlantis 1	Atlantis 2	Atlantis 3	Nautilus
13.00	Session 1: Breeding robust cultivars Chair: Marielle Muskens	Session 3: Integrated pest management Chair: Brice Dupuis	Session 5: Agronomy and tuber physiology Chair: Borghild Glorvigen	Session 7: Sustainability in a changing climate Chair: Laura Grenville-Briggs
	107 – Identifying potato cyst nematode resistance gene, Gpa5, with SMRT-AgRenSeq-d. Yuhan Wang, United Kingdom	301 – Investigating the causal organisms involved with potato early dying in South Africa. Rene Sutherland, South Africa	507 – Effect of reduced N-fertilization on nitrogen use efficiency and selected quality parameters in starch potatoes and outlook on the POTENZION project. Marcel Naumann, Germany	701 – Unravelling the molecular mechanisms of heat-induced decrease in starch content in potato tubers. Sophia Sonnewald, Germany
	108 – Diversity analysis of Rpi genes in potato. Paulina Paluchowska, Poland	302 – Patat'Up: towards the production of a low-input potato. Vincent Berthet, Belgium	508 – Impact of in-row nitrogen fertilization on potato crop. Kürt Demeulemeester, Belgium	702 – Characterizing the Stsp5g a Stsp5g b double mutant as a partial remedy for heat stress. Akiva Shalit-Kanehx, Israel
	109 – Metabolite diversification and fate of bioactive metabolites in backcrossing lines of wild and cultivated potato for resistance breeding. Karin Gorzolka, Germany	303 – Benefits of click beetle monitoring for wireworm control. Katharina Wechselberge, Austria	509 – Assessing the relationship between nitrogen use efficiency and proteins concentration in potato genotypes. Ilze Dimante, Latvia	703 – Efforts to model crop response to hot and dry environments. Jian Liu, The Netherlands
14.00	110 – Fusarium dry rot control through host encoded broad spectrum resistance in potato. Daniel Monino Lopez, The Netherlands	304 – The good, the bad and the ugly: wireworm pests and the cover crops conundrum in potato production. Bruno Ngala, France	510 – Assessing regional potato yield response to phosphorus fertilization in high-phosphorus legacy soils. Lincoln Zotarelli, USA	704 – Effects of climate change on late blight and early blight of potato. Roman Valade, France
	111 – RNAseq expression analysis of potato tubers differing in resistance to soft rot caused by *Dickeya solani*. Renata Lebecka, Poland	305 – Extension education on herbicide injury in potato. Andrew Robinson, USA	511 – Alternative herbicides for desiccation of potatoes in Norway. Kirsten S. Tørresen, Norway	705 – Investigations on nitrogen efficiency and nitrous oxide emissions under reduced N-fertilisation in starch potato cultivation in northern Germany. Hubertus Blanke, Germany
	112 – ScabEomics: *Spongospora subterranea* effectoromics for resistance breeding to powdery scab in potato. Maria de la O Leyva-Pérez, Ireland	306 – *Streptomyces* secondary metabolite effects on *Pythium*, *Colletotrichum* and *Helminthosporium*. Brad Geary, USA	512 – Test of alternatives to diquat in desiccation of potatoes. Lars Bødker, Denmark	706 – Comparison of the carbon footprint of potato cultivation and processing with other crops and products: What contribution can the potato make to sustainable production? Marcel Naumann, Germany

15.00	Poster presentations in sessions
15.15	Coffe break
15.45	Poster session
17.00	EAPR General Assembly - Atlantis 1

Wednesday July 10 Excursion day
Separate programs for each excursion, buses depart 07.30 from the Seaplane harbour.

Thursday July 11

Conference hall Atlantis 1 + 2
Plenary session – Chair: May Bente Brurberg

9.00	**Keynote 3:** Prevention and control of late blight. Alison Lees, The James Hutton Institute, Dundee, United Kingdom
9.30	**Keynote 4:** Perspectives of biocontrol of soil borne pathogens and their microbiome interactions in potato. Laura Grenville-Briggs Didymus, the Swedish University of Agricultural Sciences, Alnarp, Sweden
10.00	**Keynote 8:** Preserving potato qualities in stores in a future with increasing constraints. Nora Olsen, University of Idaho, USA
10.30	Coffe break

	Atlantis 1	Atlantis 2	Atlantis 3	Nautilus
11.00	Session 1: Breeding robust cultivars Chair: Mallikarjuna Rao Kovi	Session 3: Integrated pest management Chair: Julie Pasche	Session 4: Improved soil health Chair: Solveig Haukeland	Session 8: Post harvest Chair: Michel Martin
	113 - Salicylic-acid mediated defence against the powdery scab disease. Samodya Jayasinghe, USA	307 - Variety screening for tolerance against Candidatus Phytoplasma solani and Candidatus Arsenophonus phytopathogenicus. Benjamin Klauk, Germany	401 - Geconem: How to collectively manage genetic resistance to potato cyst nematodes? Marie-Claire Kerlan, France	801 - Towards smart potato storage: using CFD modeling and simulation to realize optimized and efficient ventilation within potato storage buildings. Petro Demissie Tegenaw, Belgium
11.30	114 - Engineering of transgene-free potato late blight resistant plants through base editing. Jack Vossen, The Netherlands	308 - Using machine learning as a predictive tool to improve potato black dot management. Marta Sanzo-Miro, United Kingdom	402 - Effects of organic amendments and cover crops on soil characteristics and potato yields. Tatiana Francischinelli Rittl, Norway	802 - Developing automatic tools in the assessment of potato qualities. Fadi El Hage, France
	115 - Field trials in Sweden of potato with changed expression of resistance and susceptibility genes. Erik Andreasson, Sweden	309 - Effect of mulch cover on wilt symptoms and rubber tubers caused by *Candidatus* Phytoplasma solani and *Candidatus* Arsenophonus phytopathogenicus. Benson Kisinga, Germany	403 - Comparing the effectiveness of real-time PCRs to simultaneously detect and identify viable *Globodera pallida* and *G. rostochiensis.* Sebastiaan van Kessel, The Netherlands	803 - Effect of water stress in potato crop on post-harvest sprouting. Margot Visse-Mansiaux, Switzerland
12.00	Lunch			

	Atlantis 1	Atlantis 2	Atlantis 3	Nautilus
13.00	Session 1: Breeding robust cultivars Chair: Domenico Carputo	Session 3: Integrated pest management Chair: Alison Lees	Sessions 5 and 7 continued Chair: Sophia Sonnewald	Session 8: Post harvest Chair: Andreas Meyer
	116 - Genomic prediction in potato breeding: status and outlook from the Nordic region of Europe. Rodomiro Ortiz, Sweden	310 - Adoption of an early warning system for the integrated management of potato late blight in Chile. Ivette Acuna, Chile	513 - The influence of late season evapotranspiration replacement rate on potato yield, quality, and economic return. Jacob Paul Meeuwsen,USA	804 - OptiGERM: a French online Decision Support System to help the industry on tuber sprout control management in stores. Michel Martin, France
	117 - Towards selection of more durable resistance to *Globodera pallida.* Julien Leuenberger, France	311 - Creating a synergy between farmers, gardeners, and other stakeholders to eradicate late blight primary inoculum and adopt IPM control strategies. Pierre Deroo, France	514 - Potato cultivation without tillage using straw mulch for sustainable agricultural intensification in Asian rice-based systems. Jan Kreuze, USA	805 - Sprout inhibitors combination for a better efficacy and rates modulations. Morgane Flesch, France
	118 - Marker type and density in tetraploid potato genomic prediction and GWAS – does it matter? Trine Aalborg, Denmark	312 - Aggressiveness of *Phytophthora infestans* isolates from four genotypes widespread in Europe. Mirella Ludwiczewska, Poland	515 - Effects of soil salinity and drought on potato production. Ke Shan, The Netherlands	806 - 1,4-Dimethylnaphthalene performance in temperature-controlled shipping containers. Henning Bergmann, United Kingdom

14.00	119 - Producing a potato pan-NLRome. Thomas Adams, United Kingdom	313 - Rating potato varieties: 30 years of experiments reanalyzed to explicit resistance and explain its variability. Delphine Chauvin, France	707 - Can drought tolerant potato genotyped be selected based on phenotypic traits? Karin I Köhl, Germany	807 - Transcriptomic changes induced by DMN exposure in dormant tubers of three potato cultivars. Emily P. Dobry, USA
	120 - Genomic selection for late blight resistance in tetraploid potato: preliminary results and impact of the minor allele frequency on predictions. Charlotte Prodhomme, France	314 - Global solutions for sustainable late blight management: Evaluating the success of 3 R-gene potatoes in Asia and Africa. Phillip S. Wharton, USA	708 - Does glasshouse trials enable to estimate drought resistance in the field? Maverick Gouerou, France / Switzerland	808 - Greening of potato tubers in grocery stores can be reduced by appropriate storage and packaging. Hanne Larsen, Norway
	121 - Targeted genotyping-by-sequencing of potato Jeffrey Endelman, USA	315 - New mutations in Alternaria solani affect disease management using SDHI / FRAC group 7 fungicides. Julie S. Pasche, USA	709 - Predicting the tolerance of potato genotypes to drought stress based on root/shoot relationship in early plant development. Dominika Boguszewska-Mańkowska, Poland	809 - Glycoalkaloids in processing potatoes and fried potato products: formation and stability. Christina Meyeers, Germany
15.00	Poster presentations in sessions			
15.15	Coffe break			
15.45	Poster session			
17.00 19.30	Guided tour of Oslo & Conference dinner			

Friday July 12

Conference hall Atlantis 1 + 2

Plenary session – Chair: Kürt Demeulemeester

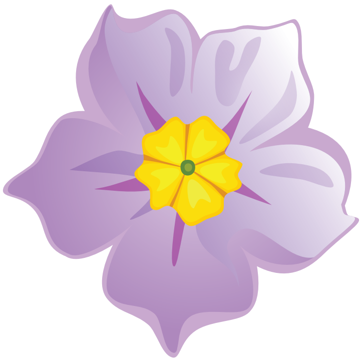
9.00	Keynote 10a: Success factors for transferring knowledge from science to growers. Borghild Glorvigen, Norwegian Agricultural Advisory Service, Norwegian Potato Forum, Norway
9.30	Keynote 10b: Linking science and industry. Ian Toth, The James Hutton Institute / University of Glasgow, United Kingdom
10.00	Coffe break

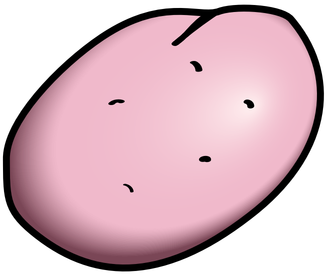
	Atlantis 1 + 2	Atlantis 3
10.30	Session 1: Breeding robust cultivars Chair: Pawel Chrominski	Session 10 Chair: Jean Pierre Goffart
	122 - Comparing yield stability of tetraploid and diploid potato. Mariëlle Muskens, The Netherlands	Workshop: Connecting research to practice Short introduction to the workshop: Global coordination of potato research through the International Potato Partnership. Iain Kirkwood, Potatoes New Zealand Connecting R &D and the potato chain in Belgium. Pierre Le Brun, FIWAP, Belgium
	123 - A universal potato research reference set - Simplifying research on a complex crop. Stan Oome, The Netherlands	
	124 - SNP-based assessment of unique and duplicated accessions in genetic resources of Nordic potatoes. Morten Rasmussen, Norway	

Conference hall Atlantis 1 + 2

11.30	Closing session
12.00	Lunch

Abstracts – Keynote presentations





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2024

Keynote: Food security

Potato: the smart crop for food security

Monica Parker

Consultant at International Potato Center, Vancouver, Canada

Potato is the crop for micro to macro investment to support food security from household to national levels. Increasingly, governments and private sector are realising the potential of potato to deliver on food security and financial growth. There is much untapped potential waiting to be realised from closing the yield gap in much of the potato producing world and developing seed systems to enable production to meet demand to provide affordable and nutritious food. International donors are investing in potato projects throughout Africa and MENA. Particularly in the MENA region, the private sector is investing in potato, governments are prioritising potato and supporting subsequent enabling environment programs. Potato can support food autonomy for MENA countries. Potato is versatile, in adaptation, production systems and uses. Potato can be grown from sea to sky, Kwale on Kenya coast to the desserts of northern Africa and the high Andes of Peru. Productions systems are adaptable to a large field, at industrial scale, or in a barrel in a refugee/IDP camp or slum, or at the household level, adapting even to humanitarian situations. Technologies enable production in diverse production systems, with one or two seasons a year with accompanying seed autonomy within commercial, rural and humanitarian conditions. When evaluating crops for prioritisation and investment at large scale, potato produces more nutritious food and calories per unit resource than the other major staple crops. Potato provides many essential nutrients and is adaptable to diverse cultural diets. Giving many reasons why potato is a smart crop for the future of food security, especially in food insecure regions.

Keynote session 1: Breeding robust cultivars

Renseq: a fast-track method for development of potato pests and disease resistance markers from genome sequences

Thomas Adams[1], Lynn Brown[2], Yuhan Wang[2], Yuk Woon Cheung[2], Micha Bayer[1], Xinwei Chen[1], Amanpreet Kaur[2], Ingo Hein[1,2]

[1] The James Hutton Institute, Invergowrie, Dundee, United Kingdom
[2] The University of Dundee, Dundee, United Kingdom

Sequencing the potato genome has provided unprecedented insights into the organisation of disease resistance genes in the third most important food crop. We developed RenSeq, a genome reduction technology tailored to re-sequence members of the nucleotide-binding, leucine-rich-repeat (NLR) family of disease resistance genes, comprising less than 0.2% of the genome.

RenSeq is instrumental in identifying and genetically characterising novel functional NLRs sourced from wild germplasm collections, offering new defences against threats such as potato cyst nematodes, viruses, and late blight. Employed as a diagnostic tool, dRenSeq enables precise identification of known functional disease resistance genes within established cultivars and breeding clones.

Our analysis of over 1000 cultivars and breeding clones has underscored the limited deployment of currently effective resistances, while also highlighting the persistent use of less effective resistances susceptible to pathogen variations. Importantly, these findings inform parental selection in breeding programmes and enable association studies for resistances effective against potato cyst nematodes and late blight. Notably, our research has identified strong candidates for H1 and Gpa5 resistance, among others.

Leveraging the wealth of data, and by contrasting sequences from functional genes and candidate genes with non-functional homologues, we have developed highly specific markers for many important disease resistance genes including those effective against potato cyst nematode, viruses, and late blight. These markers are now fully integrated into commercial breeding. Informed parental selection with these markers has expedited the breeding of new varieties, with early successes including selected clones successfully trialled internationally within five years of the initial cross. Currently, these markers are utilised to enable the stacking of complementary resistances to increase the durability of resistances.

Keynote session 2: Improved potato health

Insects as vectors for potato pathogens

May Bente Brurberg[1,2], Simeon Rossmann[1,2]

[1] Division of Biotechnology and Plant Health, Norwegian Institute of Bioeconomy Research (NIBIO), Ås, Norway
[2]Department of Plant Sciences, Faculty of Biosciences (BIOVIT), Norwegian University of Life Sciences (NMBU), Ås, Norway

In addition to the ability of many insects to damage and destroy plant crops by direct feeding, insects may act as vectors that transmit pathogenic microorganisms between host plants. It has been estimated that insects contribute to 30–40% of losses caused by plant diseases, either by transmission or by indirect effects (e.g. weakening or wounding the plant). Examples of insect vectors include aphids, thrips, leafhoppers, whiteflies, and beetles. These vectors can transmit a wide range of plant pathogens, including plant viruses, phytoplasmas, bacteria, and some fungi. For viruses in particular, the importance of insects in transmission is well documented. For bacterial diseases, however, the role of insect transmission has generally been underestimated, and only few systems have been studied in detail. Herbivorous insects graze on plant tissues that are colonized by microbial communities, including plant pathogenic bacteria, and in addition, the insects have their own microbiome, inhabiting external and internal body parts. The interaction between the specific bacteria and insect can be mutualistic, parasitic or commensal, whether they are plant pathogens or not. For some bacterial diseases such as phytoplasma diseases, insect vectors are necessary as intermediate hosts, and the vectors are often specific. Other bacterial diseases may be transmitted by a broad range of insect species. Pathogenic soft rot bacteria (SRB) belonging to the genera *Pectobacterium* and *Dickeya* cause diseases in potato and numerous other crops. Seed potatoes are the most important source of infection, but how pathogen-free tubers initially become infected remains an enigma. Since the 1920s, insects have been hypothesized to contribute to SRB transmission. We have investigated the occurrence of SRB in insects present in potato fields and identified the species of these insects to better understand the potential of this suspected source of transmission. In all tested potato fields, a large proportion of diverse insects were found to carry SRB. This suggests a need to give more weight to the role of insects in soft rot ecology and epidemiology to design more effective pest management strategies that integrate this factor.

Keynote session 3: Integrated pest management

Prevention and Control of Potato Late Blight

Alison Lees[1], James Lynott[1], David Cooke[1]

[1]Cell & Molecular Sciences, The James Hutton Institute, Dundee, United Kingdom

Potato late blight, caused by the oomycete pathogen *Phytophthora infestans*, remains a significant threat to potato crops worldwide. The disease is managed predominantly though the repeated prophylactic application of fungicides during the growing season, often at intervals of 7 days or fewer during severe epidemics. This is unsustainable for social, economic and environmental reasons. The population of *P. infestans* is dynamic, evolving over time in response to management practices. The implications of population change are twofold: new populations have traits that differ from the previous population (e.g., aggressiveness, virulence and fungicide resistance) and therefore influence blight management, and there is risk that both pathogen mating types interact to form long-lived soilborne inoculum (oospores).

Effective late blight management relies on knowledge of the source of inoculum and the conditions under which disease occurs, in combination with the efficacy of fungicides and host resistance. The population of *P. infestans* has recently undergone significant changes and resistance to commonly used fungicide active ingredients has been reported. Highly effective fungicides risk being lost as their repeated use drives selection for insensitivity in rapidly evolving pathogen populations, causing management failures and wasted treatments. Given the potential for increasing pathogen diversity in the future and concerns about further emergence and spread of fungicide insensitivity, Integrated Pest Management (IPM) strategies are more important than ever and must adapt according to the traits of the contemporary population.

Here we explore the key components of such an IPM strategy for late blight and the development and testing required to enable their successful implementation in the field. With a current emphasis on sustainable agricultural production, biological control of plant pathogens is increasingly attractive. Several tools have emerged in the last decade, but to date, biocontrol strategies remain difficult to use in practice due to their unpredictable field performance and difficulties with their integration into current cropping systems. Thus, sole reliance on biocontrol approaches in potato crop protection is considered high-risk and, at present, conventional fungicides remain the cornerstone of disease management strategies. However, there are clear opportunities to reduce the dose and application frequency of conventional fungicides through the integration of tools including biocontrol agents, plant resistance inducers, decision support systems and improved deployment of durable sources of host resistance. Forecasting and Decision Support Systems (DSS) to optimise the timing, choice, and rate of fungicide application for the control of late blight have been developed and are currently used in practice to a varying extent; the reasons for this will be discussed.

In this paper we describe how knowledge of the structure of the contemporary population of *P. infestans* in the UK and across Europe is being used, in combination with studies of host resistance and pathogen traits to improve decision making for the prevention and effective management of late blight.

Keynote session 4: Improved soil health

Perspectives of biocontrol of soil borne pathogens and their microbiome interactions in potato

Christian Andersen[1,2], Kristin Aleklett[1,3], Maja Brus-Szkalej[1], Linnea Stridh[1,4], Åsa Lankinen[1], Laura Grenville-Briggs[1]

[1]Department of Plant Protection Biology, Swedish University of Agricultural Sciences, Alnarp, Sweden
[2]Carlsberg Research Laboratory, Copenhagen V, Denmark.
[3]Department of Biology, Lund University, Lund, Sweden
[4]Lyckeby Starch AB, Kristianstad, Sweden

Biocontrol of plant diseases in open field settings remains challenging, yet alternatives to synthetic pesticides and integrated pest management approaches utilising such approaches are sorely needed, particularly in potato. Very few studies have investigated manipulation of the plant rhizosphere microbiome with the amendment of a Biological Control Agent (BCA), which is of importance for our understanding of the function of BCAs in the environment, their overall impact on soil and plant health and to ensure that such strategies are safe and sustainable. We therefore conducted a series of field trials to investigate whether amendment of *P. oligandrum* induces growth promotion in potato and further induces dynamic and temporal changes of the rhizosphere microbiome of the starch potato CV. Kuras, whilst at the same time offering protection from infection by the soil borne disease early blight. *P. oligandrum* induced significant changes in the fungal and bacterial diversity in the potato rhizosphere microbiome in a transient manner, indicating that potato rhizosphere microbial communities are highly resilient. The minor changes seen, indicate that *P. oligandrum* does not have a major impact on microbial diversity when used as an augmentative biocontrol agent. It also had a biostimulatory effect in potato in a cultivar-dependent manner, which may help to increase yield whilst at the same time lowering inputs such as fertilisers. Since cultivars respond differently to this oomycete under controlled conditions, this provides an opportunity to identify *P. oligandrum* responsive genes in the plant that might help the plant better host this or other biocontrol agents, thus improving efficacy under field conditions. Thus, there are strong indications that breeding for better hosting of biocontrol agents will be possible in the future. *P. oligandrum* was also able to suppress early blight during early disease development at the onset of plant senescence and thus may be a useful addition to the IPM toolkit in potato. Further work will investigate microbiome changes in more details and the effects of *P. oligandrum* on other soil borne diseases as well as host plant genetics that may be linked to better biocontrol or biostimulation by microbial biocontrol agents.

Keynote session 5: Agronomy and tuber physiology

New insights in seed tuber physiology

Paul C. Struik[1], Chunmei Zou[1,2], Willemien J.M. Lommen[1], Martin K. van Ittersum[2]

[1]Wageningen University and Research, Centre for Crop Systems Analysis, Wageningen, The Netherlands
[2]Wageningen University and Research, Plant Production Systems, Wageningen, The Netherlands

A seed tuber starts its life as a swollen stolon tip when tuber induction at that tip is strong enough to change the cell division plane, induce starch and patatin accumulation, and initiate tuber growth. It ends its life after having produced a cluster of stems, although it might live until the end of the bulking of its progeny tubers. Meanwhile, it has multiplied its cell number manifold, accumulated starch, proteins and nutrients, and developed a vascular system to supply the eyes with resources. It has gone through periods of active growth and development, dormancy, periderm formation, maturation, and sprouting. During sprouting it transforms and reallocates reserves to allow sprouts to develop into autotrophic stems. These different stages require both the mother plant and the tuber itself to perceive many kinds of environmental and intrinsic signals and to demonstrate an orchestrated response to all of them. In this keynote, we highlight recent insights in the physiology of seed tubers from their initiation, through their growth, maturation, storage and use. We do so at different levels of biological organisation: tuber (or stolon tip), stem, plant and crop.

A seed tuber shows different sensitivities to intrinsic and environmental factors during each event in its life. Environmental factors, plant nutrition and physiological events have strong legacy effects on what is happening later in the sequence and even on at least two generations of progeny.

Tuberization is under strict control of many internal and external factors, including light, atmospheric composition, availability of assimilates, phytochromes, gene expression, transcription factors, hormones (or hormonal balances), and metabolite availability. However, tuberization is not a status of the entire plant, but an event specific for a certain tuber site. Nevertheless, most research has focused on mechanisms at the plant level.

Molecular genetics helps unravelling tuberization mechanisms of seed tubers at the plant level. This is illustrated by the role of phytochrome. Phytochrome F (StPHYF) plays an important role in the response of tuberization to photoperiod. Genotypes that require short days to tuberize form tubers under long days when the StPHYF gene is suppressed. This is associated with degradation of the CONSTANTS protein StCOL1 and modulation of two FLOWERING LOCUS T (FT) paralogs. Grafting experiments confirm the function of StPHYF. Key proteins involved in regulating tuberization also include StCDF1, StSP6A, POTH1, StBEL5, StPHYB, StCONSTANS, StSUT4 and StSP5G.

Tuberization has a large effect on sink-source relations and carbon partitioning at the stem, plant and crop level. The signal to tuberize results in the accumulation of photosynthates, phloem loading, phloem transport and unloading of sucrose in the swelling stolon tip, followed by the conversion of sucrose into starch. Although the initial tuberization processes are triggered by a push of sucrose, gradually, the tubers become strong sinks, inhibiting further growth of above-ground biomass. These sink-source relations manifest themselves at the stem level, but are affected by competition between stems of the same plant and between plants.

How many tubers are formed per stem is highly controlled by conditions during stolon formation. Adequate moisture is essential for tuber set, but the quantity of photosynthates is important in determining how many tuber incipients will grow or be resorbed. Once the number of tubers per stem is fixed the tuber size distribution is very much a function of yield, although in specific cases leaf-tuber interactions and tuber-tuber interactions may still affect the hierarchy among tubers. This hierarchy, growth and development are also partly influenced by the micro-environment to which the tuber is exposed as determined by its position in the ridge and the rank of the stolon or stolon branch on which it is formed.

After tuber harvest, we employed GC–MS and LC–MS to examine changes in metabolite compositions in different parts of seed tubers of four contrasting cultivars during storage at different temperatures and for different durations. This approach yielded a wealth of information on changes in metabolite compositions that help identify which dynamics of specific compounds are predictive of dormancy break and various stages of physiological ageing or can describe genotype-by-storage temperature-by-storage duration interactions. Other researchers tried to monitor seed physiology by evaluating how the seed's respiration changed over time, how apical dominance of eyes or sprouts developed, which hormones were produced, how cell membranes aged, or which genes were activated.

When used as planting material, a seed tuber takes its life history with it. Taking this history into account during storage, planting and subsequent crop husbandry will enable farmers to optimize the performance of their crops.

Keynote session 6a: Precision technology in potato cultivation

Towards data-driven precision crop management of potato

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Precision farming is responding to temporal and spatial variation in crops. In the last decade, several sensor systems and digital tools have become available to capture variation in soil conditions, crop growth and/or pests and diseases. In addition, smart planters, sprayers and spreaders can be used for variable rate or spot application of inputs. Data from sensors in combination with decision support models and smart machines allow for more sustainable production. And more and more, we see science based data-driven strategic decisions on farms. In this key note, we present progress in precision planting, fertilization, irrigation, disease, pest and weed control and harvesting in potato crops. The WUR data service platform farm**maps** plays a key role in bringing the knowledge to farmers via apps. Each app consists of a model that can be accessed by API and an interface how to use it via the platform. Over 20 apps are now available in the store of the platform, including apps for scenario studies and evaluation of environmental performance of farming. A digital twin linked to farm**maps** is developed to study nitrogen dynamics in crops and between arable and diary farms. Data assimilation and crop growth models are part of the digital twin. How all these tools are used and integrated in a Farm of the Future, will be presented, including how the data can be used to report on key performance indicators and other mandatory proofs of compliance to regulations now set for Dutch farmers. Future outlook will be discussed.

Keynote session 6b: Precision technology in potato cultivation

The next generation of more efficient fertilizers in potatoes

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Potato (*Solanum tuberosum*) is a highly phosphorus (P) demanding crop, and adequate P supply throughout the entire growth period is crucial to ensure optimal yields and product quality. In the early growing season during the tuber initiation stage, P has a significant effect on tuber setting. The highest quantity of P is taken up during tuber bulking in the mid- to late growing season, and continues in the tuber maturation phase, where it improves tuber maturity. During tuber bulking, P has a critical role in carbon partitioning and starch synthesis, where several key enzymes are tightly regulated by the phosphate concentration in amyloplasts. In order to ensure optimal yield and quality of potato, it is therefore important to avoid P deficiency during the growing season. However, potatoes have a sparse and shallow root system, with up to 90% of roots located in the uppermost 25 cm of the soil. This reduces their access to nutrients with limited mobility in soil, not least P. As a result, the P use efficiency (PUE) of potatoes are generally low, and the excessive application of P used to compensate for the low PUE, results in environmental damage and economic losses. Thus, a foliar fertilization strategy where the soil is bypassed seems obvious from agronomic, environmental and economic reasons.

In the presentation I will show that potato leaves, in contrast to cereals, has a high capacity to acquire foliar P via the leaf surface and assimilate into the photosynthetic active tissue. Moreover, I will show that nanotechnology has a range of interesting perspectives to lower the risk of scorching and provide fertilizers with a range of smart properties. We have found that P ions and P containing nanoparticles (citrate coated hydroxyapatite, 25-30 nm) penetrated the leaf surface of potato through different pathways. Approximately 80% of a [33P] labeled phosphate solution were taken up within 7 days after foliar application, regardless which leaf side it was applied to, or the surface tension of the solution. In contrast, less than 20% of applied [33P] in hydroxyapatite nanoparticles were taken up when applied to the abaxial (lower) leaf side, while more than 50% were taken up from the adaxial (upper) leaf side when a trisiloxane super spreader surfactant was included to lower the surface tension. Fluorescence labelled hydroxyapatite nanoparticles were found to penetrate the leaf surface solely via stomata on the adaxial side, which is a striking observation, as this leaf side contained 25-50 times fewer stomata per unit area compared to the abaxial leaf side. However, the contact area between leaf and applied droplets were larger on the adaxial leaf side, suggesting a significant effect of leaf surface hydrophilicity (wettability) on nanoparticle uptake.

Keynote session 7: Sustainability in a changing climate

Climate adaptive water management for potato production

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Extreme events, which are attributed to climate change, are at the tail end of statistical distributions and tend to be sporadic and infrequent. Climate model simulations indicate that in a warmer climate, the likelihood of heat waves and excessive rainfall increases due to the increased intensity of the hydrological cycle. The increased frequency of adverse weather events allows more definitive statements to be made about escalating trends in temperature and precipitation intensity. Droughts in the spring and summer have led to water shortages and even to the subsequent abandonment of irrigation. Conversely, excess rainfall leads to waterlogged fields and associated yield losses (Van Oort et al., 2023). Each of these adverse events exceeds the 20-year return period, highlighting the evolving climate dynamics, and higher regional potato yields were attributed to a longer period of rainfall during the growing season (Gobin and Van de Vyver, 2021). Technological advances, including new and better adapted varieties, have resulted in increased yields but yield remains high within individual fields and across farms and regions owing to factors such as soil heterogeneity, microclimatic variations and management practices. The objectives are to assess the impact of extreme weather on potato production at the field to farm scales, and evaluate the effectiveness of climate-smart water management strategies to improve resilience and yields in potato production under varying climate and environmental conditions.

Most crop development research has focused on the soil-water-nitrogen dynamics in relation to crop phenology driven by calendar or thermal days. The crop's growth and development is closely linked to environmental conditions, making it particularly vulnerable to fluctuations in weather patterns. The crop stages with a large impact on yields include early establishment, mid-season stages around tuber setting, and harvest. The time series fraction of absorbed photosynthetically active (fAPAR), a Copernicus Sentinel-2 (S2) derived vegetation indicator at a 10 m resolution, proved successful in the retrieval of BBCH potato phenological stages, verified using field observations using digital hemispherical photography (Gobin et al., 2023). Additional evidence was provided using the Canopeo app., which was tested on fields between 2020-2023. The spatial and spectral resolution of Sentinel satellite imagery in conjunction with meteorological data, enables farmers and the agricultural sector to gain spatio-temporal insights into crop development, crop growth patterns, health status and environmental conditions affecting potato production.

Potatoes, a global staple crop, are highly sensitive to extreme weather events, presenting growers with a complex challenge. Elevated temperatures, prolonged droughts and erratic rainfall can disrupt the delicate balance required for optimal potato growth. Extreme heat can inhibit tuber formation and reduce overall yield, while prolonged drought can

Keynote session 7, continued.

exacerbate water shortages and affect key growth stages. Conversely, excessive rainfall can lead to waterlogging, which adversely affects root health and creates conditions conducive to disease. Given the current pace of climate change, understanding and mitigating the impact of these extreme weather events on potato growth and yield within and across fields helps develop climate smart agricultural practices, thereby ensuring production security.

Adapting potato production to the challenges of climate change and extreme weather requires the implementation of climate-smart water management strategies. The use of time-series satellite imagery and meteorological data for crop monitoring provides the necessary spatio-temporal data space and knowledge for predicting yields under varying environmental conditions and improving agricultural water management. Results of time-series analysis and geo-processing help growers to detect changes in vegetation indices, pinpoint growth stages and identify stressors and anomalies, enabling them to implement precision farming practices. Supplemental irrigation and climate-adaptive drainage are emerging as promising practices to mitigate water related stress and ensure consistent yields, although their effectiveness depend on timely application in line with crop phenological development. Field-level practices such as plastic mulching, climate-adaptive drainage and strategic irrigation are complemented with farm-level strategies such as insurance coverage, cooperative farming initiatives and renewed contract agreements. As extreme weather events increasingly influence yield variability, understanding the spatio-temporal dynamics is essential for efforts to build resilience within potato production systems.

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Keynote session 8: Post harvest

Preserving potato quality in storage in a future with increasing constraints

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The primary objectives of storing a potato crop are to extend crop availability beyond harvest, minimize losses, and maintain the desired quality. There are increasing external constraints putting pressure on the ability to reach these objectives and necessitating proactive responses in cultivar selection, storage design, technology and management, and industry expectations. Constraints generate innovation but it may also be accompanied by higher costs. The economy of problem solving can put further constraints on what is necessary to store potatoes. Constraints will differ depending upon growing region and market, but primary issues affecting the potato storage sector include climate change, energy demand, sprout suppression capabilities, and availability and cost of resources and labor. Variability in traditional weather patterns will necessitate adjustments in storing for quality. This can prompt changes in storage design and use of insulation, ventilation capacity, supplemental refrigeration, and evaporative cooling or drying capabilities. The evolution and sophistication of climate-controlled storages will help integrate weather forecasting and intuitive prediction with decision-support monitoring to further manage the crop. Crop data at harvest combined with in-pile and storage sensors will feed into the decision-support system to help store the crop efficiently and effectively. Having interpreted data will help a storage manager make a science-based decision on setting control parameters of the storage, especially early in the storage season when decisions are critical to minimize losses due to disease and evaporation. Using environmental sensors within the storage to preemptively respond to an issue before further loss arises will be another tool to utilize. Unfortunately, responding to a change in climate or weather may put greater dependency upon power and electricity to store for quality. Energy initiatives and optimizing the use of ambient cooling, variable frequency drives, solar, wind, and other innovative means to minimize the impact of high energy costs and demands will need to be further incorporated into management decisions. Constraints in the application of agrichemicals, in particular sprout inhibitors, will force the use of cultivar selection with extended dormancy length, colder store temperatures, and novel and program approaches to suppress sprouting. Breeding and identifying resilient cultivars to withstand the demands and conditions of postharvest handling, defect and disease tolerance, desired dormancy, and market quality maintenance under stress-inducing environments will help respond to current and future constraints. The necessity of storing potatoes cold will further dictate the need for cold resistant sweetening cultivars for the process markets. Cultivar breeding and selection will be a vital solution to preserving quality under increasing constraints and attributes of storability may play a greater role in cultivar selection and acceptance. Knowing the quality and storage limitations of a cultivar will avoid situations of unmet expectations if the cultivar is not inherently suited for storage. Loss in storage comes in multiple forms: direct losses due

Keynote session 8: Post harvest, continued.

to defect damage and disease development and water and carbon loss due to evaporation and respiration and indirect losses due to not meeting the acceptable quality specifications. Regardless of the type of loss, both create a reduction in a marketable and consumable crop. External constraints will place further pressure on the potential for crop loss, which will force an evolution of a systems approach to minimize loss and maintain the volume of potatoes needed for food production. The principles of storage design and management will become more robust. Innovation, research, and technology will continue to be relied upon as the industry moves forward with identifying solutions to these emerging constraints.

Keynote session 10a: Connecting research to practice

Success factors for transferring knowledge from science to growers

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The area of Norway is 323,806 square kilometres, and cultivated land constitutes 3.5% of this area. Potatoes are cultivated on 11,505 ha, which is 1.17% of the cultivated area. Total potato yield is 305,000–385,000 tons per year. Norway has a total of 37,561* farmers. About 64% of them are members and owners of the Norwegian Agricultural Extension Service (NLR). Of a total of 1,336* potato farmers ca. 77% have an ownership share in NLR.

Transferring knowledge from science to growers in a way that turns the results into practical use is a challenge. The message may be unclear or explained in a difficult way, it may be very complicated, or the receiver is not able to accept or understand the message. This discussion of knowledge transfer is based on the fact that the farmer is a member of NLR.

Research must be open to issues raised by growers or industry partners. Advisors are the spokespeople for the farmers and the challenges they face in their daily work. It is more likely for a researcher to receive support and interest from farmers and industry when the issues are relevant and interesting to them. Ownership of the project through reference groups, hosting field experiments and being involved in a project facilitates the transfer of the results from research to the growers.

A good relationship with the farmers is valuable for the advisors when they convey the results. It is easier for the advisor or the research team to get the message through to the grower if she trusts the spokesperson. Good connections can be attained by facilitating physical meetings and thereby generating good opportunities for discussions.

Get the trailblazers on your side. In all societies there are always people that are in front of the development. A trailblazer is a person within the farming community that other farmers look to and listen to. This person can host a field experiment or test a new model in the forecasting system etc., and thereby become involved in a project. Field days, seminars, or meetings with news from the research, together with good conversations over a cup of coffee, are good arenas for transferring knowledge from science to growers.

Publish new knowledge in a way that is easily receptive. Translate difficult scientific language to a language easy to understand. Transform new knowledge into practical use which can be implemented in agriculture directly. Show calculations with economic or biological positive effects.

* www.ssb.no = Statistics Norway, 2023

Keynote session 10b: Connecting research to practice

National Potato Innovation Centre (NPIC) for the UK and beyond

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Potato is a major crop in the UK and throughout Europe and is key in government strategies worldwide (including in China, India and Sub-Saharan Africa) to attain food security by ensuring a reliable and sustainable supply of healthy food. The climate and biodiversity crises require rapid development of crop cultivars adapted to warmer environments to be grown in low input sustainable systems, while loss of plant protection products mean that new solutions to pest and disease control become ever more important.

We are proposing to establish a National Potato Innovation Centre (NPIC) at the James Hutton Institute in Dundee, Scotland, which will comprise a state-of-the art innovation facility managed in partnership with stakeholders across academia, industry and government, both nationally and internationally. The NPIC will be part of a creative cluster that will deliver solutions for industry, generating new findings, innovative products and highly skilled jobs in new industries.

We are meeting with academic partners, as well as industry and government to identify major industry challenges where science can offer a potential solution, both now and in the future. Challenges to potato cultivation are often similar between nations and the Centre is looking to work with scientists and industries in other countries to coordinate efforts to ensure the best research and knowledge delivery to the global potato industry.

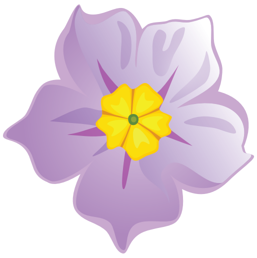
We are currently in discussions with the International Potato Partnership (IPP) and the International Potato Centre (CIP) to see how a more joined up approach globally can help potato growers, from subsistence farmers to those that work with large multi-nationals. Information being collected about the main needs of industry through the IPP show a remarkably similar list, helping to identify major targets for international collaborative research and knowledge exchange.

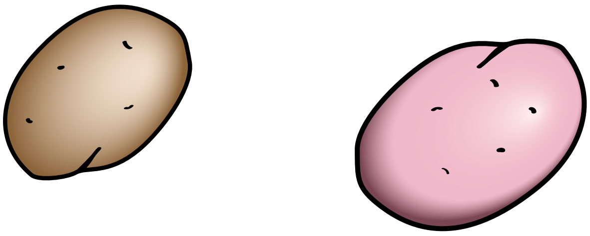
We see this as the beginning of a longer process and would welcome involvement from other interested academic and industry groups.

In this presentation, we will describe our vision for a Potato Innovation Centre and how working with international partners will help to coordinate global scientific endeavours and potato industry resilience.

Abstracts – Session 1

Breeding robust cultivars





101

The role of Yip1 proteins in membrane trafficking and potatoes’ resistance to stress

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The high demand for human foods under unstable water resources and changing climate is a serious threat to food security in the world. Among food crops, the potato contributes highly to global food security due to its cultivation conditions and nutritional value. However, environmental stress critically influences potato production. Plants respond to stresses through multiple signalling pathways that involve membrane-bound proteins that modulate plant responses to stress. The Yip1 domain-containing proteins are membrane-bound proteins that are known to be involved in plant stress response by regulating the intracellular trafficking of stress-responsive proteins and membrane-bound receptors involved in plant responses to stress. Here, we aim to identify and characterize the Yip1 domain-containing proteins in the genome of potatoes by genome-wide analysis. Several Yip1 proteins revealed expression patterns in potato tissues during developmental stages in response to induced drought and heat stress. Cis-regulatory elements analysis reveals binding sites for various transcription factors involved in responses to stress, light, and plant hormones in the putative promoter sequences of putative Yip1 promoters. Despite the strong conservation of the putative Yip1 family proteins of potato, gene expression analysis, and promoter analysis indicate different roles for the members of the Yip1 family in potato tissues during rooting and tuberization. Understanding the role of Yip1 proteins in potato stress tolerance could lead to the development of new strategies and tools to improve the ability of potato to withstand stress conditions, ultimately enhancing global food security.

102

Phenotypic and genotypic screening for nitrogen and phosphorus efficiencies in potato (*Solanum tuberosum* L.) genetic resources

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Improving nutrient efficiency of cultivated potato (*Solanum tuberosum L.*) could reduce fertiliser application as well as nutrients leaching from the soil solution while ensuring high quality standards and satisfactory yields. Due to their limited root system, potatoes cannot acquire nutrients from deeper soil layers, making them especially prone for nutrient deficiencies. The main aim of this study was to explore the natural variation among set of potato germplasm for nitrogen and phosphorus efficiency potentials and identification of molecular markers related to nutrient efficiency. A phenotyping experiment was conducted on 220 potato accessions from IPK's Gross Luesewitz Potato Collections (GLKS), along with 20 modern varieties. The experiment was conducted under greenhouse condition in a hydroponic system with modified Hoagland solution as substrate. Two nitrogen treatments – high N (15mM N L^{-1}) and low N (1.875mM N L^{-1}) and two phosphorus treatments – high P (30mgP L^{-1}) and low P (3mgP L^{-1}) – were applied to screen each genotype for its response to N or P deficiency stress. At the end of a 21-day trial period, shoot and root biomass were measured. Chlorophyll contents of the leaf epidermis were measured on day 14 and 21 of the trial period. In order to compare the genotypes for their stress susceptibility or tolerance, stress tolerance indices (STI) based on their shoot and root biomass were calculated. Results from the phenotyping screening showed a very high variability among the gene bank accessions regarding both shoot and root biomass. The STI for shoot biomass ranged between 0.17–1.99 for the N experiment and between 0.16–2.58 for the P experiment. Similarly, the STI for root biomass ranged between 0.06–2.08 for N and 0.08–2.90 for P. The majority of the genotypes showed an increase in their root:shoot ratio under stress conditions. Furthermore, roots exhibited an extensive variation in architecture and development. In conclusion, we observed a high variability among the potato accessions, not only regarding shoot biomass, but also in terms of root biomass development at an early stage of plant growth, forming a good basis for breeding towards nutrient efficient potatoes. Currently, a genotyping by sequencing (GBS) analysis is under progress. It is the basis for conducting a genome wide association study (GWAS) to elucidate markers associated with stress tolerance. Simultaneously, N and P contents of the harvested plant shoots are being analysed.

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103

Innovative potato breeding through FIXATION and RESTITUTION – the happy medium between conventional tetraploid and diploid F1 hybrid breeding

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Conventional potato breeding is based on the vegetative propagation of superior descendants identified within segregating tetraploid progenies. This numbers game is characterized by a slow pace of genetic improvement. Global efforts to move towards a fast pace diploid F_1 hybrid breeding system have made considerable progress over the past decade. However, transforming a tetraploid outcrossing crop into a selfing diploid one is not without problem. Once the original hurdle of self-incompatibility was overcome, the most substantial challenge of inbreeding depression was exposed. Other challenges such as the composition of heterotic groups must be addressed before F_1 hybrid varieties can compete with tetraploid cultivars in terms of marketable yield. Despite these challenges, diploid self-compatible clones offer genetic advantages, particularly in terms of stacking resistance genes, which cannot be ignored amid climate change and the associated rise in disease pressure. Thus, we ask whether the F_1 hybrid scheme is the only option available to potato breeders who want to benefit from self-compatible diploids. In our opinion there is an alternative, a happy middle between the conventional and the F_1 hybrid breeding schemes. We named this interploidy breeding scheme Fixation-Restitution breeding. This approach utilizes self-compatible recurrent parents for faster breeding, bringing favourable alleles like resistance genes to homozygosity. Unlike the F_1 hybrid approach, homozygosity is reach at *some* rather than at *all* loci, hereby contributing to the fixation of genetic gains while minimizing inbreeding depression. The genetic makeup of these partially inbred diploids can then be transferred to the tetraploid level via 4x × 2x crosses. Such interploidy crosses are enabled by a meiotic restitution mechanism resulting in the production of unreduced pollen. Clonal selection will identify heterotic tetraploid descendants that combine the high yield potential of the tetraploid parent with the fixed beneficial alleles from the diploid parent. By integrating the strengths of diploid and tetraploid breeding, we believe that Fixation-Restitution breeding can yield multi-resistant cultivars of agronomic value before F_1 hybrid breeding reaches maturity. Last but not least, we will show that, over the past five years, our research in potato sexual reproduction has provided the molecular tools necessary to implement this innovative breeding system.

104

Development of new potato varieties for north of Norway

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Over the last years, Norway has increased its consumption of vegetables and berries. The Ministry of Health is encouraging this trend. This has led to that the Norwegian farmers have expanded the production and trade, all over the country. During the last twenty years, the demand of high-quality vegetables has reached new heights. For potatoes, the skin needs to be set, nice and shiny, with no sorts of spots. To achieve this “goal”, it’s necessary that the potatoes are mature when harvested, and with as little symptoms of diseases as possible. Based on this, it has been a big need for new potato varieties suitable for growing in northern part of Norway, adapted to the short growing season, and with as strong resistance against diseases as possible.

The climate at the latitude 69°N is characterized by low temperatures and midnight sun in half the growing season. During mid-summer it’s up to 23 hours netto photosynthesis a day, in good weather conditions. It’s snow in the mountains when planting potatoes, and snow again in the mountains when harvesting. Despite a little longer growing season because of climate change, the period for growing potatoes is still short, about 100 days. “To buy them some more time”, farmers who are producing potatoes on a large scale, pre-sprout the seed potatoes, and have invested in efficient equipment for spring and autumn work in the fields, helping to prolong the short growing season.

Some potato farmers up north, together with Graminor (plant breeding company in Norway) and Norwegian Agricultural Extension Service, has collaborated since 2006, looking for new potato varieties for growing in the Artic. This work has been organized as periods of 3-years project, led by the innovative potato farmers Evy and Olav Grundnes, in Målselv municipality of northern Norway.

When searching for new potato varieties, we bear in mind not only demands for good yield, good locking and nice eating quality, but also strong resistance for different diseases, low fertilizer input and that it will store well for at least 8 months.

The project is also collaborating closely with the packing company Tromspotet AS which is located to “Senja” in the middle of the county of Troms. The company are owned (51 %) of the potato-producers in Northern Norway. They do 5000 tons of potatoes pr year. 50 % for packaging and 50 % for pealing and sous-vide production, proximately 10 variants of ready meals (mostly side dishes).

This long-term work is, and has been, a collaboration between a wide group of stakeholders and financiers. We have found a few, promising potato varieties over the years, but are still looking, for new, in a constantly changing market.

105

Transcriptomic dynamics and biochemical insights into anthocyanin-enhanced tolerance to *Rhizoctonia solani* in potato

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Anthocyanins, known for their antioxidant properties, play an important role in protecting plants against environmental stresses. However, their involvement in the response against potato necrotrophic fungi remains underexplored. This study aimed to decipher the molecular response underlying anthocyanin-mediated tolerance to *Rhizoctonia solani* in cultivated *Solanum tuberosum*. Two varieties with varying anthocyanin content were used: Musica, with white tubers and shoots, and Blue Star, accumulating anthocyanins in all the tissues. Musica exhibited a 75% reduction in tuber production after Rhizoctonia infection, while Blue Star showed complete tolerance. The tolerance of Blue Star was further evidenced by biochemical parameters, particularly the increased levels of photosynthetic pigments, which were conversely reduced in Musica. RNAseq analyses revealed distinct transcriptomic responses to the infection in Musica and Blue Star. Among the four differentially expressed genes (DEGs) specifically identified in Blue Star, *StSGR* (related to chlorophyll catabolism and senescence) was downregulated 2-fold after infection, aligning with the observed phenotype. Musica exhibited 156 DEGs related to cell wall modification and hormone signaling, suggesting an attempt to respond to *Rhizoctonia*, though unsuccessful. Notably, the anthocyanin R2R3 MYB TF gene *StAN2* was significantly upregulated in Musica, despite the absence of anthocyanins in infected tissues. Functional studies showed that transgenic tobacco overexpressing *StAN2* produced elevated levels of phenolamides, implicated in biotic stress signaling, along with anthocyanins. They also displayed an increased tolerance to *Botrytis cinerea*, another necrotrophic pathogen. Overexpression of *StAN2* produced changes in vascular tissues, as also evidenced by promoter localization experiments. Altogether, these results highlighted that the absence of anthocyanins in Musica, despite activating the molecular complex responsible for their production, correlated with higher sensitivity and robust transcriptomic response to the attack compared to Blue Star. Our functional studies revealed that the metabolism accompanying *StAN2* activation may be associated with other changes, such as phenolamide accumulation that could enhance tolerance to stress. Ongoing studies aim to unravel the molecular mechanisms that alter the burst of reactive oxygen species (ROS) by anthocyanins, utilizing genome editing approaches.

106

Predictability of breeding further improved by doubled haploid technology

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To support potato breeders, Fytagoras has developed a method to produce diploids from tetraploid potato. Diploid breeding offers precision in identifying characteristics, facilitating faster and more efficient variety development.

Potato breeding aims to combine positive traits in one plant, primarily achieved through crossing plants with different characteristics. However, the tetraploid nature of current potatoes, with four sets of chromosomes, leads to high heterozygosity, making outcomes unpredictable. To overcome this disadvantages, some breeders work with diploid potatoes, which can be propagated by tubers or seeds. For both diploid and tetraploid breeding programs the availability of diploid lines makes the outcome from crossings more predictable, and the breeding process more efficient and faster.

The Fytagoras method for diploid plant production is based on DH technology and has proven to be effective for many genotypes already. DH methodology is based on the use of haploid cells with a single set of chromosomes. Cells are isolated from flower buds, cultured, and induced to divide in a controlled laboratory environment. As a result tissue culture plants are produced, while the whole process may take 6-9 months. The DH method provides breeders with a diverse set of plants; every new plant is in principle unique. Typically breeders request 30 to 50 plants per donor, allowing for individual analyses, and subsequent crossings and selections.

The same technique can be used to produce pure homozygous diploid lines in just one step. In contrast, inbreeding would never provide complete homozygosity, while also a large number of backcrossing would be needed, and so is time consuming. Pure homozygous potatoes have identical homologous chromosomes, so lethal or weak alleles are eliminated, as they cannot survive without a strong counter allele being present. In diploid potatoes, homozygous lines are foundational for F1 hybrid seed production, ensuring genetically identical offspring. Pure homozygous lines also are vital for genetic research processes like chromosome mapping and marker detection.

DH technology can mean a major step in potato breeding, offering speed and efficiency.

107

Identifying potato cyst nematode resistance gene, Gpa5, with SMRT-AgRenSeq-d

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Potato is the third most important food crop in the world. Diverse pathogens threaten sustainable crop production but can be controlled, in many cases, through the deployment of disease resistance genes belonging to the family of nucleotide-binding, leucine-rich-repeat (NLR) genes.

To identify functional NLRs in established varieties, we have successfully established SMRT-AgRenSeq in tetraploid potatoes and have further enhanced the methodology by including dRenSeq in an approach that we term SMRT-AgRenSeq-d. The inclusion of dRenSeq enables the filtering of candidates after the association analysis by establishing a presence/absence matrix across resistant and susceptible potatoes that is translated into an F1 score. Using a SMRT-RenSeq based sequence representation of the NLRome from the cultivar Innovator, SMRT-AgRenSeq-d analyses reliably identified the late blight resistance benchmark genes *R1*, *R2-like*, *R3a* and *R3b* in a panel of 117 varieties with variable phenotype penetrations. All benchmark genes were identified with an F1 score of 1 which indicates absolute linkage in the panel.

When applied to the elusive nematode disease resistance gene *Gpa5* that controls the Potato Cyst Nematode (PCN) species *Globodera pallida* (pathotypes Pa2/3), SMRT-AgRenSeq-d identified nine strong candidates. These map to the previously established position on potato chromosome 5 and are potential homologs of the late blight resistance gene *R1*.

108

Diversity analysis of Rpi genes in potato

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Phytophthora infestans causes late blight, a highly destructive potato disease which has challenged global agriculture for centuries. Costs associated with crop losses and chemical control of late blight are estimated to be more than € 9 billion per year. Therefore, host resistance appears to be an environmentally friendly and cost-effective alternative to limit the disease impact.

Genes involved in resistance to *P. infestans* (Rpi genes) have been discovered in wild potato species (Solanum spp.), and some of the Rpi genes have been introduced into potato cultivars. However, we do not know which Rpi genes are present in the many potato genotypes. The goal of our work is to investigate the incidence of eleven Rpi genes and to analyze their diversity in potato cultivars grown in Poland and Norway using an Amplicon Sequencing (AmpSeq) approach. The 183 potato cultivars were selected based on resistance to late blight and acreage of cultivation. In addition, 98 breeding lines and 54 genotypes of wild potato species were included.

The entire coding sequences of Rpi genes were amplified, barcoded and sequenced using PacBio high fidelity long read technology. So far, each of two libraries (120 and 123 PCR products; seven Rpi genes) produced more than 4 million reads with an average length of 4.067 bp. We have confirmed the presence of these seven Rpi genes in 243 potato genotypes and detected new variants of them (from two to 14 amplicon sequence variants per gene). The AmpSeq strategy proved to be reliable and efficient. Data on the distribution and sequence diversity of the Rpi genes can facilitate new breeding strategies and lead to the discovery of new Rpi variants in both cultivars and wild potato species.

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109

Metabolite diversification and fate of bioactive metabolites in backcrossing lines of wild and cultivated potato for resistance breeding

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Solanum tuberosum is susceptible towards many microbial and fungal pathogens like *Phytophthora infestans* or *Alternaria solani*, and is attacked by insect herbivores such as the Colorado potato beetle (CPB). Only few or even no resistance loci are available for resistance breeding, that is the most sustainable and most ecofriendly way to protect plants while saving energy, costs and crop protection measures. Wild potato species demonstrate a multitude of resistances against many pathogens and pests and are therefore promising reservoirs for new resistance traits. Secondary metabolites can be key players in the plants' adaptation to biotic and abiotic stresses. However, while crossing wild and cultivated *Solanum* species to transfer genes for bioactive compounds, breeding barriers often have to be overcome, e.g. by somatic hybridization.

A set of 159 backcrossing lines from somatic hybrids of five different wild potato species and *Solanum tuberosum* was screened for its metabolite diversification and the fate of bioactive metabolites using metabolite profiling via liquid chromatography – mass spectrometry. More than 5000 features were detected and compared.

The BC1 lines from the same parents demonstrated a huge metabolic variation already in the first backcrossing cycle. New compounds were found in the lines which were not detectable in the parental species. Some of these were identified as general stress-related compounds and might derive from suboptimal metabolic balance due to genomic imbalance. A highly bioactive metabolite against several potato pathogens and insect pests, identified in previous studies, demonstrated extreme ranges from zero to very high abundances in the BC1 generation. The metabolic dataset was further correlated to CPB larvae survival and feeding tests revealing new potentially bioactive compounds that might be utilized for resistance breeding.

We postulate that a metabolite-based selection of lines containing high levels of bioactive compounds and low levels of stress-related compounds in early plant growth stages is a promising perspective to speed up resistance breeding.

110

Fusarium dry rot control through host encoded broad spectrum resistance in potato

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Potato dry rot is a major threat to global potato production, causing postharvest losses ranging from 6% to 25%, with occasional reports of losses reaching up to 60% (Tiwari et al. 2020). Dry rot in potato is caused by soil-borne fungi from the *Fusarium* species complex, being *F. sambucinum*, *F. culmorum* and *F. solani*, the most relevant species (Stefańczyk et al. 2016). Current measures to control potato dry rot are scarce, which together with the limited resistant cultivars available and the emergence of fungicide-resistant strains have made this disease more threatening for potato cultivation. In this research, a germplasm of 300 wild *Solanum* genotypes were screened for *Fusarium* resistance using a stem inoculation assay. Twenty accessions from 15 different *Solanum* species, which included *S. chacoense*, *S. stoloniferum*, *S. tarijense*, *S. berthaultii*, *S. demissum*, *S. albicans* and *S. morelliforme*, showed resistance to at least one of the tested species (*F. sambucinum* and *F. solani*).

In order to study the *Fusarium*-resistance spectrum, the different resistant *Solanum* accessions were inoculated using a diverse set of eleven different potato-infecting *Fusarium* isolates. This resistance spectrum analysis resulted in the identification of broad spectrum resistant *Solanum* accessions, such as *S. stoloniferum*, *S. demissum* and *S. albicans*. Resistant accessions have been used to generate segregating populations in order to identify the resistance loci involved in the different resistant *Solanum* accession. It remains elusive what the resistance mechanisms of these newly identified resistance sources are, but their value for resistance breeding is evident. This research contributes to the identification of the *Fusarium* (a-)virulence and resistance mechanisms which will guide future strategies to develop durable resistant potato varieties.

111

RNAseq expression analysis of potato tubers differing in resistance to soft rot caused by bacteria *Dickeya solani*

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Soft rot of potato tubers caused by several species of pectinolytic bacteria is an important constraint to potato growers worldwide. Resistance to these bacteria is a complex polygenetic trait. A higher level of resistance than in tetraploid potato cultivars was found in diploid interspecific hybrids of *Solanum tuberosum* and wild *Solanum* species. The most resistant individuals and the most susceptible ones were selected within the mapping population DS-13 evaluated in previous studies [1]. For RNAseq expression analysis fragments of tuber tissue were collected 8 and 24 hours post inoculation with bacteria *D. solani* from tubers inoculated in wounds (B), not inoculated (NT) and wound-water-treated tubers. (W) . Bulks were prepared from resistant (NTR, BR, WR) and susceptible (NTS, BS, BR) individuals. Sequencing was performed using the NovaSeq6000 (Illumina). Genes of high ($\log_2 FC \geq 2$) different expression within the bulks, were then selected and verified in single potato individuals. These genes are related to stress response, resistance to bacteria, pathogenesis, resistance genes, defence mechanisms, pathogen recognition, wound healing, and suberization. Most of them were also found to be differentially expressed in bulk analysis of RNA collected 24 hours post-inoculation of potato tubers. Functional enrichment analysis of obtained data was performed using Gene Ontology and Kyoto Encyclopedia of Genes and Genomes (KEGGs). According to KEGGs the pathways involved in “Protein processing in endoplasmic reticulum”, “2-oxocarboxylic acid metabolism”, “Biosynthesis of amino acids”, “Citrate cycle”, “Carbon metabolism”, “Spliceosome”, “Ribosome” were commonly significantly enriched in BS vs BR, WS vs WR, NTS vs NTR. Additionally, “Valine, leucine, isoleucine degradation”, ”Protein export” and “Glutathione metabolism” were enriched in BS vs BR up-regulated genes.

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[1] Lebecka R. et al., 2021. Plant Pathol. 70:1745-1756.

112

ScabEomics: *Spongospora subterranea* effectoromics for resistance breeding to powdery scab in potato

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Powdery scab in potato is caused by the obligate pathogen *Spongospora subterranea* sp. *subterranea* (Sss). Lesions in the tubers affect marketability and provide entry points for other pathogens. Moreover, Sss can spread Potato MopTop Virus (PMTV) which can cause spraing. Efforts to breed for Sss-resistant varieties are hampered by troublesome phenotyping methods due to instable Sss inoculum.

Effectors are molecules that manipulate host cells facilitating the infection. However, some effectors that are recognized by special receptors from the host (R proteins), result in resistance, often mediated by a hypersensitive response (HR). Such effectors are called avirulence proteins (Avr). Agrobacterium mediated production of such proteins in the host was exploited as a simplified phenotyping system for resistance screening and breeding.

In order to identify potential effectors in the Sss genome, we re-sequenced over 20 different isolates from 15 different countries in 5 continents. We mined Sss genomes and selected 5 candidate effectors based on their predicted secretion, diversity across different isolates and their gene expression.

These candidates were transiently expressed in different potato genotypes with different susceptibility to powdery scab. Surprisingly, one candidate produced rapid and specific cell death when expressed without secretion signal peptide in a susceptible genotype. The speed, intensity and genotype specificity are reminiscent of a HR. This is the first effector of *Spongospora subterranea*. The response was specifically found in the most susceptible genotype. This indicates that recognition could be involved in susceptibility, rather than in resistance. Further characterisation of the plant receptor would offer the potential to detect and eliminate powdery scab susceptibility from breeding material in a fast and cost-effective manner. New insights about Sss effectors will allow further effector mining, either to eliminate susceptibility from cultivated potato or to screen for resistance in cultivars and wild species.

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113

Salicylic-acid mediated defense against the powdery scab disease

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Potato powdery scab is a soilborne disease caused by *Spongospora subterranea f. sp. subterranea* (*Sss*). The main symptoms are root galling and tuber blemishes. In addition, *Sss* vectors the potato mop-top virus (PMTV) that causes tuber necrosis. Both pathogens reduce the economic value of potato and impede foreign trade. Effective control methods are currently unavailable, emphasizing the need to investigate the source of genetic resistance. In this study, we employ potato hairy roots as a tool to study gene expression in response to *Sss* and validate gene involvement via gene editing. Following *Sss* inoculation, we observed differential expression of plant defense-related genes in the hairy roots. Our analysis of defense marker gene expression led us to hypothesize the pivotal role of salicylic acid (SA)-mediated defense against *Sss*. To further investigate the impact of SA-mediated defense on *Sss* infection, we generated a series of transgenic hairy root lines. These lines included those overexpressing an SA receptor, *SlNPR1*, and those with another SA receptor, *StNPR3*, knocked down using CRISPR/Cas9-based gene editing. Our results showed that reduced *Sss* propagation was observed both in the *SlNPR1*-overexpressed lines and the *StNPR3*-edited lines. Consistent with these results, pretreating hairy roots with SA also led to reduced *Sss* propagation. Our findings collectively suggest the involvement of SA-induced defense mechanisms against *Sss*. Furthering our investigation, we conducted transcriptomics (RNA-seq) to unravel the tripartite interplay between potato, *Sss*, and PMTV. Big data analysis of these results pointed towards the additional involvement of the SA-mediated defense and other mechanisms in countering these pathogens.

114

Engineering of transgene-free potato late blight resistant plants through base editing

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Genome editing offers tremendous opportunities for adapting crop varieties to emerging environmental stresses. Current challenges are to develop editing tools, delivery systems for a crop of interest, and to pinpoint the target sequences in the genome. In potato transgene free delivery is preferred because removal of the integrated tools through selfing is not an option. Here we report the development of a transient *Agrobacterium*-mediated transformation system for stable CRISPR-Cas mediated mutation without T-DNA integration. To optimize the protocol we targeted the kanamycin resistance gene (*nptII)* in a previously transformed plant. An efficiency of up to 31% was obtained for the knockout of the single copy *nptII* kanamycin resistance gene. From all the *nptII* mutants, 69% did not contain T-DNA integrations in the genome, which highlights the high efficiency of this method to generate transgene-free mutant plants. Next, we deployed this tool to engineer resistance against *Phytophthora infestans*, the causal agent of potato late blight. Accessions from the tetraploid species *Solanum agrimonifolium* are susceptible to late blight when they are homozygous for the *SaLIP5-2* allele. It differs by two codons from the SaLIP5-1 allele that provides dominant broad spectrum resistance to *Phytophthora infestans*. Through the *Agrobacterium*-mediated transient transformation tool we targeted both codons using customised base editors to convert the *SaLIP5-2* allele into the *SaLIP5-1* allele. The codons were individually and simultaneously edited with efficiencies of 17-32% and 4-8%, respectively. Moreover, the regenerants which had acquired the *LIP5-1* allele through the edits of both codons, had also acquired full late blight resistance. This case study provides the first proof of principle for the engineering of transgene-free potato late blight resistant plants through base editing. Because a naturally occurring allele is reconstructed the resulting improved plants are indistinguishable from classically bred plants.

115

Field trials in Sweden of potato with changed expression of resistance and susceptibility genes

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Potato cultivation is threatened by various disease and abiotic stresses that could increase with climate change. Plant breeding approaches implementing knock-out of susceptibility genes (S-genes) are of growing interest, in addition to the use of resistance genes (R genes). S-genes are generally more robust than R-genes and can confer broad-spectrum disease resistance but are usually not that effective as R genes.

Late blight, caused by *Phytophthora infestans*, is the most devastating disease in potato production. Here, we show full late blight resistance in a location in southern Sweden with a genetically diverse pathogen population with the use of GM potato stacked with three R genes over three seasons. In addition, using this field trial, we demonstrate that in-the-field-intervention among consumers led to change for more favorable attitude generally towards GM crops (Bubolz et al 2022; GM Crops and Food 10.1080/21645698.2022.2133396). This gives a base for cisgenic approaches that are currently undertaken.

Here we also present field evaluations of known CRISPR/Cas9 S gene potato mutants, during four consecutive years that indicate increased resistance to late blight without any significant trade-off in terms of yield penalty. Furthermore, the field trials showed increased resistance to common scab, and the mutant lines exhibit increased resistance to early blight pathogen *Alternaria solani* in controlled conditions. In controlled simulation or salinity, mutant plants made larger fresh mass than the background cultivar.

We studied immune responses of potato plants using quantitative proteomic techniques and identified a protein with an unknown function, here named Parakletos. *Parakletos* overexpression in the model plant *Nicotiana benthamiana* decreased the reactive oxygen species (ROS) and cytosolic calcium (Ca^{2+}) bursts induced by flg22, while *Parakletos* silencing increased both those. Furthermore, *Parakletos* silencing in *N. benthamiana* enhanced the plant's resistance to *Phytophthora infestans* and *Dickeya dadantii*, while its over-expression promoted infection. In *Parakletos*-silenced plants, transcript analysis revealed increases in expression of defense-related genes in response to flg22. We also assessed the effects of CRISPR/Cas 9-mediated knock-out in potatoes and found that it improved plant resistance toward biotic and abiotic stressors. *parakletos* mutant plants offer improved resistance to *P. infestans*, *A. solani* and *Pseudomonas syringe* as well as increased plant tolerance to salt stress. Moreover, field trials corroborated that *parakletos* mutant lines have enhanced resistance to *P. infestans*.

116

Genomic prediction in potato breeding: status and outlook from the Nordic Region of Europe

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An approach that integrates genomic prediction into selection strategies yields greater short-term genetic gains for desired traits compared to traditional phenotypic selection in potato breeding. This transformative shift is being adopted elsewhere, the Nordic Region of Europe. Drawing on almost a decade of comprehensive field, greenhouse, and lab research conducted by SLU's Svenska potatisförädling, this method proves invaluable for identifying parents based on their estimated breeding values. Likewise, it serves a dual purpose of predicting outcomes in untested sites within target populations of environments or for unobserved genotypes. Notably, it effectively purges deleterious alleles within inbred potato populations. This strategy also shows promise in selecting high-yielding bred germplasm in early generations, as evidenced by *in silico* breeding or field trials at Nordic latitudes. The accuracy of predictions appears to be markedly influenced by genotype, whether in inbred or hybrid offspring, regardless of the testing site or year. Multi-environment modeling further enhances prediction accuracy. Genomic best linear unbiased predictors (GBLUPs) play a crucial role in selecting breeding clones with varying inbreeding levels in early stages, using a model based on a training population evaluated in 4-plant plots employing an augmented design. In large potato breeding programs with hundreds of full-sib F_1 family offspring, GBLUPs may also enable a two-stage selection process; first choosing the best among the F_1 full-sib family offspring, and subsequently selecting the best breeding clones within each family. Hence, the potential applications of genomic prediction in future potato breeding endeavors extend to both population improvement and cultivar development. Envisaged in such an approach, it would significantly impact potato breeding efficiency. Multi-environment, multi-trait genomic prediction methods using partial least squares emerge as the most effective approach for estimating breeding values related to tuber yield and quality in this tetrasomic polyploid tuber crop ($2n=4\times=48$ chromosomes), which ranks third among the staple crops feeding the world's growing population.

117

Towards selection of more durable resistance to *Globodera pallida*

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Breeding efforts have been made to create potato varieties resistant to *Globodera pallida*. Currently, most of these resistant varieties carry *GpaV*$_{vrn}$ Quantitative Trait Loci (QTL)[1]. However, the resistance conferred by this QTL has been overcome by nematode populations in controlled conditions and in the fields in some parts of Europe [2,3]. The resistance variability observed in potato genotypes containing *GpaV*$_{vrn}$ may be attributed to additional genetic factors. Newgeneration genotyping technologies, like Genotyping-By-Sequencing (GBS), and advanced statistical models, such as the Multi-Locus Mixed Model (MLMM), have been shown to be effective in refining the detection of genomic variants associated with relevant traits and identifying molecular markers useful for breeding programs [4].

We developed a GWAS approach using MLMM on a panel of 249 advanced breeding clones which were phenotyped for resistance to *G. pallida* population 2/3 (Chavornay population) (Geconem national research program) and genotyped using GBS technology (G2PSol H2020 project) and SolCAP array (LDpot INRAE project). We successfully identified relevant molecular markers specifically linked to *GpaV*$_{vrn}$ loci. Additionally, we discovered another QTL on chromosome 9, previously unknown in our panel, which likely corresponds to *GpaVI* locus[1].

Subsequently, we identified sets of SNP markers linked to these two QTL and converted them for PACE (PCR Allele Competitive Extension) technology. The concordance between the SNP genotyping data obtained from GBS and PACE, as well as the genotype-phenotype association at each PACE marker set, were confirmed in a subset of the GWAS panel and in a validation panel.
This study led to the development of novel SNP markers closely linked to *GpaV*$_{vrn}$ and *GpaVI*. The genetic regions associated with these markers are derived predominantly from a potato clone which is currently used by breeders. In conclusion/To conclude, this study provides useful tools for breeding potato varieties with a high level of resistance to *G. pallida* by pyramiding QTLs which likely improve durability of resistance[5].

118

Marker Type and Density in Tetraploid Potato Genomic Prediction and GWAS – Does It Matter?

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Genomic prediction and genome-wide association studies are becoming widely employed to support potato breeding using genomic selection and for the identification of trait-underpinning QTLs. Elite cultivars are tetraploid and highly heterozygous but also share many common ancestors and generation-spanning inbreeding events. Consequentially, many SNP markers are not in 1:1 relationship with a single allele variant but instead shared over several alleles that might exert varying effects on a given trait. The impact of such redundant 'diluted' predictors on the statistical models underpinning GWAS and genomic prediction have scarcely been evaluated, despite the potential impact on the accuracy and performance of the models. We evaluated the impact of marker location, -type, and -density on genomic prediction and GWAS of five key performance traits in tetraploid potato (chipping quality, dry matter content, length/width ratio, senescence, and yield). A 762 offspring panel of a diallel cross of 18 elite cultivars was genotyped-by-sequencing, and markers were annotated according to a reference genome. Genomic prediction models (GBLUP) were trained on four distinct marker subsets (non-synonymous [29,553 SNPs], synonymous [31,229], non-coding [32,388], and a combination) and robustness to marker reduction was investigated for each subset. Trait prediction abilities were similar across all marker types, only non-synonymous variants improving yield predictive ability by 16 %. Marker reduction response did not dependent on marker type but rather on trait. Traits with high predictive abilities, e.g. dry matter content, reached a plateau using fewer markers than for traits with intermediate- low correlations, such as yield. Our results suggest using non-synonymous variants does not enhance performance of genomic prediction of most traits. In addition, single-marker regression GWAS was performed for each trait and marker subset to evaluate the impact of marker type. Major known QTLs were identified by GWAS and were reproducible across exonic and whole-genome variant sets for dry matter content, length/width ratio, and senescence. In contrast, minor QTLs detection was marker type dependent.

119

Producing a potato pan-NLRome

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Potatoes *(Solanum tuberosum*) are a critical food crop, with approximately 375 million tonnes produced globally in 2022 (FAOSTAT, 2023). However, potato production is constrained by numerous phylogenetically diverse plant pathogens, resulting in economic losses, threatening global food security.

A key mechanism of disease resistance in plants involves intracellular resistance (*R*) genes. These *R* genes typically comprise a single class of nucleotide-binding, leucine-rich repeat (NLR) genes. Through the use of enrichment-sequencing based approaches (termed RenSeq), the genome complexity can be reduced for sequencing, lowering the cost and allowing for the assembly of all the NLR genes present in an individual, termed an NLRome. The decrease in sequencing costs in recent years has meant that studies of an entire species NLR complement are now feasible, as first shown in Arabidopsis (Van de Weyer et al., 2019). However, we have shown that in order to accurately represent the NLRome in potato, highly accurate long reads, such as PacBio HiFi, are required (Wang et al., 2023).

Cultivated potato has a large number of extant relatives among wild tuber-bearing Solanum species native to the Americas. A collection of these is held in trust by the James Hutton Institute, making up the Commonwealth Potato Collection (CPC). This collection has been shown to harbour traits that are not present in cultivated potato accessions, including disease resistance traits, such as *H1* against the potato cyst nematode *Globodera rostochiensis* (Castelli et al., 2003) and *Rpi-blb4* against the oomycete pathogen *Phytophthora infestans* (Li et al., 2023).

We have sequenced over 100 accessions of diploid tuber bearing Solanum wild species and landraces from the CPC with PacBio HiFi-based RenSeq (termed SMRT-RenSeq) to assemble their NLRomes. Through the use of transcriptomics on a subset of samples, we have successfully annotated the NLRomes of these individuals. This provides an insight into the diversity and evolutionary dynamics within this key group of genes. The resulting pan-NLRome is a valuable resource to the potato research community and could potentially lead to the deployment of novel resistances to a wide range of pathogens.

120

Genomic selection for late blight resistance in tetraploid potato: preliminary results and impact of the minor allele frequency on predictions

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Breeding for durable resistance to late blight is challenging in potato. Usually, markers are used in breeding programs to facilitate the identification of genotypes harboring *R* genes. However, we think combining oligogenic and quantitative resistance, where multiple loci have a quantitative effect, is needed to increase the durability of resistance. Combined with marker assisted selection (MAS), genomic selection might be a useful tool to breed for varieties containing both types of resistance. Our aim is to explore the possibilities offered by genomic selection in a panel of genotypes where qualitative and quantitative resistance segregate and to evaluate the impact of the minor allele frequency (MAF) on the predictions accuracy.

The panel used for the genomic predictions was composed of 244 genotypes and varieties from three French breeding programs. This panel was designed for GWAS analysis for late blight resistance. The genotypic dataset was made of 6798 SolCAP SNPs and 68 additional markers representing 329 different alleles, including markers specific for known late blight *R* genes. Two different MAF of 0.05 and 0.0125 were tested in the models. The rAUDPC were measured in 2013, 2014 and 2015 in the western part of France (oceanic climatic conditions). Three different models (RKHS, Bayesian RR and Bayes B) were used for the predictions. Cross validations were performed with varying training population sizes (50, 100, 150 or 200 genotypes).

Overall, the bigger the training population, the higher the correlations between observed and predicted rAUDPC. Bayes B performed better than other models, especially when the training population size was equal to or higher than 100. With a MAF of 0.05, the maximum observed correlation between phenotypes and predictions was 0.68 using a training population of 200 genotypes (rAUDPC measured in 2013). Decreasing the MAF to 0.0125 led to a significant increase in correlations, reaching nearly 0.8 using Bayes B in 2013 and 2014 (with a training population of 150 genotypes). Interestingly, one year could be confidently predicted using the data obtained the previous years.

Our first results showed the interest of reducing the MAF for the prediction of late blight resistance when dealing with material where *R* genes can be found at low frequency. Although the panel used was not designed specifically for this purpose, late blight resistance could be predicted with interesting reliability which holds promises for the usefulness of genomic selection for breeding varieties with complex resistance to late blight.

121

Targeted genotyping-by-sequencing of potato

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Targeted genotyping-by-sequencing combines trait-specific markers with thousands of genomic markers at an attractive price for linkage mapping and genomic selection. A "mid-density" panel for potato, based on multiplexed PCR, was originally designed in 2020 and updated in 2023 to have nearly 4000 genomic SNPs and diagnostic markers for pest resistance (PVY, wart, golden cyst nematode), maturity, self-compatibility, tuber shape, and skin color. A higher density version, based on probe hybridization, was also developed in 2023 with 22,000 targets. Interpretation of the micro-haplotypes was facilitated by the availability of phased genome assemblies for *S. tuberosum* dihaploids. The application of these technologies for genomic selection and genetic mapping in the University of Wisconsin potato breeding program will be presented.

122

Comparing yield stability of tetraploid and diploid potato

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Agrico Research is a potato breeding company located in the Noordoostpolder, a large seed potato production area in The Netherlands. A part from the conventional tetraploid breeding program, since the mid-eighties, we have spent about 10 percent of our capacity on breeding at the diploid level. The work started with diverse dihaploid material obtained through classic induction of tetraploid varieties. These were inter-crossed with various accessions of diploid *S. phureja* (now *S. tuberosum* cultivar group Andigena). Over the years, a slow but steady increase of agronomic performance (yield, tuber shape, cooking and frying quality) was obtained. Typically, the breeding work was carried out in and around our own premises and, as a consequence, diversity of environments for selection was limited. Since diploid potato has a lower allelic variation per locus, we wondered how the stability of yield of our most advanced diploid clones would be in comparison to tetraploid potato. Therefore, we investigated the yield and yield stability of our ten best diploid clones in comparison to ten tetraploid varieties. Both ploidy groups were selected to represent a range of maturity classes. Yield was determined in replicated trials in four consecutive years at two or three different locations in the Netherlands and France resulting in datasets for 11 environments in total. We determined yield and dry matter yield and studied yield stability by plotting the genotype main effect (G) plus genotype-by-environment (GE) interaction (GGE). It turned out that the yield of some of the diploid clones was higher than some of tetraploid varieties and that the yield of diploid genotypes was as stable as that of the varieties. However, for dry matter yield, it was found that diploids performed consistently less than the tetraploid varieties if maturity class was taken in consideration. Furthermore, since both older and newer varieties had been selected, evidence was obtained that potato breeding did not result in any gain of dry matter yield within maturity classes.

123

A universal potato research reference set – Simplifying research on a complex crop

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For many years, HZPC has been working on harnessing the genetics of the potato. We do this through advanced clonal tetraploid breeding, as well as through diploid hybrid breeding. Over the last decade, we have built up many resources to help us in deciphering the polyploid (and often polygenic) traits that are found in this crop. As potato is genetically also one of the most diverse crops on the planet; there are very many traits hidden in the cultivated germplasm. We feel it is time to start exploring this crops' germplasm to the fullest, and we cannot do this alone: We need your help! For this purpose, we have set up a program that we hope will enable many researchers to start exploring this complex, polyploid crop, as easy as if they are working on the model species *Arabidopsis*.

124

SNP-based assessment of unique and duplicated accessions in genetic resources of Nordic potatoes

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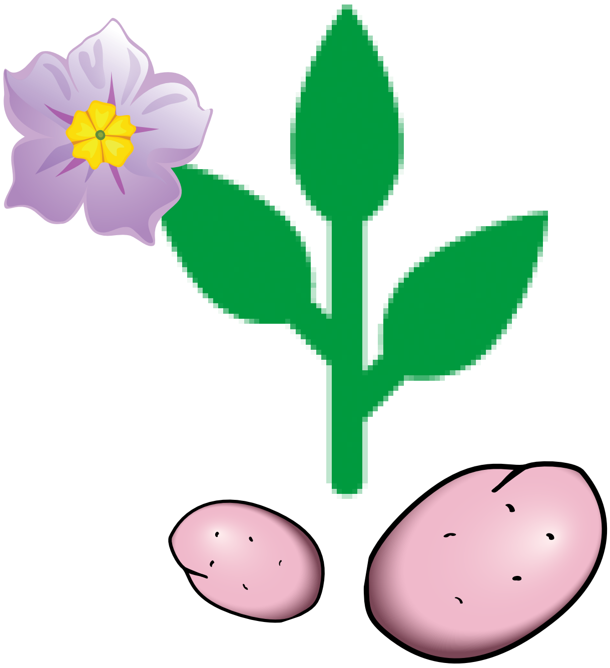
Collections of Nordic potato varieties exist at the Norwegian institute of Bioeconomy Research, NIBIO, at the Nordic Genetic Resource Center, NordGen, and at the Leibniz Institute of Plant Genetics and Crop Plant Research, IPK Groß Lüsewitz. The collections include landraces, older varieties from early years of Nordic breeding programs, and heirloom varieties, of which some are suspected to be variants of early, regionally well-known varieties. Diverse microclimates of the region and strong dependence on potato in traditional diets, has allowed large numbers to survive and remain in local use, particularly in Norway. NIBIO conserves and provides access to potato accessions of Norwegian origin for predominantly domestic use. Norway's strict phytosanitary regulation complicates access to the Nordic potato collection at NordGen. Both collections have received new accessions, predominantly from private donors, raising concerns about potential duplicates and the need for comprehensive identification. Traditionally varieties and landraces have frequently traveled across borders finding use in similar climates in neighboring countries. The extensive German potato collections at IPK, one of the largest and oldest in Europe, encompass a substantial portion of Nordic accessions that predate the Nordic collections. Similarly, the German collections hold many early and widespread varieties, historically used in the Nordic region, hence of large value as reference for identifying and characterizing potato accessions in Nordic collections.

In recent years, Single Nucleotide Polymorphisms (SNPs) have emerged as a powerful tool for genetic analysis. In this study, 356 accessions from the three collections – NordGen, NIBIO, and IPK – were genotyped using an Infinium 22K SNP array (TraitGenetics, Germany). After filtering on minor allele frequency and variability, 13,252 SNP markers were retained for further analyzes. This high-throughput genotyping approach enabled the identification of duplicates and the establishment of genetic relationships among accessions. The results identified unique accessions, revealed suspected landraces as variants of well-known regional older cultivars and identified duplicates across collections. The findings of this study will contribute to the efficient management and utilization of Nordic potato genetic resources for research breeding and training and identify unique heirloom varieties for food innovation and specialty production.

Abstracts – Session 2

Improved potato health



201

Aggressiveness and behavior of different pectinolytic bacteria species involved in potato blackleg disease

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Blackleg causes high economic losses for the seed potato industry worldwide. The disease is caused by bacteria belonging to the genera *Pectobacterium* or *Dickeya*. Recent developments in sequencing technology led to refine their taxonomy. Since 2016, the number of described species has increased from 12 to 33, highlighting their great genetic diversity. To date, few data are available about their specific behavior on potato host.

In order to compare the aggressiveness of 5 different *Pectobacterium* and 2 *Dickeya* species, we inoculated the pathogens on tubers just before plantation in trial fields. Each inoculum consisted in a mix of 5 strains belonging to a same species. Then, different parameters reflecting the aggressiveness and fitness of the inoculated strains were observed, as blackleg expression or vertical transmission in harvested tubers.

The results showed differences between species for all the parameters studied, highlighting different colonization strategies on potato host. Moreover, the qPCR analysis of blackleg symptoms obtained after inoculation with a mix of strains belonging to two different species can reveal a possible antagonistic relation between pectinolytic bacteria species association. Finally, a metabarcoding sequencing approach performed to monitor each inoculated strain revealed the predominance of one strain in each analyzed symptom, not always the same, highlighting a pioneer effect during the symptom development.

202

A microscopic examination of potato root infection by *Pectobacterium atrosepticum*

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Bacteria belonging to the genera *Pectobacterium* and *Dickeya* cause significant losses due to disease in a wide range of crops and other plants worldwide, with potato being the most economically important. While different species are responsible for losses in different countries, *Pectobacterium atrosepticum* (Pba) is the main cause of potato losses in the UK, causing blackleg disease of potato plants and soft rot of tubers. Disease is thought to initiate from contaminated mother tubers when environmental conditions, including heavy rainfall and waterlogging, favour disease development. However, our recent data shows that under heavy irrigation, Pba infection can also cause disease directly from the environment and that the presence of soil-borne free-living nematodes (FLN) may help to mediate Pba entry into the growing plant. Studies in the Netherlands have shown that the closely related bacterium *D. solani* is able to enter the plant directly via the roots, although the environmental conditions and mechanisms responsible are currently unknown.

Using three different microscopy methods; light, confocal and lightsheet, we analysed the movement of Pba both on and into the roots of actively growing potato plants. While experiments using FLN were inconclusive, our data shows that entry into the root systems of these plants only occurred following physical damage, in this case caused by laser ablation, and that once inside the plant the bacteria moved freely within the pectin-rich middle lamella between cells. However, we did not find evidence of entry into the xylem and therefore we require a better understanding of how bacteria entering via the roots move into the stem to cause disease.

203

Bacterial wilt of Potato: A Threat to Food Security in sub-Saharan Africa

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Potato is an important food security crop and source of household income for many rural smallholder farmers in sub-Saharan Africa (SSA). Despite the importance of potato, its productivity remains at 4–9 t ha^{-1}, largely due to diseases, of which bacterial wilt caused by *Ralstonia solanacearum* species complex (RSSC) is the most important. Latently infected propagation material such as potato seed tubers are known to be a source of long distance spread of the pathogen and pose a threat to crop production and contribute to pathogen dispersal. The potato seed system in SSA is largely informal, and unrestricted regional and cross-border movement of seed potato occurs frequently. The unregulated seed movement in the regions and cross-border poses a great threat in disseminating RSSC strains to un-infected areas and have been introducing new strains from abroad as well. Here, we will give insight into the potato seed system in sub-Saharan Africa; distribution, pathogenic diversity, epidemiology of RSSC strains, and the state of the art for management of bacterial wilt under small holder farmers' perspective. Components of the bacterial wilt management strategies examined include diagnostics and surveillance, prevention and control of infection using phytosanitation and use of bacterial wilt free seed, and management of disease through the breeding and promotion of varieties, and cultural practices. We highlight key research areas that need prioritization and conclude by examining the outlook for bacterial wilt management in potato from SSA perspective.

204

Pepper ringspot virus (PepRSV), the latest threat to the South African potato industry

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Over the last four years, a Tobravirus, named Pepper ringspot virus (PepRSV) was found to infect potato crops (*Solanum tuberosum*) in South Africa (SA). To date, PepRSV has only been reported from Brazil, where it infects pepper, tomato, artichoke and *Bidens* weed species, but not potatoes. In SA, PepRSV cause brown arcs and flecks in the tubers, a symptom also referred to as spraing. In light of the importance of the commercial potato industry in SA and its use as a subsistence and cash crop for many households, the PepRSV disease is an important priority for investigation. During this DALRRD-funded research project, two molecular detection methods for PepRSV were established. The detection efficiency of the qRT-PCR method was shown to be able to detect one infected leave in a sample of 100 leaves, making the method appropriate for use in potato certification scheme, where for a zero tolerance disease, a sample of 4605 leaves/tubers needs to be tested per unit, to ensure a 99% probability of 0.1% disease detection. Widespread testing by the ARC in 2023 revealed the presence of PepRSV in the Free State (Warden, Kroonstad, Bultfontein, Theunissen, Bethlehem), Limpopo (Dendron, Vivo, Polokwane), North West (Skeerpoort, Christiana, Bloemhof, Vryburg) and KwaZulu-Natal (Moorivier, Winterton). The potato cultivars affected include Mondial, Sifra, Panamera, Allison, UTD and Lanorma. A nematode transmission trial with *Nicotiana benthamiana* in pots was carried out and it was found that PepRSV is being transmitted by *Nanidorus minor*, a trichodorid found widespread in SA. A host range study using nematode transmission in pots are currently being carried out and this results will also be discussed.

205

Losses from seedborne Potato Virus Y infection dependent on strain and variety

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The economic impact of seedborne *Potato virus Y* (PVY) to commercial producers is difficult to assess as it is largely dependent on variety and PVY strain. A field study to evaluate foliar and tuber reactions on five potato varieties (All Blue, Chieftain, French Fingerling, Yukon Gold, and Russet Burbank) against three PVY strains (O, NTN, and N-Wi) was set-up in 2018. PVY inoculation, seed production, and foliar and tuber evaluations were done in greenhouses, 2015–17. Progeny tubers (G3) from greenhouse-grown plants, testing positive for PVY by ELISA, were planted in a field trial near Othello, WA. A split-plot design with four replicates was used with variety as the main plot and strain as the sub-plot. Foliar observations of PVY symptoms were recorded 63 days after planting (DAP) and tubers were harvested 102 DAP. Tuber yields, grades, number per plant, quality, and defects were recorded. Gross return was estimated using local market prices for WA. Averaged across cultivars, grower gross return of each plant infected with PVY^{O}, PVY^{NTN}, $PVY^{N\text{-}Wi}$, was reduced by 55%, 22%, and 20%, respectively, relative to the non-infected control. The three strains also reduced individual plant yield by 64%, 21%, and 18%, respectively. Reductions in gross return from PVY^{O} infection ranged from 13% to 89% among varieties; PVY^{NTN} and $PVY^{N\text{-}Wi}$ gross return losses ranged from 0% to 54%, and losses were not always significant. Gross return for individual Russet Burbank plants infected with PVY^{O} was reduced by 79%. If these values were applied to a commercially-grown Russet Burbank field, WA growers would experience an economic loss of US$104 ha^{-1} for every 1% of PVY^{O} infection, assuming a clean field was worth US$12,355 ha^{-1}. Across 400 hectares of potato production, the loss from 1% infection would be US$41,600. A similar level of PVY^{NTN} or $PVY^{N\text{-}Wi}$ infection in Russet Burbank might cost WA growers up to US$14,830 per 400 hectares of production.

206

Operator influence on roguing efficacy for controlling potato virus Y (PVY) in seed potato fields

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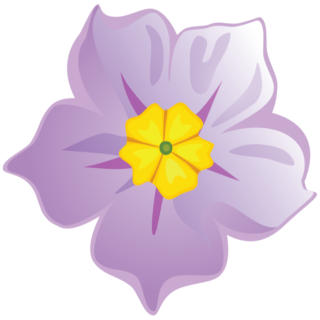
Roguing, the manual removal of potato plants displaying symptoms of viral or bacterial infection, as well as those with atypical appearances for the cultivar, plays a crucial role in controlling Potato Virus Y (PVY) in seed potato fields. The primary objective is to diminish the percentage of inoculum in the field, thereby reducing further virus spread. Given PVY's transmission by various aphid species and its significant economic impact on the European potato sector, effective roguing is essential. Operators conduct plant removal before crop inspection by the official seed certification service to ensure compliance with certification tolerances. The quality of roguing depends on factors such as the severity of symptoms and the operator's ability to recognize them.

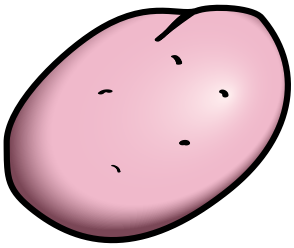
A three-year field study was conducted, involving the planting of 11 tuber samples of cv. Celtiane infected at various levels in 11 lines of 100 plants each. Upon emergence, leaves were sampled from each plant and analyzed via enzyme-linked immunosorbent assay (ELISA) to detect virus presence. Trained operators, numbering five to six annually, assessed the number of infected plants in each line. The study calculated the percentage of infected plants that went undetected by the operators.

Results indicated that operators generally observed a higher number of infected plants than reality. The first year they saw 1% more infected plants, while they saw respectively 11% and 18% more infected plants in the second and the third year. Significant discrepancies were noted among operators, with overestimations ranging from 3% to 21% of infected plants. Additionally, operators occasionally underestimated the number of infected plants, occurring in 37%, 8%, and 16% of plots in years 1, 2, and 3, respectively. Minimizing these underestimations is crucial for maximizing roguing efficacy.

Abstracts – Session 3

Integrated pest management





301

Investigating the causal organisms involved with potato early dying in South Africa

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Symptoms resembling potato early dying (PED) has been observed in potato fields in the Limpopo Province, South Africa. The disease causes potato plants to age prematurely and eventually die back which leads to reduced yield, with smaller tubers and low tuber quality. A two-season survey was conducted within the potato production area in the Limpopo Province in South Africa. Numerous fungal, oomycete, pectolytic bacteria and nematode genera were isolated from plants showing symptoms of PED.

The dominant fungal genera included *Alternaria* spp., *Colletotrichum* spp., *Fusarium* spp., *Macrophomina* spp., *Pythium* spp., *Rhizoctonia* spp. and *Verticillium* spp. *Colletotrichum coccodes* and *V. dahliae* were co-isolated at high rates from plants collected during both growing seasons (91% and 71%, respectively), and are believed to be the main causal organisms of PED in South Africa. Pathogenicity testing showed that both *C. coccodes* and *V. dahlia* were pathogenic. Stem and leaf symptoms, similar to those observed in the field on plants infected with *C. coccodes* alone, were not evident in the glasshouse until an extended time period post-inoculation. Most of the *V. dahliae* isolates tested caused symptoms of leaf chlorosis and necrosis, followed by total wilting of the plant, which was similar to the PED symptoms observed in the field. The interaction between *C. coccodes* and *V. dahliae* requires further investigation.

The high number of *Pectobacterium* species isolated indicates that this pathogen was prominent. Pathogenicity testing revealed that aerial stem rot could not be reliably distinguished from PED symptoms at an advanced stage, which explains why so many plants, that were sampled, were infected with the pectolytic bacteria. The interactive role between *Pectobacterium* spp. and *V. dahliae* should not be ignored. Over the two growing seasons, *Pectobacterium* spp. were isolated in conjunction with *V. dahliae* (23% and 38%, respectively).

From the soil and root samples, a low number of nematodes including the plant feeding *Meloidogyne* spp. and *Pratylenchus zeae* were observed and it is believed that nematodes do not to play a major role in PED in the Limpopo Province of South Africa. Management strategies for PED must take into account the disease complex and understanding the biology of the pathogens involved. It is clear that *V. dahliae*, *C. coccodes* and *Pectobacterium* spp. are major contributors to PED in South Africa and should be the focus of management strategies.

302

Patat’Up: towards the production of a low-input potato

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Potato cultivation in Wallonia holds economic and cultural significance, but its heavy reliance on inputs poses risks at environmental, health, and economic levels. The Patat’Up project aims to address these challenges by integrating various levers to create alternative, ecologically intensive, and resilient potato production systems, both for fresh markets and for industrial processing. This involves using robust varieties, implementing innovative cultivation techniques to reduce inputs and better respect the soil, and assessing the processing capabilities of selected potatoes to make sure they can be effectively used and valued by operators. The project emphasizes a multifactorial approach, evaluating the technical, environmental, and economic aspects of the different cultivation models studied. Regular consultation with industry stakeholders is planned throughout the project to ensure that practical solutions aligned with their needs.

The project is divided in two phases. In the initial period (2022-2023), micro-field trials aimed to identify key levers for reducing input usage while maintaining high yield and good quality. The applicability of these techniques to large-scale production was a crucial consideration. The second phase, commencing in 2024, focuses on integrating these levers into two low-input itineraries, comparing them to a conventional itinerary across technical, environmental, and economic dimensions. The selected levers are focused on the use of robust varieties and innovative cultivation practices.

Regarding robust varieties, the project explores potato varieties with late blight tolerance to potentially delay fungicide interventions and identifies those with optimal nitrogen use efficiency.

In terms of innovative cultivation practices, the project examines various haulm desiccation systems, including crushing & spraying, haulm pulling, thermal, and electric methods. It also assesses the effectiveness of localized spraying at the ridge’s top, combined with mechanical weeding of the sides, to reduce herbicide usage. To address insecticide reduction, multi-spectral sensors and mapping techniques are employed to detect Colorado Potato beetle (CPB) outbreaks, aiming to minimize insecticide application. Additionally, the project introduces a mechanical approach to CPB monitoring with the Colorado Beetle Catcher.

303

Benefits of click beetle monitoring for wireworm control

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Wireworms are a major pest of potatoes. Significant crop losses and the limited availability of soil-based insecticides call for practical solutions. Soil tillage is considered to be an effective method of wireworm control, especially when carried out during or shortly after the egg-laying period. On the one hand, tillage reduces the number of viable eggs and immature larvae, which are particularly susceptible to desiccation. On the other hand, it is thought that click beetles prefer to lay their eggs in densely vegetated areas rather than in bare soil. The challenge is that there are several species of click beetles. They differ considerably in their biology, in the emergence of the adult beetles and therefore in the time of egg laying. Knowledge of the local species composition and their swarming period is necessary to determine the best time for soil cultivation. For this reason, click beetle monitoring with species-specific sexual pheromones has been carried out in Austria since 2019. Monitoring data are currently available online at www.warndienst.lko.at.

Successful control strategies need to take into account the biology of wireworms, be manageable, and be economically viable. One of the aims of the “Wireworm Control” project is to test the applicability of the click beetle monitoring as a decision-making tool under practical conditions.

The effectiveness and practicability of tillage measures are investigated in field trials. The trials are carried out on several sites with different climatic conditions and with crop rotations adapted to the site conditions. Tillage is carried out as permitted by the crop and according to the activity phases of the dominant click beetle species. The results on the feasibility and effectiveness of tillage against wireworms will be presented based on the results from three trial sites in Austria.

304

The Good, The Bad and The Ugly: wireworm pests and the cover crops conundrum in potato production

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The use of cover crops in Agri-ecosystems has increased in recent years, partly due to the need for biodiversity conservation, concerns about the leaching of soil nutrients under bare soils, pest and pathogen pressure and the dwindling crop protection options available to growers. The choice of which cover crop to cultivate varies according to the needs of the growers, crop rotation sequences, seed prices and their adaptability to the local conditions. Soil biodiversity conservation studies involving cover crops often focus on beneficials, with little or no attention to the detrimental proportion of the population. Recent observations (Percommune) have shown belowground pest and beneficial population build-up in soil under reduced tillage relative to conventional tillage.

Here we investigated cover crop effect on the oviposition of adult click beetles and larvae development for *Agriotes sputator* (Coleoptera: Elateridae) under polytunnel. Newly hatched larvae were then exposed to the same set of cover crops, which included *Fagopyrum esculentum* (buckwheat), *Brassica juncea* (Ethiopian mustards), *Raphanus sativus* (fodder radish) or *Lolium perenne* (English ryegrass) and compared with bare soils under glasshouse pot experiments. Different larvae sizes of *A. sputator* were equally challenged with tubers of potato var. Monalisa in pot experiments to observe damage intensity.

Bare soils and buckwheat significantly reduced the number of newly formed larvae as compared with the English ryegrass. Likewise, the number of neonate larvae were reduced on mustard and fodder radish, but to a lesser extend as compared with buckwheat. Larvae mortality post hatching was 60% and 75% under buckwheat and bare soils on average respectively, as compared with 10%, 15% and 25 % under mustard, ryegrass, and fodder radish respectively. Damage on potato tubers was less intense for smaller sized larvae and intensity increased with larvae sizes.

Results highlight the significance of cover crop choices in rotation with potatoes under wireworm infestation or fields at risk of infestation. Results also show that larvae sizes could be indicators for expected damage on potato tubers in a rotation under infested plots. Further studies are in process to better understand these phenomena.

305

Extension Education on Herbicide Injury in Potato

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The number of herbicide injury problems in potato are more commonplace, causing many questions by potato growers. Injury from herbicides can be a result of soil carryover, herbicide residues in seed, or exposure of plants to herbicides. As a result, potatoes can have poor emergence, chlorosis, necrosis, growth reduction, misshapen tubers, reduced yield and nonacceptable residues. The objective of this Extension project has been to demonstrate various herbicide injury symptoms to assist potato growers in improved i dentification, educate growers on how to test for herbicides, and mitigating such difficult situations. Determining if injury is caused by herbicides or another source will be important in managing and marketing potatoes.

306

Streptomyces secondary metabolite effects on *Pythium, Colletotrichum* and *Helminthosporium*

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Potato tuber pathogens *Pythium*, *Helminthosporium*, and *Colletotrichum* have detrimental effects on potato tuber quality and yield. *Streptomyces* bacteria are known for producing secondary metabolites with antifungal properties. Streptomycete bacteria are found in all regions of potato growing soil and can also be found on the tuber surface, some are known as pathogenic but many isolates are not pathogenic and compete with other microorganisms at the tuber surface environment. Isolates of *Streptomyces* collected from tubers surfaces all over North America have shown inhibitory effects towards *P. ultimum* and *H. solani* in Petri dish assays. Tests were conducted in a lab, greenhouse, and field setting to determine if the inhibition was observed outside of a Petri dish. We found a powder formula that kept 50% of the added Streptomyces spores viable for a period of three to six months. Isolates with inhibitory effects towards *H. solani* were applied as a powder on seed tubers infected with H. solani and grown in a greenhouse. *Helminthosporium* was not identified on the progeny tubers, but some isolates significantly limited *C. coccodes* compared to the control. This experiment was repeated in a field setting where *C. coccodes* was again the primary disease on progeny tubers. In the field, isolates showed no inhibitory effect towards *C. coccodes*, but fungicide seed treatment Maxim MZ did. Isolates with inhibitory effects towards *P. ultimum* were applied as a powder onto wounded tubers in a storage study. One hour later the tubers were exposed to *P. ultimum*. Isolates did not limit *P. ultimum* compared to the control. Isolation and identification of the secondary compounds was attempted with mass spectrometry, but attenuation with the isolates may have reduced effectiveness against the fungi. Our data suggests that Streptomyces may reduce tuber infections due to *Pythium*, *Helminthosporium*, and *Colletotrichum* under controlled conditions but there was no efficacy under field conditions.

307

Variety screening for tolerance against *Candidatus Phytoplasma solani* and *Candidatus arsenophonus phytopathogenicus*

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A change in climate directly influences the emergence and spread of plant pathogens. The rise in temperatures in particular enables invasive insect species to settle in new regions. Associated with the settlement of invasive insects, various immobile pathogens such as viruses and bacteria can be transferred to plants. *Pentastiridius leporinus*, a planthopper that has been spreading massively in south-west Germany, particularly in the Rhine valley, expanded its host range to potatoes. Both the phytoplasma *Candidatus Phytoplasma solani* (stolbur) as well as *Candidatus Arsenophonus phytopathogenicus* can be transferred to potato plants by *P. leporinus*. In 2022, typical symptoms such as aerial tubers, leaf discoloration, wilting plants and rubbery tubers were discovered, leading to yield and quality losses. Due to the socioeconomic value of potatoes in south-west Germany and an inefficient direct control to *P. leporinus*, cultural practices such as variety choice should be focused to minimize the economic loss. Therefore, field trials were conducted in 2022 and 2023 in Bingen, Germany, including 21 varieties. Each variety was repeated three times. The plots were allocated using a randomized block design. In both years, *P. leporinus* was found on yellow sticky traps. The wilting process of the potato plants were visually assessed in July and August. The rAUDPC was calculated to quantify the wilting process. Furthermore, the proportion of rubber tubers were determined for each plot. Hierarchical clustering was conducted to identify varieties with a lower level in both wilted plants as well as rubber tubers. In general, all varieties showed both symptoms in both trial years. Thereby, the calculated rAUDPC ranged between 12 to 58 % in 2022 and 9 to 70 % in 2023. A weak positive correlation was found between rAUDPC and proportion of rubber tubers, but only in 2022. However, the clustering including both responsible variables revealed 6 varieties with a better performance in both symptoms and years. Upcoming PCR analyses of the tubers will provide more precise information between the correlation between infestation and symptoms. More detailed investigations for clarifying the mechanisms of better tolerance, which could be vector-based or pathogen-based, is needed.

308

Using machine learning as a predictive tool to improve potato black dot management

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Potato black dot, caused by the fungus *Colletotrichum coccodes*, produces macroscopic black sclerotia that develop into silvery brown lesions on the tuber skin, negatively affecting the aesthetic appearance of the tubers and, as a consequence, reducing the suitability for pre-pack markets. The soilborne pathogen infects tubers in the field, but symptoms tend to manifest during postharvest cold storage. Despite strategies to manage and control potato black dot disease in the field and during storage, there is a research gap concerning how pre- and postharvest factors interact and affect black dot development during potato cold storage. Alongside minimising the incidence of the disease, there is a need for objective assessment methods to predict the progression of the disease during storage. The study aimed to use machine learning techniques to integrate pre- and postharvest strategies for improving the management of black dot disease.

Field trials over a two-year period followed by postharvest cold storage were used to critically evaluate how the preharvest factors of fungicide application and crop duration affect black dot disease development. Daughter tubers were stored under continuous air flow for 10 months at 3 °C and > 90% of relative humidity. During postharvest cold storage, tubers were sampled monthly to visually assess black dot incidence (% of tubers affected by black dot) and severity of the lesion (% of tuber surface affected by the disease lesion). Empirical data obtained was used to develop different regression and classification models (binary and multiclass) using random forest algorithms to predict the percentage of black dot lesion severity.

The best results were observed when classifying either unmarketable tubers (> 12.5% area of the tuber affected by potato black dot lesion) or marketable tubers (< 12.5%) where a 90% accuracy was achieved. However, the main limitation of the models was the unbalanced nature of the datasets used. Precision and recall values for the minority class (tubers affected by the disease) ranged from 0.46 to 0.64 suggesting that further work should include a more diverse dataset to achieve a better model's overall performance. The results demonstrated the benefit of integrating pre- and postharvest factors to predict potato storability and the potential use of random forest, contributing to a better disease management, and resulting in a reduction of food loss and waste within the UK potato supply chain.

309

Effect of mulch cover on wilt symptoms and rubber tubers caused by *Candidatus Phytoplasma solani* and *Candidatus Arsenophonus phytopathogenicus*

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In recent years, potato production in south-west Germany has been affected by the emerge of the phytoplasma *Candidatus Phytoplasma solani* (stolbur) as well as *Candidatus Arsenophonus phytopathogenicus*. The planthopper *Pentastiridius leporinus* has been identified as vector. Typical symptoms such as aerial tubers, leaf discoloration, wilting plants and rubbery tubers were discovered in many fields, leading to yield and quality losses. Due to the socioeconomic value of potatoes in south-west Germany and an inefficient direct control to *P. leporinus*, cultural practices should be focused to minimize the economic loss. One option appears to be covering the potato rows with a layer of mulch. It is known that aphids are irritated by a change in the color contrast between the soil and the plant as well as the change in the odor, which disrupts their function as a vector. Therefore, field trials were conducted in 2022 and 2023 in Bingen, Germany, testing mulch cover (with and without) on 21 varieties. As mulch materials, lucerne hay was used at a rate of approximately 2 kg/m² at around 40 days after planting. In both years, the presence of *P. leporinus* was confirmed using yellow traps. The wilting progress of the potato plants was visually assessed in July and August. The rAUDPC was calculated to quantify the wilting progress. Furthermore, the proportion of rubber-like tubers was determined. In both years, the mulch cover led to a significant reduction in the proportion of rubber-like tubers across all varieties. The proportion of rubber-like tubers decreased from 19.3% and 21.8% in the control to 6.4 % and 7.6 % with mulch apllication in 2022 and 2023, respectively. Mulch cover also reduced the rAUDPC by around 10 % in both years, and increased tuber yields by 27 and 39 % in 2022 and 2023, respectively. No significant interactions between variety and mulch cover were identified. Further research on the type, amount and timing of mulch application is required to improve the performance and to understand its interaction to vector community.

310

Adoption of an early warning system for the integrated management of potato late blight (*Phytophthota infestans*) in Chile

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Potato late blight, caused by *Phytophthora infestans*, is the most important disease affecting the potato crop in the world, decreasing yield by more than 50%. It is a disease that occurs under conditions of moderate temperatures and high relative humidity. Early warning systems are tools that use models based on environmental conditions to predict the risk of disease development. In Chile, early warning system for late blight was developed and implemented and it is available on the http://tizon.inia.cl platform. However, the monitoring of the adoption of knowledge by farmers is of great relevance for the evaluation of the impact of the technological intervention. The objective of this study was to evaluate the adoption of early warning systems by small farmers in an integrated control management of late blight. Therefore, for this, small farmers were trained in the integrated management of late blight during 4 seasons. At the beginning of this project in the year 2018, baseline surveys were conducted with potato farmers, mainly from the Puqueldon Commune, Chiloe Island, Los Lagos Region. The technical advisors who support these farmers were also considered in this survey. This survey served as the basis for the first measurements of the indicators contemplated in the design of this project. At the end of the project, in 2023, a follow-up survey was conducted among the beneficiary farmers to evaluate progress in terms of late blight management and the use of early warning systems. The technical advisors surveyed, mentioned late blight as one of the main diseases causing damage to the potato crop and 95% of them, in addition, indicated that they had observed damage in the farmers they advised. Farmers, on the other hand, use mainly fungicide to control the disease. Comparing the initial and final situation, positive changes are observed in relation to disease control and identification of the disease. In relation to disease control, there is an increase in the adoption of IPM and control strategies, so farmers now use more than one technique for control and, also, fungicide applications are initiated at the right time. In good agricultural practices, farmers have become aware of the proper use of chemical products and the proper use of application equipment. Finally, a better understanding of the early warning system and its implementation has been achieved, leading to an increase in the use and timing of chemical control.

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311

Creating a synergy between farmers, gardeners, and other stakeholders to eradicate late blight primary inoculum and adopt IPM control strategies

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Sources of primary inoculum responsible for early outbreaks of late blight are well known. However, only a small number of farmers have adopted prophylactic measures, and a major factor is underestimated: management at a landscape scale. The Hauts-de-France region has more than 100,000 ha of potato crops, which represents two-thirds of French production. The potato crop is highly dependent on chemical protection due to the exploding characteristic of late blight disease and early infections. Reducing its dependence is crucial for human and environmental health.
Through a systemic approach, the SYNAPTIC project aims to show that integrated control of potato late blight – including landscape-scale management of primary inoculum – would enable significant reductions in pesticide use, maintaining acceptable crop protection. This project brings together farmers, gardeners, engineers and industrialists from the Hauts-de-France region and aims to work on varied and interconnected topics.

Firstly, the SYNAPTIC project is dedicated to charting primary inoculum sources, by identifying primary inoculum sources around fields, monitoring spores in the air with spore traps and analysing strains genotypes. Secondly, gardeners and farmers habits and their reluctance towards changing them are surveyed. Then, IPM strategies and prophylaxis measures are tested through field pilots, and efforts are made to help gardeners adopt virtuous practices.

To date, spores' traps results are disappointing as few spores are sampled during substantial outbreaks, whereas *P. infestans* genotypes are well known, 36_A2 representing the large majority. Surveys reported that gardeners have risky habits towards disease management, mainly because of a lack of knowledge, whereas farmers have safer habits, but they highlighted the need for more resistant cultivars that are adapted to the market, requiring network adjustment. The five farmers followed through field pilots are willing to adopt IPM strategies as long as they are well advised and rewarded. In addition, a cultivar showcase has been presented to gardeners, and the participative science app VigiMildiou has been introduced to spread information about late blight and localise inoculum sources in real-time. Complementary work by ARVALIS has shown encouraging results in substantial reductions in fungicide input, showing good protection with a combination of IPM levers.

312

Aggressiveness of *Phytophthora infestans* isolates from four genotypes widespread in Europe

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Phytophthora infestans is an oomycete pathogen within the kingdom *Stramenopiles*, which causes late blight in potato and tomato. During infection the pathogen secretes effector proteins that suppress the defense system of the plant. Plants have evolved to recognize effectors, resulting in an evolutionary cycle of defense and counter-defense in plant–microbe interactions. The pathogen reproduces both asexually and sexually, resulting in constant development of new clonal lineages with different levels of aggressiveness. The lineages are routinely defined by analysis of up to twelve simple sequence repeat (SSR) markers, but little is known about the functional genes (effector repertoire) and the aggressiveness of isolates within the lineages. We have analyzed this by testing aggressiveness of 28 isolates representing four clonal lineages, EU13_A2, EU34_A1, EU37_A2 and EU41_A2 that are widespread in Europe. Five leaves of susceptible potato cultivars Craig's Royal, Irys and Tarpan were inoculated in three repetitions on two dates. The aggressiveness was determined by latency period (days), lesion diameter (mm) and sporulation intensity (number of sporangia/ml). The isolates of the genotype EU37_A2 were the most aggressive of the tested isolates. To analyze the effector repertoire, we amplified and sequenced several effector genes using Illumina Miseq and PacBio, but bioinformatic processing and analysis remain to be done.

The research leading to these results has received funding from the Norwegian Financial Mechanism 2014–2021, project DivGene: UMO-2019/34/H/NZ9/00559

313

Rating potato varieties: 30 years of experiments reanalyzed to explicit resistance and explain its variability

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Late blight is a disease caused by the oomycete *Phytophthora infestans* on potato and other Solanaceous crops. Currently, control of this pathogen makes potato the most frequently treated arable crop in France. With pesticide use reduction in mind, two potential solutions are the use of resistant varieties and Decision Support Systems (DSS). However, resistance assessment to potato late blight is currently not informative enough to be optimally implemented into DSS, so potential synergies between these two means of control are not fully exploited.

We aimed at creating an epidemiologically informative resistance rating scale, based on the analysis of epidemic progress curves. We used a 28-year dataset of late blight observations on a number of potato varieties (cultivars and hybrids) to generate a classification of epidemics and evaluate the respective influences of the host, the pathogen and climate on the type of epidemic observed. To achieve this, we fitted a logistic model to observed disease progress curves, applied a PCA to the parameters descriptive of the curves, and built clustering trees. We then used random forest models to evaluate variables importance on the belonging of epidemics to one or another cluster.

We kept 5 types of epidemics: no epidemics (NoE), weak late and fast epidemics (WLF), intermediate late and slow epidemics (ILS), severe late and fast epidemics (SLF) and severe early and fast epidemics (SEF). The variety was the most important predictor of epidemic type. For varieties predominantly associated with NoE or SEF, shifts between epidemic types across years were driven by humidity, and for varieties associated with WLF or SLF by climate and pathogen composition, especially diversity. Our results also pointed out to a depreciation of high-level resistance between 30 and 50 years after variety introduction. Furthermore, low and high types of resistance were dependent on pathogen population composition, so description and monitoring of *P. infestans* are crucial to better predict epidemics on potato. In conclusion, a more informative rating of varieties based on epidemic parameters is possible and would provide benefits for the combined use of DSS and host resistance.

314

Global Solutions for Sustainable Late Blight Management: Evaluating the Success of 3 R-Gene Potatoes in Asia and Africa

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The USAID Feed the Future Biotechnology Global Potato Partnership developed bio-engineered potatoes with 3 R-gene late blight resistance. For Asia, the Simplot/MSU construct (Rpi-blb2, Rpi-vnt1, and Rpi-mcq1) was inserted into farmer-preferred varieties Granola and Diamant. In Africa, CIP's construct (RB, Rpi-blb2, and Rpi-vnt1) was inserted into Shangi, Tigoni, and Victoria. Studies, conducted in Bangladesh, Indonesia and Kenya, assessed the efficacy of these constructs in factorial randomized complete block trials. In Indonesia, Diamant and Granola 3-R gene lines were compared to non-transgenic Diamant and Granola in 3 confined field trials. In Kenya, 3 R-gene lines (Shangi, Tigoni, and Victoria) were compared to non-transgenic lines at three locations. In Bangladesh, Diamant 3 R-gene lines were compared to non-transgenic Diamant at four locations. Late blight ratings began upon symptom appearance in non-sprayed control plots, continuing weekly until harvest. No late blight was observed in 3 R-gene plots, indicating complete resistance to *P. infestans* strains in all three countries. This data, combined with regulatory information, will be used for the development of dossiers to be submitted to the national biosafety authorities of each country for commercial release of the 3 R-gene potato.

315

New mutations in Alternaria solani affect disease management using SDHI / FRAC group 7 fungicides

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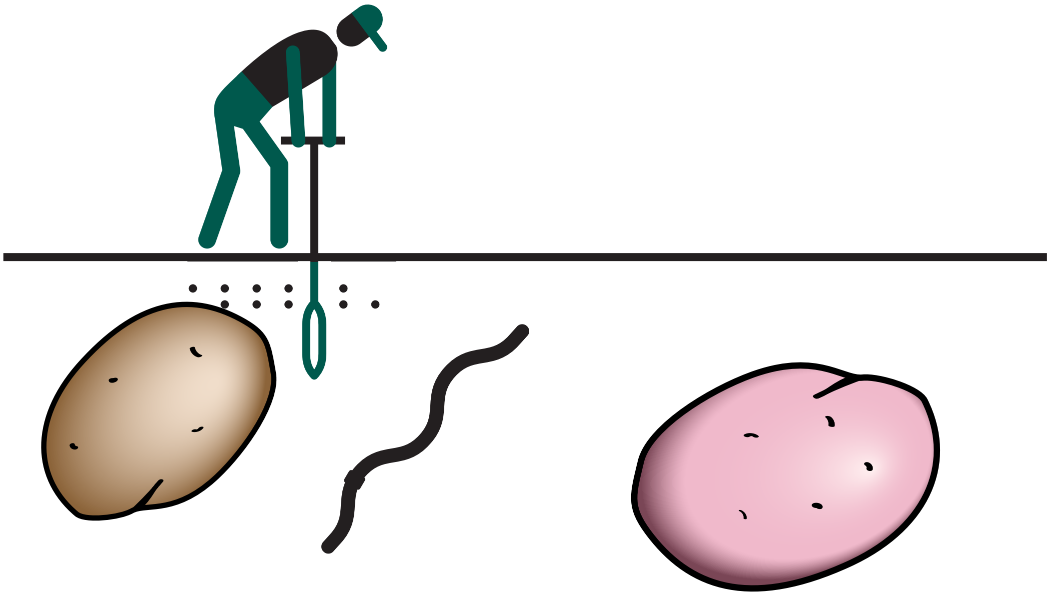
The potato industry in North America relies heavily on the application of foliar fungicides for the management of early blight. Resistance to single-site mode-of-action fungicides has plagued pathogens in the species *Alternaria* for decades. Five mutations in the Sdh gene of *A. solani* previously identified by Mallik et al. result in reductions in the efficacy of SDHI / FRAC group 7 fungicides. *Sdh* gene mutations were characterized in nearly 1,500 *A. solani* isolates collected in 2020, 2021, and 2022 using methods previously developed by Mallik et al. Over 60% of isolates were found to have none of the five mutations previously identified in the *Sdh* gene. The SdhB, C, and D sub-units of a sub-set of 29 *A. solani* isolates displaying reduced-sensitivity to the SDHI / FRAC group 7 fungicides fluopyram and pydiflumetofen (adepidyn) were sequenced. Isolates were collected from numerous potato growing regions in North America. We uncovered two novel mutations in the SdhB and SdhD sub-units of these 29 *A. solani* isolates, and some isolates contained more than one mutation. Reduced-sensitivity to fluopyram and pydiflumetofen (adepidyn) was observed in *in vitro* fungicide sensitivity assays when compared to baseline isolates. This was further supported by greenhouse evaluations conducted across a range of fungicide concentrations where disease control was significantly reduced in some isolates. Results from both *in vitro* ($r = 0.877$; $P < .0001$) and greenhouse ($r = 0.859$; $P < .0001$) assays indicate cross-sensitivity in most isolates across the two SDHI / FRAC group 7 fungicides. These results aid in our understanding of fungicide resistance development in *A. solani*, and our ability to make relevant disease management recommendations. Fungicide efficacy should be closely monitored in potato fields and *A. solani* isolates tested for fungicide sensitivity if reduced efficacy is observed.

Abstracts – Session 4

Improved soil health



401

Geconem: How to collectively manage genetic resistance to potato cyst nematodes?

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Quarantine potato cyst nematodes (PCN) *Globodera pallida* and *G. rostochiensis* are major pests in Europe, but few knowledge exist about population and virulence levels in France. The recent discovery in the north of Europe of virulent populations against resistant potato varieties has raised questions in the French potato sector. In this context, the French research project Geconem (2019–2023), was set up to explore ways to collectively manage varietal resistances to PCN populations by combining analyses of epidemio-surveillance data (WP1); population characterisation (WP2); farmer practises (WP3); development of new molecular markers (WP4) and phenotyping of new resistant genotypes (WP5). The main objectives of the WP1 were to aggregate knowledge and data from the National Competent Authority (in charge of the National monitoring programme) and FN3PT/OPs (in charge of pre-planting tests for seed potato sector) for mapping the presence/absence of *G. pallida* and *G. rostochiensis* and their evolution over time. Twenty years of observations were compiled for 11 out of 13 French metropolitan regions and an interactive map was created for the exclusive use of the consortium.

In WP2, nematode populations were characterised by analysing soil samples collected in infested fields identified in WP1 to determine the species and virulence levels against a range of resistant varieties. Out of 34 soil samples collected, 17 were successfully analysed. Controlled condition tests did not allow the identification of virulent populations but highlighted some behaviour variations.

In WP3, individual and collective strategies of the different potato actors to limit nematode dispersion and promote resistance sustainability were analysed. The study was conducted at various organisation scales (cooperative, regional and national scale). The interviews carried out with a range of potato actors revealed that the subject is taboo, there is a generalized lack of knowledge, which hinders the possibility to develop collective strategies. To initiate the circulation of information, a workshop gathering 20 actors of the French potato industry was organised, and three posters were presented at a technical meeting in Northern France.

Development of molecular markers associated with resistance factors to *G. pallida* and *G. rostochiensis* from different sources of resistance was the objective of WP4. SNP markers identified by genetic association approach and the efficiency of markers from literature linked to resistance are presented at this congress by Leuenberger et al and by Marhadour et al respectively.

In WP5, resistant clones were phenotypically characterized in laboratory and in natural infested fields. The two field experiments showed that resistant clones reduce significantly the number of larvae in the soil.

402

Effects of organic amendments and cover crops on soil characteristics and potato yields

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Intensive potato production may reduce the soil organic matter content (SOM), which may impact several soil functions and increase the incidence of potato diseases. We examined if cover crop and addition of organic materials may counteract these effects. Organic materials were one application of biochar mixed with liquid digestate (BLD); solid digestate (SD); or farmyard manure (FYM); with or without winter rye as cover crop, in a field with regular potato growing. Organic amendment increased SOM, especially for FYM and BLD, while cover crop did not affect SOM. Yet, cover crop increased tuber yields in the second year, and reduced the severity of potato diseases by 10% in post-harvest potatoes in both years. In the second year, the number of marketable potatoes after storage increased by 37% with cover crop. Organic amendments did not affect potato yield or quality, but the proportion of marketable potatoes tended to be higher in the amended soil. By lab incubation, BLD showed the largest potential for SOM storage, up to 32 years, followed by FYM and SD. Cover crops and organic amendments is recommended in potato production, especially for early potatoes where there is sufficient time after harvest to establish a good cover crop.

Link to full article: https://acrobat.adobe.com/link/review?uri=urn:aaid:scds:US:dfee7c97-f832-3229-9e1f-a3ae361742d4

403

Comparing the effectiveness of real-time PCRs to simultaneously detect and identify viable *Globodera pallida* and *G. rostochiensis*

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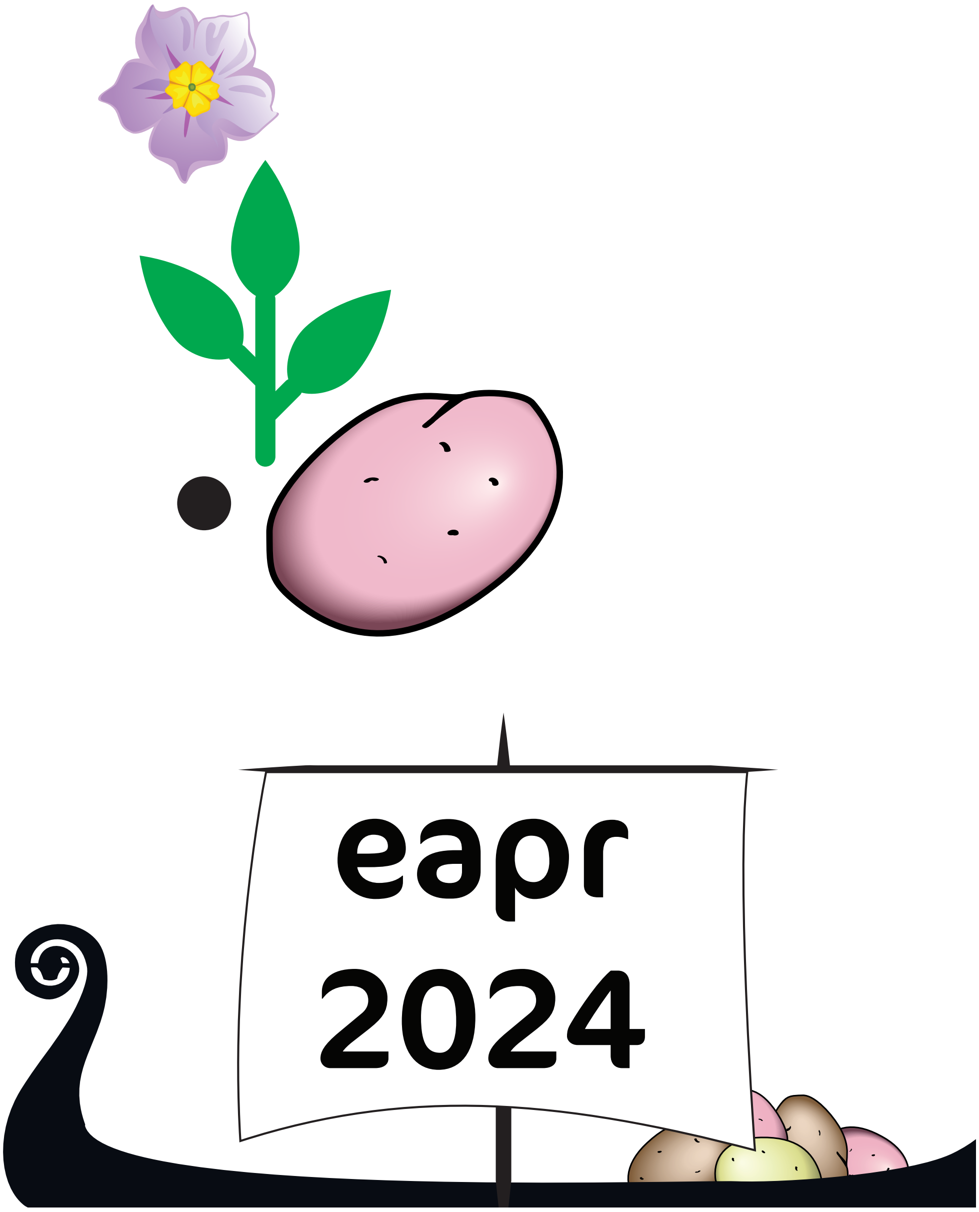
Recently, the Commission Implementation Regulation (CIR) 2022/1192 has been published by the European Union, prescribing regulations on eradication measures for quarantine potato cyst nematodes including mandated assays for species identification. The CIR 2022/1192 provides a derogation on the use of Beniers et al. (2014) real-time PCR as the validation process was still ongoing. In this study, the validation of a modified version of the Beniers real-time PCR was carried out, following EPPO Standard PM 7/98. Furthermore, the performance was compared to the conventional PCR of Bulman & Marshall (1997) and the Gamel et al. (2017) real-time PCR, both DNA based, which are mandated by CIR 2022/1192. Additionally, the effect of cyst viability was compared for the two real-time PCR assays. The modified Beniers real-time PCR met all validation performance criteria, with analytical sensitivity of 1 living egg for both targets *Globodera pallida* and *G. rostochiensis*. The viability assays showed that the DNA based Gamel real-time PCR provided positive results for non-viable, non-infectious cysts in contrast to the modified RNA based Beniers real-time PCR. Based on the results of this study, the modified Beniers qualifies for the detection and identification of viable *G. pallida* and *G. rostochiensis* and performs at least equally well as the other two PCR assays. To encourage the development and improvement of diagnostic protocols, it is suggested that diagnostic laboratories performing official surveys are provided with the freedom to use relevant internationally recognized diagnostic protocols when properly validated in-house, according to EPPO Standards.

Abstracts – Session 5

Agronomy and tuber physiology



501

Is plant maturity a reliable indicator of bruise susceptibility?

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Plant maturity at the time of vine kill or harvest is one of the factors that has previously been reported to be related to bruise susceptibility, but the nature of the relationship is not well understood. Tuber samples were collected from 20 locations in commercial fields in Idaho and Oregon, USA during both the 2020 and 2021 growing seasons. Fields were selected to represent commonly grown cultivars and included one field of Russet Burbank, Ranger Russet, Umatilla Russet, and Clearwater Russet each year. Vine maturity was visually rated at each in-field location just prior to hand-harvesting 20 tubers that were subjected to controlled impact tests and evaluated for blackspot bruise incidence, severity, and depth. Three additional tubers from each field location were assessed for nitrogen (N) and tyrosine content. Most of the fields were exhibiting large variations in vine senescence when tuber samples were collected in early September; however, vine senescence level was not a good indicator of bruise susceptibility. For example, vine senescence was positively correlated with bruise severity in Umatilla Russet in 2020 and Clearwater Russet in 2021, but negatively correlated with bruise severity in Russet Burbank in 2020 and Ranger Russet in 2021. Consistent relationships were found between tuber N content and tyrosine content. In all eight fields across four different cultivars tyrosine increased as tuber N content increased (significant correlation in five locations). Tyrosine also increased in seven of the eight locations as plant senescence increased (significant correlation in three locations). However, neither tuber tyrosine content nor N content was consistently related to any of the gauges of bruise susceptibility measured. In fact, the relationship between tyrosine content and bruise susceptibility was weakly negative in both years. This is opposite to what would be expected if tyrosine was limiting the extent of darkening after impact damage.

502

Environmentally triggered russeting – an overview

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Potato tuber skin is a protective corky tissue consisting of suberized phellem cells. A clean, shiny appearance characterizes smooth-skinned varieties compared to the darker hue of russeted potatoes. The rough skin of russeted cultivars is a desired, genetically inherited characteristic; however, russeting of smooth-skinned cultivars often occurs under undefined suboptimal growth conditions (i.e., environmentally triggered russeting) and is rejected by the consumer. Pathogens do not cause the phenomenon, and the direct causes in the field are unclear. An update will be presented on the factors involved in the development of smooth-skin russeting – from the field to the skin cell level. Anatomically, in russet, the old outer layers of the corky skin cells remain attached to the newly formed layers instead of being sloughed off. In the field, russeting is more common in sandy soils. Nevertheless, the application of calcium (Ca) reduced the rate of affected tubers and the severity of the russeting. The positive effect of Ca could result from its direct interaction with the skin via the soil solution. However, high soil potassium may compete with Ca binding to the corky material of the skin, negatively affecting the skin finish. High soil temperatures were also shown to result in russeting by increasing the thickness of the skin and altering skin-related gene expression. Recently, we studied the involvement of epigenetic modifiers in regulating the smooth skin russeting disorder. Epigenetic regulation governs plant response to extreme growth conditions and allows phenotypic plasticity by regulating gene expression levels. Global DNA methylation analysis indicated a significant reduction in the percentage of 5-methylcytosine in russet vs. smooth skin. The expression level of selected DNA methyltransferases was reduced accordingly, whereas DNA demethylase activity did not change between the skin types. Assuming that DNA methylation provides stringent regulation or fine-tuning of gene expression in controlling phenotypic variation, it can be suggested that reduced DNA methylation reflects weak control of skin developmental processes, resulting in the formation of russeted skin instead of smooth.

503

Quantifying differences in source-sink relations between hybrid potato plants grown from two types of propagules

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Ware or seed tubers can be produced from diploid hybrid potato plants using two different types of starting materials or propagules: true seeds or seed tubers derived from true-seed-grown plants, also called seedling tubers. These propagule types produce plants with distinct architectural development and biomass allocation patterns, resulting from differences in source-sink relations. As the potato plant architecture contains aboveground leafy (source) branches and belowground (sink) branches (stolons and tubers), dynamic interactions between source and sink branches determine the growth and development of the whole plant. To understand these interactions and their consequences for plant and crop growth in two propagule types, a combination of experimental and modelling approaches was designed. First, branching and biomass allocation patterns of plants grown from true seeds and seedling tubers from the same genotype were studied in a greenhouse experiment. Photosynthetic parameters of representative leaves from different branches were determined. Compared to seedling-tuber-grown plants, true-seed grown plants produced a more branched and compact architecture; the change of biomass investing from leafy branches to tubers was slower. Moreover, as branching is highly plastic in plants from both propagule types and strongly affected by stem density, understanding their branching responses to stem density is essential. Results from a two-year field experiment showed that, at any density, more sympodial branches were produced in true-seed-grown plants affecting light interception and biomass partitioning; tuber size distribution shifted towards smaller tuber sizes as density increased, and this effect was stronger in true-seed-grown plants. To quantify the dynamics of contribution of source branches to photosynthesis and assimilates partitioning to sink branches within the whole plant for both propagule types, a functional-structural plant model is being developed based on the data from our experiments and literature. The model will simulate architectural development and growth of plants in 3D explicitly describing above and belowground branching and source-sink relations. The function of individual branches and their contribution to crop growth, especially tuber production, can be quantified. This study aims to provide insight in source-sink relations in hybrid potato plants grown from two propagule types which can benefit sustainable tuber production.

504

Agronomy of field transplanted hybrid potato crops

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Introducing hybrid breeding in potato (*Solanum tuberosum* L.) requires novel, efficient cropping systems for potato production based on true potato seed (TPS). Such systems address the limitations of conventional seed tuber-based systems, including low multiplication rates, high degeneration rates, and high costs of transport and storage. Of the possible cultivation pathways of TPS, we introduce and discuss the potential of field transplanting nursery-raised TPS seedlings as an alternative system for seed and ware production. First, we discuss key factors that influence the success or failure of the system as well as the critical field crop management factors to consider for a successful transplanted crop. Additionally, we highlight the results attained from various studies conducted on the influence of crop management factors on yield and yield components of field transplanted hybrid potato crops. A field transplanting system will require the successful production of seedlings in the nursery, a successful establishment of transplanted seedlings in the field, and successful crop management to attain a productive seed or ware crop. On crop management factors, using field studies, we assessed the contribution of nutrients — nitrogen (N) and partially phosphorus (P) — and the choice of tillage system on transplant crop growth, yield and yield components. While clear N effects were observed on both above- and below-ground yield components, seasonal and locational differences also contributed to variation in response to N. Crop responses to P were, however, not conclusive. The choice of tillage system used at transplanting also influenced both canopy development and yield attributes specifically due to varying crop densities associated with each tillage system. Systems with higher planting densities had the higher values for above-ground parameters including ground cover percentage and area under the ground cover curve than those of lower densities. Additionally, yield and tuber numbers were affected by tillage and genotype. These results coupled with other studies contribute to the existing knowledge on transplant systems and will contribute to further studies and demonstrations of practice of the feasibility of a field transplanting system for hybrid potato. Conclusively, while transplant crops differ significantly from seed tuber-based crops, the field transplanting system still promises a fast, efficient and sustainable production of seed and ware potato.

505

Promoting international collaboration in potato breeding to transfer frost tolerance from wild species *Solanum commersonii* into native potato cultivars from the Andean region and the Altiplano

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The Andean region endures climate-related challenges with significant impact on ecosystems and livelihoods. One example is unexpected frosts during the potato growing season which are responsible for substantial losses in yield. The development of new varieties with enhanced resilience to extreme climate is thus very important. The US Potato Genebank (USPG) in cooperation with Peruvian partners and farmers promoted breeding efforts intended to use the wild potato species *Solanum commersonii* (*cmm)* to transfer cold hardiness into Peruvian native cultivars. This species has outstanding levels of cold tolerance and cold acclimation capacity. At the USPG, several breeding families were created using (a) a somatic hybrid *cmm* + *S. tuberosum* (*tbr*) as male and, (b) different Peruvian cultivars of *S. tuberosum sbsp. andigenum* (*adg*) as females. Seeds of these families were sent to Peru and tested, in the Andean highlands and the Altiplano, for frost tolerance, desirable tuber traits and good yield. Over years of multi-location selection and evaluations, some breeding lines were identified with consistent expression of those traits. This resulted in advanced clones from which two were released as new cultivars because of their exceptional frost tolerance and superior field productivity that outyielded many established cultivars in the region. These cultivars were named *Wiñay,* a Quechua word meaning *"to grow"* and *Llapanchispaq* (meaning "*for all of us"*), released in Peru in 2018 and 2022, respectively. This project, developed through international cooperation, exemplifies how scientific efforts in combination with breeding, germplasm exchange and use of diversity can enhance crop resilience and sustainability and contribute to global food security.

506

Revolutionizing Seed Potato Production System in Africa and Asia

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Limited access to quality seed poses a significant challenge for the potato subsector in Africa and Asia. Previous efforts have focused on enhancing the quality and quantity of seed potatoes available to farmers, with a particular emphasis on addressing the bottleneck in the seed value chain — namely, the insufficient quantity of early generation seed (EGS) for field multiplication. Minitubers have traditionally served as the starting point for seed multiplication. Over the past decade, the International Potato Center (CIP) has promoted aeroponics and sand-hydroponics rapid multiplication technologies for minituber production. This has resulted in a remarkable increase in the supply of high-quality seed potatoes in Africa and South America. More recently, CIP has introduced Rooted Apical Cuttings (RAC) in Africa and Asia as a revolutionary approach to EGS production. The technology was originally developed years ago by scientists from the Vietnamese Research Center for Experimental Biology and CIP. RAC are rooted transplants produced in a screenhouse from tissue culture plantlets. The three technologies, aeroponics, sand-hydroponics, and RAC, differ in multiplication rates, investment costs, profitability, required skills, infrastructure needs, and associated risks. Among the three rapid multiplication technologies, RAC stands out for significantly increasing EGS volumes in a short period (30–50% increase in EGS within the initial six months depending upon the environmental conditions). RAC seedlings eliminate concerns about seed dormancy, allowing for optimal seed production during the short window of 2–3 months between planting seasons, but it requires constant irrigation and careful management from transplanting until vegetative development. While these technologies are integral to the seed value chain, success in scaling requires careful consideration of the specific context, enabling policy and socio-economic environments. Key recommendations include raising awareness and developing effective marketing strategies to promote not only the adoption of these technologies, but also the development of value chains for certified seed and ware potatoes. Additionally, efforts should focus on ensuring the adequate multiplication of RAC into commercial seed to enhance accessibility for smallholder farmers in Africa and Asia.

507

Effect of reduced N-fertilization on nitrogen use efficiency and selected quality parameters in starch potatoes and outlook on the POTENZIO^N project

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The joint research project POTENZIO^N (Potentials for increasing nutrient efficiency and reducing nitrogen emissions in starch potatoes) aims to identify starch potato varieties, mineral nutrition / fertilization systems, and cultivation methods that serve as a knowledge basis for an optimized, N-efficient, and low-emission cultivation systems for starch potatoes. The focus is on field trials under practical farming conditions and additional modeling to evaluate starch potatoes and management options for their potentials to increase nutrient efficiency and reduce nitrogen (N) emissions while maintaining tuber quality.

A first field trial was set up at the Reinshof experimental farm in Göttingen in 2021 carried out with three N-fertilization levels (N1 = no N addition; N2 = 120 kg N ha^{-1} and N3 = 160 kg N ha^{-1}) as well as with two starch potato varieties (Eurotonda and Avamond) and, for comparison, with a table variety (Milva). Depending on the calculation method and variety used, higher nitrogen use efficiency (NUE) was found with lower N-fertilization. In addition, tuber dry matter and starch content decreased with increasing N-supply in the table variety, but not in the starch varieties. Furthermore, only the starch variety Avamond responded with a significant increase in yield, dry matter content, and starch yield to increased N-levels. With increasing N-supply, crude protein content increased in all varieties, while the pure protein content remained unchanged. To achieve an approximate optimum between yield, quality and NUE, the result of this experiment recommends a reduction of N fertilization to the N2 level for Eurotonda and Milva varieties.

In 2022 and 2023, comparable trials were set up at three different locations. Once again, the aim was to investigate the responses of the potato varieties in terms of yield, starch yield and various quality parameters with regard to different N fertilization levels. The field studies were complemented by a storage experiment. Initial results show that reduced N fertilization had hardly any negative effects on starch yield and numerous quality parameters. Further quality analyses have not yet been completed – for example, the composition of the proteins in the tubers is currently being analysed as well as the amino acid profile and the glycoalkaloid content.

508

Impact of In-Row Nitrogen Fertilization on Potato Crop

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Residual soil nitrate levels post-potato harvest frequently remain elevated, attributed in part to the inherently low nitrogen (N) efficiency of potatoes, primarily stemming from underdeveloped root systems. Potatoes exhibit limited N uptake from soil depths beyond 60 cm, and the minimal overlap of plant roots in adjacent rows worsens this inefficiency. To address these challenges, a focused approach involving in-row fertilization has been explored to optimize the placement of fertilizer in proximity to seed potatoes. This targeted method aims to enhance nitrate utilization, reduce residual soil nitrate, and concurrently maintain yield and quality. Another efficient method to minimise N-leaching is to give about 70% of the total need by planting and the other 30% 6 weeks after planting. This should also lead to a better utilization of the given N with less risk of nitrate leaching in spring by heavy precipitation.

During 2020 and 2021 we set up randomized block trials on in-row nitrogen application. In these trials, the highest yields were often found at the plots with row fertilisation. Depending on the season, reduced fertilisation (70% or 80% of the advised dose) was even sufficient. Post-harvest nitrate residue results were less easy to explain as we had not always a clear link with the fertilisation given.

In 2022 and 2023, row fertilisation was further tested via on-form experimentation (OFE) by growers who had adapted planting machinery available. Each year 6 fields were monitored and broadcast and in-row nitrogen application were compared. The results suggest a reduced nitrogen dose in the row does not lead to lower yield.

Demonstrating that N inputs can be reduced by e.g. row fertilisation is important given the increasingly stringent regulations in Flanders that impose ever stricter fertilisation standards to meet the European Nitrates Directive and to enhance the water quality.

509

Assessing the Relationship between Nitrogen Use Efficiency and Proteins concentration in Potato Genotypes

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A two-year study was conducted in Latvia at the Priekuli site (57°19′ N, 25°20′ E) of the Institute of Agricultural Resources and Economics (AREI). The study explored the effects of nitrogen use efficiency (NUE) on potato tuber protein levels under varying levels of plant-available nitrogen. The study concentrated on crude protein concentration (CPC), crude protein yield (CPY), and the relative abundance of patatin (PRA) in 19 potato genotypes subjected to four nitrogen management strategies (an organic field without supplemental fertilizers and three integrated strategies with nitrogen fertilizer applications of 60, 120, and 180 kg ha^{-1}), each with four replications throughout the trial. Genotypes had a significant impact on all the traits studied. Results demonstrated that nitrogen availability significantly affected CPC, with the highest average CPC recorded at the 180 kg ha^{-1} nitrogen availability level and the lowest average at the 60 kg N ha^{-1} level. A significant negative correlation between CPC and NUE was observed, suggesting that genotypes with enhanced NUE tend to have lower CPC levels. Conversely, a significant positive relationship was found between CPY and NUE, with the maximum CPY reaching 1.36 t ha^{-1} under the 120 kg N ha^{-1} treatment. This positive correlation implies that genotypes with greater NUE (thus – higher yielding) tend to be more effective at protein production per area, irrespective of CPC. The nitrogen treatment did not have a significant effect on PRA, while significant differences were found in the PRA across the cultivar with PRA values ranging from 9% to 36%. A significant, albeit weak, negative correlation was found between NUE and PRA of the genotypes, indicating that high NUE genotypes may have low PRA and vice versa.

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510

Assessing regional potato yield response to phosphorus fertilization in high-phosphorus legacy soils

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The State of Florida has implemented Best Management Practices (BMPs) for vegetable production, utilizing soil test-based fertilizer application recommendations to ensure compliance with Florida's water quality standards statute. In 2010, Mehlich-3 (M3) replaced Mehlich-1 (M1) as the standard soil extractant for phosphorus (P) recommendations in Florida. Consequently, the majority of M3 soil testing results from potato-growing areas indicated high P levels, leading to no recommended P-fertilizer application, despite observed yield responses to applied P-fertilizer. This study aimed to regionally evaluate potato growth, P uptake, total and marketable yield responses to various P-fertilizer rates and determine a critical soil P value for soil tests. Six potato production areas were selected based on M1 soil test levels ranging from 34 to 350 mg/kg and M3 levels from 73 to 648 mg/kg. P-fertilizer rates ranged from 0 to 250 kg/ha of $P2O5$, following a randomized complete block design with four replications. Data were collected over two consecutive years for the 'Atlantic' potato variety, with repeated measurements of soil and plant tissue taken at specified stages throughout the growing season. The study quantified the effects of P-fertilizer rates on soil P levels, plant biomass, plant P content, tuber specific gravity (SG), and potato yield. Plots without P-fertilizer application yielded between 24.0 to 48.2 Mg/ha, representing 42% to 83% of the relative yield, respectively. Significant linear responses of tuber yield and plant P uptake to P-fertilizer were observed for sites with soil P tests below M1 (115 mg/kg) and M3 (196 mg/kg). Total plant P uptake ranged from 18 to 59 kg/ha of P, while P accumulated in tubers ranged from 15 to 40 kg/ha of P.There was no effect of P-fertilizer rates on tuber SG, averaging 1.084±0.003 and 1.082±0.007 in 2022 and 2023, respectively. These findings suggest that current interpretations of soil P concentration using M3, which is set at 45 mg/kg, inaccurately predict potato yield response to added P-fertilizer. Consequently, the current soil P critical ranges for potatoes, based on M3 extractable soil P interpretations, overestimate soil available P for potatoes in northeast Florida sandy soils, requiring modification accordingly.

511

Alternative herbicides for desiccation of potatoes in Norway

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Desiccation of the potato canopy before harvest is a common practice, in order to regulate tuber size, induce tuber maturity, promote skin set, improve tuber release from the vine, ease harvest and reduce incidence of fungal infestations such as *Phytophthora infestans*. A common procedure is to apply defoliant (desiccation) herbicide(s) uniformly on the canopy 1-3 weeks prior to harvest. Since the herbicide diquat (marketed as e.g. Reglone) was banned in 2020 in the EU and Norway there is a need to find other solutions for desiccation. In a series of trials in period 2021-2023 (3 sites per year) we have been testing the alternative herbicides pelargonic acid (Beloukha) and acetic acid (UgressNIX Trippel Effekt) in comparison with carfentrazon-ethyl (Spotlight Plus, registered in Norway) and pyraflufen-ethyl (Mizuki, used on emergency derogation the last years in Norway). We tested the products alone or in different combinations (dose rates, timings, addition of oil or adjuvant). We tested the effect in the cultivars 'Folva' (medium amount of haulm, difficult to desiccate) and 'Asterix' (high amount of haulm). Preliminary results showed that acetic acid was more promising for desiccation than pelargonic acid. The addition of oil or adjuvant did not have a significant effect. Two applications with e.g. pyraflufen-ethyl + carfentrazone-ethyl, or two times acetic acid, was necessary. The treatment with three applications (1/4 normal dose (N) pyraflufen-ethyl + 1/1 N pyraflufen-ethyl + 1/1 N carfentrazone-ethyl) gave the best desiccation or was among the treatments giving the best desiccation. The cultivar 'Folva' was more difficult to desiccate than 'Asterix', especially if the treatment started before the potato plants had initiated natural maturation.

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512

Test of alternatives to diquat in desiccation of potatoes

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Denmark is currently the only country in Europe with a major potato production not having the PPO inhibitors pyraflufen-ethylene and carfentrazon registered as chemical desiccants in potato. In Denmark, pyraflufen-ethyl is the only PPO inhibitor registered with a dosage of 2 x 10,6 g a.i./ha after flailing, which is not sufficient for obtaining 100 percent desiccation. Pelargonic acid has been registered but is not an economical feasible desiccant in seed potatoes with a green canopy.

Since 2020, several alternative strategies have been tested in plot trials and on-farm trials e.g. flailing followed by propane gas burning, mechanical haulm destruction with MSR Crown Crusher, haulm pulling with Vegniek DiscMaster, electric weeding by XPower and a wide range of other strategies. The alternative techniques have been tested in different potato varieties at different growth stage, physiological age, soil types and nitrogen levels. Danish potato fields are very heterogeneous with a large topographic variation and a fluctuating texture both within and between field. Plot trials and on-farm trials have shown that mechanical haulm destruction can be an alternative but in some unpredictable cases lead to regrowth and leaving a high number of green and wounded potatoes on the surface. Using mechanical defoliation, soil texture, precision in bed formation and the technical skills in general are of paramount importance for the efficacy. A slower canopy destruction and regrowth lead to a slower skinset and a higher risk for tuber blight and virus infection in seed. The primary mode of action of the PPO inhibitor is the disruption of protoporphyrinogen oxidase which require green growth. Nitrogen level should be reduced but not more than 10–15 percent.

There is no silver bullet in desiccation of potatoes in the absence of diquat and only one available PPO inhibitor. However, different combination of mechanical canopy destruction with lower dosage PPO inhibitor, propane gas burning or hybrid electric desiccation may be alternatives in farm saved seed and in mature ware and chips potatoes. For certified seed production, haulm destruction in potatoes is still a major challenge.

513

The influence of late season evapotranspiration replacement rate on potato yield, quality, and economic return

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What is the ideal irrigation level for maximizing potato economic return following peak canopy development? Should the predicted evapotranspiration (ET) rate be fully replaced, or should it be altered? Research was conducted near Othello, Washington across three years, 2018-20, to answer these questions. Five processing potato cultivars: Alturas, Clearwater Russet, Ranger Russet, Russet Burbank, and Umatilla Russet received five irrigation treatments: 40%, 60%, 80%, 100%, and 120% replacement of modeled ET. Irrigation treatments were implemented when canopies of all varieties were predicted to peak in size at approximately 1500 day-degrees (base temp of 7.2°C) and 95 to 110 days after planting. ET was measured and predicted using a combination of environmental data, soil moisture sensors and the field soil-water balance method. Economic return of Clearwater R., Ranger R., and R. Burbank was maximized by irrigating with 100% ET replacement across the last eight weeks before vine kill (155 days after planting). Alturas and Umatilla R. economic return was maximized by irrigating with 80% ET (20% less irrigation) late in the season. Alturas and Umatilla R.'s economic return increase was due largely to improvements in tuber quality. In Alturas and Umatilla R., reducing late-season irrigation led to increased tuber specific gravity, improved market and US No.1 yields, and improved tuber size distribution. Across the five potato cultivars, specific gravity decreased as irrigation level increased. As irrigation level declined, the incidence of growth cracking in Alturas tubers also declined. Reducing late season irrigation by 20 to 40% significantly improved fry color lightness on all five cultivars. This research will provide potato growers with improved irrigation management guidelines while maintaining their economic return.

514

Potato cultivation without tillage using straw mulch for sustainable agricultural intensification in Asian rice-based systems

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Asia's population is projected to increase by 14% (668M people) until 2050. About half of the increase (317M) is due to India, whereas Bangladesh's population is expected to increase by 40M people. Potato is a key crop in Asia and an important source of nutritious food and income. It grows in (sub) tropical conditions as a winter crop (Nov-March). Suitable for rice-based systems, early-maturing varieties fit in between two cereal seasons, which is often left fallow. Potato can be cultivated without tillage using straw left over from the rice harvest as mulch (PZTM) and represents a climate-smart regenerative agricultural practice which has several benefits. We will present data from three years of on-station and on-farm field trials in Bihar state in India and two years data of Bangladesh's saline-affected delta region (Khulna). A nutrient management experiment was carried out at ICAR-Central Potato Research Institute (CPRS), Patna, from 2021 to 2023 under PZTM in a randomized complete block design with three replications. Results indicated a 30% increase in nutrient use efficiency with PZTM compared to conventionally tilled (CT) potato. In a seperate experiment at CPRS and two on farm sites, PZTM was compared to CT tillage for two cultivars in a split plot design with 4 replications. Average yields varied from 38-43 and 35-42 t/ha for 'K. Pukhraj' and 'K. Jyoti', respectivliy under PZTM compared to 33-38 and 30-36 t/ha under CT while kg CO2 e/ha and irrigation water input were reduced by 40% each. In Bangladesh experiments were conducted at three locations in the Khulna district in southwestern Bangladesh. PZTM was compared to CT using two varieties and laid out in a strip plot design with four replications. Results showed 'Alu72' and 'Alu78' produced average yields of 20-34 and 15-27 t/ha under PZTM whereas yields under CT were 5-10 and 4-10 t/ha accross the three sites. At the same time several soil health parameters were improved already after one season of PZTM cultivation. Compared to traditional potato farming, this method reduces irrigation, fertilizer needs, and costs. Yields rise, soil health improves, and farmers' profits increase. Rice crop residues, usually burned, serve as mulch, lowering air pollution. Predictions suggest it can scale to 33.6 Mha in South and Southeast Asia.

515

Effects of soil salinity and drought on potato production

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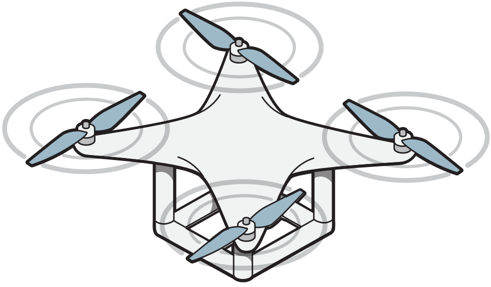
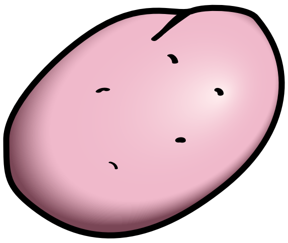
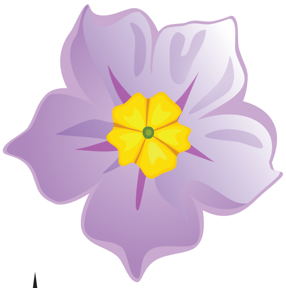
Soil salinity and drought are major environmental constraints to potato production, especially in coastal and arid production areas. They cause unfavourable soil conditions for potato root growth and functioning. Potato root systems may adjust their spatial distribution to optimize water and nutrient uptake. Understanding root responses and characterizing root traits in various temporal drought and salinity stress regimes are essential to developing resilient crops. Furthermore, above-ground leaf photosynthesis and carbon assimilation are likely to be restricted due to adverse soil conditions and limited root growth, which, subsequently, decreases yield and affects yield components. Due to global climate changes, the increasing frequency of dry spells and the problems associated with salinity in irrigated and coastal areas frequently result in the co-occurrence of drought and salinity stress in agro-ecosystems. However, the combined effects of salinity and drought on potato growth and development, including those of shoots and roots, and their interactions, are not yet known. A first field experiment was conducted at the Unifarm of Wageningen University, The Netherlands. A split-split-plot design was applied with six modern cultivars, two water regimes and two salt regimes to investigate the factorial impact on potato growth, development, and yield. Those six cultivars were contrasting in maturity type, salinity tolerance, and drought tolerance. The canopy development of water-limited crops was delayed and, in some cultivars, also reduced but could recover to some extent once frequent rainfalls occurred. Canopy cover dynamics also showed cultivar differences, with late cultivars reaching maximum soil cover, even under water-limited conditions, while early cultivars could not recover after drought stress. Salinity stress was severe and resulted in detrimental effects on above-ground development, impeding canopy cover increase and causing accelerated leaf senescence. The combined stress of soil salinity and drought reduced yield compared with a single stress. The results obtained in this work provide useful insights into adaptive responses and can help develop and calibrate the WOFOST (WOrld FOod STudies) model for potato, which will be used later to design the potato ideotypes for enhanced resilience under combined soil salinity and drought stress.

Abstracts – Session 6

Precision technology in potato cultivation







601

Risk maps in VIPS deliver late blight warnings at high spatial resolution

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Infection warnings for potato late blight based on location specific weather data have been issued through the online Norwegian decision support system VIPS (www.vips-landbruk.no) for the past two decades. Many farms are far from the nearest weather station, resulting in less relevance of the warnings, proving the need for development of a service with a higher geographic resolution.

VIPS is an open-source digital platform which can alert farmers and advisors of pest risks in important agricultural and horticultural crops. It provides easy access to information needed by advisors and growers to assess the need for plant protection measures at an early stage. The late blight warnings based on the Nærstad model (Hjelkrem et al, 2021) works by calculating risk values related to spore production and infection. The model includes criteria for spore survival, like solar radiation and precipitation, and the risk of blight development is a function of amount of viable released spores and duration of leaf wetness. To calculate the RISK value, these weather parameters are required on an hourly basis: Temperature, rainfall, relative humidity, leaf wetness, wind speed and short-wave radiation. Leaf wetness and solar radiation are typically only measured at well-equipped weather stations, so till now the model outputs have been linked to locations with available weather data combined with corresponding weather forecasts, producing pest predictions valid only for the location of each weather station and the nearby area. Predicting late blight infections for the total potato growing area of Norway has thus not been possible.

Gridded high-quality weather data with the necessary weather parameters has recently been made freely available for the Nordic-Baltic region by the Norwegian met office. The weather data has a spatial resolution of 1x1 km and an hourly temporal resolution and is a combination of reanalyzed data for the past and 66-hour forecasts. All the required parameters for running the Nærstad model are provided, except for leaf wetness. This can however be estimated using the other parameters provided.

In VIPS, we have developed a framework for calculating and displaying risk maps for pest prediction models using gridded weather data. The framework can be used on any gridded weather data source and the risk maps are served as a Web Map Service (WMS). It can be displayed on VIPS, in standalone GIS clients such as QGIS or by implementing a client for your own purpose. The risk map for the Nærstad model is one example of this, made publicly available at www.vips-landbruk.no.

Hjelkrem, A.-G. R., Eikemo, H., Le, V. H., Hermansen, A., & Nærstad, R. (2021). A process-based model to forecast risk of potato late blight in Norway (The Nærstad model): model development, sensitivity analysis and Bayesian calibration. Ecological Modelling, 450, 10.

602

Potassium Management Strategy in Starch Potatoes

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Precision agriculture (PA) in potatoes involves more precise fertilization, seeding and use of pesticide and irrigation to increasing the net-economy and reducing the impact on the environment. In this article, we will discuss the use of variable rate of potassium fertilization as a PA in starch production. In Denmark, potatoes for starch production are often grown on depleted sandy soils with low potassium content. However, soil samples in field trials have shown a greater variation than expected and an optimum potassium application variating from 0 to 250 kg K/hectare.

Based on 13 field trials, there is a linear relationship between the plant available potassium content in the soil and the economical optimal potassium application. However, the time for soil sampling is critical due to the risk for leaching of potassium during winter and spring on especially sandy soils.

In the decision support system CropManager, it is possible to graduate potassium to starch potatoes according to the results of soil samples based on GPS and time of sampling etc. A prescription map is sent wireless to the tractor. CropManager will adjust the prescription map according to expected yield, type and price of potassium fertilizer, and other types of fertilizers containing potassium.

603

Using drone-retrieved multispectral data for phenomic selection in potato breeding

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Predictive breeding approaches, like phenomic or genomic selection, have the potential to increase the selection gain for potato breeding programs which are characterised by very large numbers of entries in early stages and the availability of very few tubers per entry in these stages. The objectives of this study were to (i) explore the capabilities of phenomic prediction based on drone-derived multispectral reflectance data in potato breeding by testing different prediction scenarios on a diverse panel of tetraploid potato material from all market segments and considering a broad range of traits, (ii) compare the performance of phenomic and genomic predictions, and (iii) assess the predictive power of mixed relationship matrices utilising weighted SNP array and multispectral reflectance data. Predictive abilities of phenomic prediction scenarios varied greatly within a range of -0.15 and 0.88 and were strongly dependent on the environment, predicted trait, and considered prediction scenario. We observed high predictive abilities with phenomic prediction for single plant yield (0.45), maturity (0.88), foliage development (0.73), and emergence (0.73), while all other traits achieved higher predictive ability with genomic compared to phenomic prediction. When a mixed relationship matrix was used for prediction, higher predictive abilities were observed for 20 out of 22 traits, showcasing that phenomic and genomic data contained complementary information. We see the main application of phenomic selection in potato breeding programs to allow for the use of the principle of predictive breeding in the pot seedling or single hill stage where genotyping is not recommended due to high costs.

604

Screening a breeding program for nitrogen use efficiency using drone imagery

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On the sandy soils used for potato production in the US, up to 60% of applied nitrogen (N) can be lost to the environment. Nitrogen leaching from agricultural production in Minnesota has devastating environmental consequences locally and as far away as the Gulf of Mexico. One way to mitigate N loss is to reduce N required and therefore applied, by planting varieties with low N requirements. Potato varieties vary in their N requirements and those with lower requirements are often described as N use efficient. Nitrogen Use Efficiency (NUE) is a complex trait made up of multiple components and although NUE is traditionally measured in terms of yield, N also has an impact on tuber size and appearance. For a potato variety to be meaningfully efficient it must maintain both yield and quality traits under low N conditions. We have found variation within our breeding program for components of NUE as they relate to yield and quality traits. However, these studies were necessarily limited in scope (under 15 clones) because they required labor intensive sampling of vines and tubers from the field in order to measure plant N content. To effectively breed for NUE, we need methods that allow us to quickly screen large numbers of clones in early generations. Models are available for predicting N status of clones from drone images. However, these have only been validated in a small number of popular commercial russet clones. We expanded these machine learning models to apply to the range of clones in the University of Minnesota (UMN) potato breeding program. To accomplish this, we developed a new training data set that included 75 clones across four market classes (russets, chips, red fresh market potatoes, and yellow fresh market potatoes). Each clone was grown in replicated fifteen hill plots for two years at four N levels (recommended, 66% of recommended, 33% of recommended, and no added N). Multispectral drone images were collected at seven time points between emergence and senescence. Yield and quality traits were measured at harvest. Additionally, tuber and vine samples were collected from the field before senescence to determine biomass accumulation and N content. This data set was used to develop a new model to predict N status, NUE, and its components from multispectral drone images, as well as identify clones with high NUE in the UMN potato breeding program for potential release or use as parents. This tool will allow us to screen large numbers of clones early in the breeding process for NUE thus facilitating selection and breeding.

605

In-season potato crop nitrogen status assessment from satellite and meteorological data

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For a conventional potato crop, splitting nitrogen (N) application is recognised as an efficient strategy to improve tuber yield and quality and to mitigate N losses to the environment. This approach requires the assessment of in-season crop N status (CNS) for decisions on supplemental mineral N fertiliser application. This study focuses on the assessment of potato crop biophysical variables useful to establish CNS. Field, satellite and meteorological data were collected in farmer's fields during 3 years (2017–2019) with contrasted meteorological conditions. Degree days (DD) and water balance from planting date were computed from meteo data, and a selection of relevant vegetation indices (VIs) was derived from Sentinel-2 reflectance. Multiple linear regression (MLR) and random forest regression (RFR) models predicting shoots biomass, shoots N content and shoots N uptake from a combination of meteo and/ or satellite-based variables were defined and evaluated. The best combinations integrate DD and two to four VIs and perform with cross-validation RMSE of about 0.38 DM t ha−1, 0.41%, 21 kg ha−1 for MLR and 0.32 DM t ha−1, 0.31%, 19 kg ha−1 for RFR. Despite these performances, MLR was shown to be more robust. From these estimated variables, two methods are proposed to derive total N uptake and nitrogen nutrition index. The most relevant method uses shoots N uptake and biomass. Such empirical models can be implemented into decision support systems intended for farmers or other users wishing to improve their potato N fertilisation towards sustainable management and practices. It allows future estimation of in-season supplemental N fertiliser to be applied to reach a targeted tuber yield.

606

Combining remote sensing and crop growth model for better decision support on water and nitrogen management in potato crops

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Optimizing water and nitrogen management of potato cultivation benefits both the financial result and the environmental impact. For example, splitting the nitrogen application reduces the expense on fertilizer and avoids nitrogen leaching, denitrification, volatilization and GHG emission . However, since the environmental impact is not a direct financial reward, and potential yield loss results in a direct financial loss, there is a barrier for farmers to start with nitrogen optimization.

Precision agriculture provides farmers with tools to optimize their farm management. The smart farming platform Farmmaps (Been et al., 2023) provides several precision agriculture apps for potato growers. There are, among others, advice apps for irrigation and for top dress N application. However, when and what to do on which moment requires insight in the development of the crop. A crop growth simulation model (CGSM) can provide a farmer with these insights and give support on their crop management.

On Farmmaps a CGSM for potato, called Tipstar, is integrated. This model uses the field location to retrieve the relevant input parameters, like soil composition and ground water levels, and weather data. Together with the crop recordings of the farmer a digital twin of the field and crop is created, providing information on the conditions on a daily basis. With these data the potential yield of a field is calculated, ignoring possible water and nitrogen shortages. Next to the potential yield, the actual yield is calculated, including possible water and nitrogen shortages. Observations of the crop growth using remote sensing are used to correct the simulation in real-time, to overcome the limitation that the model provides only an approximation of the actual crop growth. This so-called data assimilation is realized with an ensemble Kalman Filter.

Weather data is used for the growth up to the current date. Calculations for the remaining part of the growing season are performed using 30 years of historical weather. The prediction provides the farmer insight in potential stress, both for water and nitrogen. Also scenarios can be compared, providing insight in the agronomical and financial impact of intended water or fertilizer applications, e.g. the need for a second or a third N-application during the season. Examples of the use of the digital twin in 2023 will be presented.

References

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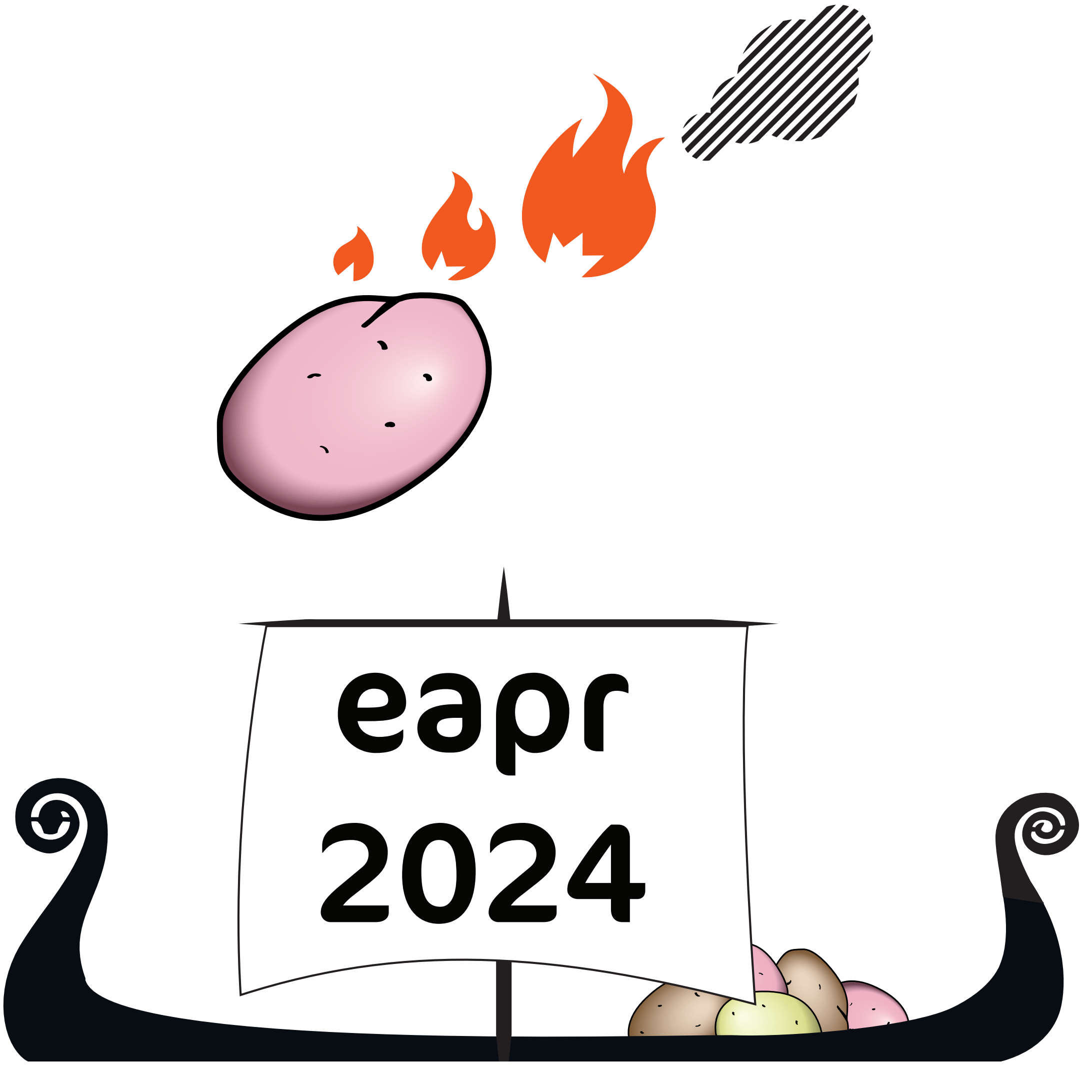
Abstracts – Session 7

Sustainability in a changing climate



701

Unravelling the molecular mechanisms of heat-induced decrease in starch content in potato tubers

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Potato (*Solanum tuberosum*) tubers are critical to feed an increasing world population while also serving as feed and feedstock for many industrial applications. Tubers are rich in starch, and provide essential amino acids, minerals, and vitamins. However, increasing temperatures due to global warming threaten its production, impair tuber yield and quality. We investigated elevated temperature-induced tuber starch reduction in about 180 potato cultivars. Overall, tuber yield and starch content were significantly decreased by elevated temperatures, with large variations in the degree between individual genotypes. These phenotypic data were used in a genome-wide association study which led to the identification of QTLs. Current analyses attempt to verify the relationship of a highly significant QTL to the heat-mediated starch loss and to identify potential candidate genes.

Out of the large panel of cultivars, sixteen were selected for a detailed analysis of starch metabolism. These varieties were considered susceptible or tolerant based on their level of heat-induced starch reduction. Lower tuber starch contents in heat were associated with a decreased activity of sucrose synthase, a key enzyme for starch formation, in all genotypes. Global transcriptome analysis of growing tubers from eight genotypes revealed a general down-regulation of starch biosynthesis genes and an up-regulation of starch degrading enzymes under heat stress, not distinguishing between susceptible and tolerant genotypes. Quantitative PCR analysis indicated that genotypes with a greater reduction in starch content under heat showed a stronger decrease in the expression of granule-bound starch synthase1 (GBSS1), which is important for starch granule initiation and strongly dependent on sucrose levels. This suggests that under elevated temperatures a decreased substrate availability and a reduced sink strength may restrict tuber starch accumulation. This is most likely caused by negative effects of heat on photosynthetic assimilate (sucrose) production and allocation to tubers. To investigate this in more detail, the effect of elevated temperature on leaf physiology, metabolism and transcriptional changes were investigated in two (out of the sixteen) contrasting cultivars. The results indicate that, among other processes, photosynthesis was severely affected in the heat-susceptible cultivar.

702

Characterizing the *Stsp5g a Stsp5g b* double mutant as a partial remedy for heat stress

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Elevated temperatures have detrimental effects on yield and quality of field crops and vegetables. Climate change effects are felt already with higher frequencies of heat events and are predicted to further challenge agriculture. Potato, *Solanum tuberosum*, is one of the most important food crops produced and consumed worldwide and is greatly affected by elevated temperatures. The potato tuber is formed at the tip of an underground modified branch called a stolon. The initiation of tubers at the stolon tip is induced in part by systemic signals originating from the leaves. A central signal is tuberigen, the protein product of the *SELF PRUNING 6 A* gene (*StSP6A*). StSP6A is regulated at multiple levels and is effected by endogenous and external signals. Under heat stress conditions potato tuberization is repressed. In these conditions *StSP6A* mRNA has been shown to be post-transcriptionally degraded by small RNAs generated by the *SUPPRESSING EXPRESSION OF SP6A* gene (*SES*) whose expression is upregulated in heat. Another negative regulator of *StSP6A* is the *StSP5G* gene however its role is mainly know with respect to the photoperiodic pathway central to photoperiodic sensitive potatoes such as the landrace *Solanum tuberosum ssp. Andigena*. Modern potato cultivars have reduced sensitivity to photoperiod mainly due to mutant alleles of the *CYCLING DOF 1* gene (*CDF1*), which relieve *StSP6A* of *StSP5G*'s negative regulation. Nevertheless conflicting results have been reported showing in some modern varieties, an increase of *StSP5G* expression correlating with heat stress. One recent study showed that this is at least in part due to the *CDF1* allele present. In our study three different *Stsp5g a Stsp5g b* double CRISPR mutants were identified in the *S. andigena* background. In long days all showed early flowering and tuberization. One line showed more branching and two had elongated tubers. In short day one line was tested showing more and larger tubers vs. control. Under heat stress in short days we find indications of earlier tuberization in mutant lines suggesting a role in heat stress response. We discuss our current findings and present future avenues of research.

703

Efforts to model crop response to hot and dry environments

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Potato is an essential crop for global food security. However, the adverse effects of climate change on potato production require robust adaptation strategies. Crop growth models (CGM) are essential tools for exploring adaptation strategies and providing decision support for growers. Unfortunately, existing CGM, such as WOFOST, have limitations in accurately simulating potato responses to high temperatures and drought. We aim to investigate and model the effects of episodic high temperature and drought on potato development, growth and productivity through experiments and modelling. We conduct field experiments in India (three seasons, starting in November 2022), South Africa (two seasons, starting in January 2024) and the Netherlands (one season, starting in April 2024). In India and South Africa, potato crops are affected by early-season high temperatures (> 30 °C). We use intermittent drip irrigation to create dry periods artificially. The Indian experiments have six irrigation treatments with one cultivar (Kennebec). In South Africa, the experiments have two irrigation treatments and two cultivars (Mondial and Sifra) in the field and a rain shelter experiment (Sifra). In the Netherlands, we will elevate the soil temperature before and after tuber initiation using Innovator. We monitor the soil moisture and temperature and canopy temperature with proximity sensors and remote sensing technologies to increase the data resolution. Four destructive harvests are performed over the season for all sites. For CGM, the Indian and South African results demonstrated that the WOFOST-Potato model underpredicted the leaf area index (LAI) in the early season due to the negative effects of early-season high temperatures on photosynthesis. However, the model overpredicted late-season dry matter production because it overpredicted LAI in the late season. For agronomic practices, the Indian experiment demonstrates that frequent deficit irrigation is a valid water-saving strategy when water or power shortage occurs. We found that irrigation of 65% potential evapotranspiration (PET) on alternate days produced similar yields as 100% PET irrigated weekly or fortnightly. No significant yield differences were found between weekly and fortnightly irrigation. However, alternate days of irrigation produced significantly higher yields than lower irrigation frequencies. The yield differences were attributed to the canopy development rate and lifespan.

704

Effects of climate change on late blight and early blight of potato

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Late blight, caused by *Phytophthora infestans,* and early blight, caused by *Alternaria* species, are major threats to potato crops. In France, these diseases regularly thrive throughout the growing season due to favorable weather conditions, characterized by mild or warm temperatures and high humidity. Disease models were used to predict to what extent climate change is likely to affect the evolution of blight epidemics in different regions of France up to the year 2100. Simulations were carried out to highlight French locations with potential future higher risk of potato's diseases.

Epidemics of late blight and early blight were simulated with the Decision Support System Mileos®, which uses hourly weather data (temperature, relative humidity and precipitation). Climate projections on a daily basis come from three climate models: KNMI-EARTH, CNRM-ALADIN63 and KNMI-RACMO22E. The scenario RCP 8.5 was used to get two climate datasets: 1950-2005 (the reference simulation) and 2006-2100. These data were downloaded from the website DRIAS (www.drias-climat.fr) for eight French locations (Hondschoote, Saint-Quentin, Evreux, Fagnières, Ouzouer, Pontivy, Bordeaux and Avignon). The Waichler and Wigmosta method, implemented in the R package fruclimadapt, was used to transform the daily data into hourly data. The disease simulations were performed each year from March 1st to September 30th (which basically corresponds to the growing period). Epidemic indicators used were the daily values and the sum of weight of contaminations during the growing period for *P. infestans* and the weight of contaminations for *Alternaria*. A physiological model, named pdays, was used to determine the beginning of potato's susceptibility to *Alternaria* with a threshold of 400 cumulative pdays for mild-early cultivars.

The three periods studied were the "reference period" (1975-2004), the "near future" (2020-2049) and the "far future" (2070-2099). Simulations suggest that, in the future, the late blight risk would be globally higher in June and July than during the reference. The differences of cumulated risk indicators between the reference and both future periods would be less significant in August and September. The duration of early blight risk period would increase in the future with an earlier start in the year, regardless of potato physiology. This study shows that the risk of late blight and early blight would increase earlier with climate change for all areas.

705

Investigations on nitrogen efficiency and nitrous oxide emissions under reduced N-fertilisation in starch potato cultivation in northern Germany

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Since the late 19th century, the concentration of N_2O in the atmosphere has steadily increased, with agriculture being the primary contributor. Nitrogen (N) emissions in agriculture are mainly caused by fertilization. Gaseous N losses occur as N_2, NO, NH_3, or the potent greenhouse gas N_2O, which is produced by microbial processes during denitrification and nitrification in the soil. Nitrate leaching further exacerbates the issue by contaminating groundwater, which has led to the designation of “red zones” in Germany. In response to this, stricter fertilizer regulations were issued, mandating a 20% reduction in N-fertilization.

The often low efficiency of N-fertilization and the associated risk of high N-losses are well-known in potato cultivation. The available data for processing potatoes under field conditions is rather limited and the potential for improvement in cultivation is considerable.

The aim of this joint research project POTENZIO^N (‘Potentials for increasing nutrient efficiency and reducing nitrogen emissions in starch potatoes’) is to quantify nitrogen utilization and losses through the comparative cultivation of different starch potato varieties and to identify resource-efficient, low-emission cultivation systems that meet legal requirements.

For this purpose, different fertilizer quantities and types were applied (CAS or fermentation residues 144kg/ha and 180kg/ha, unfertilized control). Stable ^{15}N isotopes were used to trace N in soil samples, tubers and aboveground biomass. Gas emissions were intensively monitored using the closed-chamber method. Leaf measurements with Dualex showed the nutrient supply and photosynthetic performance of the plants during the growth phase.

The cumulative N_2O emissions remained at a very low level throughout the entire cultivation period and the subsequent winter, with variations occurring only in the intensity and temporal pattern of occurrence. Overall, there was generally no significant difference in total N_2O emission between treatments. Instead, temperature, soil texture and water saturation appear to be the crucial factors. Remarkably, phases in which the soil consumed N_2O were only recorded late in the growing season. In summary, the starch yield per hectare of the N-efficient potato varieties has not decreased under a 20% reduction in N-fertilization.

The study provided important results for assessing the relevance of greenhouse gas emissions in starch potato cultivation and the potential for fertilizer savings. Further research will focus on capturing the causes and influencing factors of N_2O formation in even greater detail.

706

Comparison of the carbon footprint of potato cultivation and processing with other crops and products: What contribution can the potato make to sustainable production?

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The potato is one of the world's most important staple crops and ranks fourth after maize, rice and wheat. In addition, global potato production is currently increasing steadily. In future, consumers will demand more products that are produced and processed in a sustainable way. Therefore, the aim of this study was to investigate, based on a literature review, to what extent the production and processing of potatoes can be classified as sustainable compared to other crops with regard to the release of CO_2-eq. The term CO_2-eq was used as a metric measure to compare the emissions of different greenhouse gases (GHG) according to their global warming potential (GWP). It was remarkable that the cultivation of fresh potatoes produces around 50% less GHG emissions compared to wheat, barley, oats, rye and maize if only part of the value chain (*cradle-to gate*) is considered as the system boundary. Especially for potato cultivation, some important parameters could be identified that cause higher emissions of CO_2-eq—these include the provision of seed potatoes, the amount of nitrogen fertilizer used, irrigation in the field and the associated emissions (N_2O, NH_3 and CO_2) as well as humus decomposition. In terms of the cultivation conditions, conventionally and organically produced potatoes were considered with regard to their release of CO_2-eq. It was found that the organic cultivation of potatoes releases an average of 0.072 kg CO_2-eq/kg of product, which is 56 % less CO_2-eq compared to conventional cultivation (0.129 kg CO_2-eq/kg of product). It was also found that the higher the degree of potato processing, the more CO_2 equivalents are released. The production of French fries (1.444 kg CO_2-eq/kg of product), chips (1.969 kg CO_2-eq/kg of product), and mashed potato powder (1.740 kg CO_2-eq /kg of product) cause significantly higher CO_2-eq than other starchy products such as wheat bread (0.846 kg CO_2-eq/kg of product) or pasta (1.122 kg CO_2-eq/kg product). Overall, it should be noted that the amount of CO_2-eq produced and released depends on many factors, which is why the reduction of GHG emissions is only possible through various adjustments. Nevertheless, it can be stated that the potato performs relatively well in terms of CO_2-equivalent emissions compared to many other crops and can therefore be classified as sustainable.

707

Can drought tolerant potato genotyped be selected based on phenotypic traits?

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As climate change model predict altered precipitation patterns and increased drought risks, drought-tolerant crops are required to ensure yield stability. Potato shows a high crop (calories) per drop (water supply) ratio, but is drought-sensitive. Breeding of drought tolerant genotypes can be done by selection on yield in arid environments, but the process takes decades. Hence, we developed a metabolite/transcript-based selection model (DOI:10.1111/pbi.12840) that efficiently selected tolerant, but failed to select against sensitive genotypes (DOI: 10.3389/fpls.2020.01071). Therefore, we tested whether a second selection layer based on phenotypic markers derived from automatic phenotyping systems can improve the selection. Our test population comprised 63 *Solanum tuberosum* ssp. *tuberosum* genotypes selected from a population segregating for drought tolerance. The validation population contained 13 genotypes from the test population plus 7 unrelated cultivars. We determined drought tolerance indices for these genotypes based on tuber starch yield in three test systems representing Central European drought stress scenarios. Shoot growth was monitored continuously with an automobile laser scanner to estimate features like plant height, leaf area and leaf movement. We developed a data evaluation pipeline to determine descriptive parameters for the growth of control (c) and drought-stressed (s) plants. Logistic regression yielded the parameters initial slope (k), inflection point (Tm) and maximum (Max) for plant height and leaf area. For leaf angle, means were estimated for six intervals of the diurnal cycle and three different age ranges (vegetative, tuber initiation, tuber filling). Analysis by general linear model revealed significant genotypic variation for all features. Leaf movement and growth curve parameters for plant height were significantly affected by the treatment and varied between years. The relatively small environment effect on leaf area made the trait a good candidate for tolerance selection. Decision tree analysis selected Tm(leaf area)(s), plant height(c) at the end of the vegetative growth and the leaf angle(c) before noon as the most important features for tolerance class prediction. Multiple regression analysis on data from the genetically more diverse validation population confirmed leaf area and leaf position parameters as predictive tolerance traits.

708

Does glasshouse trials enable to estimate drought resistance in the field?

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The potato (*Solanum tuberosum L.*) is important in meeting food security worldwide. Potato crops are vulnerable to drought periods leading to yield reductions of about 30% to 60% classifying drought as a primary abiotic stress affecting potato plants. The severity of alterations induced by water deficit depends on the potato varieties. However, the phenotypic responses of a particular genotype, including resource allocation to tubers, vary depending on the growing site, and the environment. Given that, we are also expecting variations in phenotypic response of the plant between glasshouse and field trials. Glasshouse trials have shorter growing periods, enabling to conduct experiments more quickly and obtain results in a shorter time frame. It could then be used as a driver of variety selection for drought tolerance.

In this study, we evaluate drought resistance of 50 varieties in the field and in the glasshouse by measuring 32 plant growth traits (e.g. tuber weight per plant, harvest index, above-ground dry mass, root/shoot) to estimate differences in plant growth between both trials conditions. Each trial was conducted with plant in control condition, fully irrigated, and plant in stress condition, that undergo periods of water deficit.

It has been observed that field plants yield twice more tuber weight compared to glasshouse plants, regardless of water condition. Stems in the field are smaller, thicker, lighter, and more numerous compared to those in glasshouse trials. Leaf are wider but thicker in the glasshouse and there is a higher root biomass production in glasshouse trials. Then, it has been found that the harvest index is the variable the most correlate to tuber weight per plant in field and glasshouse, explaining more than 30% of tuber weight variability. Finaly, two common traits of drought resistance, above-ground fresh mass and harvest index, have been found between both field and glasshouse trials. These traits classify varieties of swiss trials according to their drought resistance and explain more than 90% of tuber weight variability.

Conducting glasshouse trials to forecast field trial yields during drought could be highly beneficial. Such an approach might obviate the need for yearly drought condition in variety trials.

709

Predicting the tolerance of potato genotypes to drought stress based on the root/shoot relationship in the initial period of plant development.

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Plant Breeding and Acclimatization Institute- National Research Institute in Radzików Division Jadwisin Poland

According to the literature and our observations, in the first period of development, potato genotypes growing in ideal conditions show slight differences in the root/sprout ratio. Differences in the relationship: the underground part (roots) and the above-ground part (sprouts) become more visible between varieties under drought stress conditions. In such conditions, potato plants produce relatively more roots and less above-ground mass, but variety differences in the root/sprout ratio may be very high (Mukul et al. 2016). Based on these relationships, it is possible to select genotypes in which the development of the root system in drought conditions is better than others, already in the initial period of plant growth.

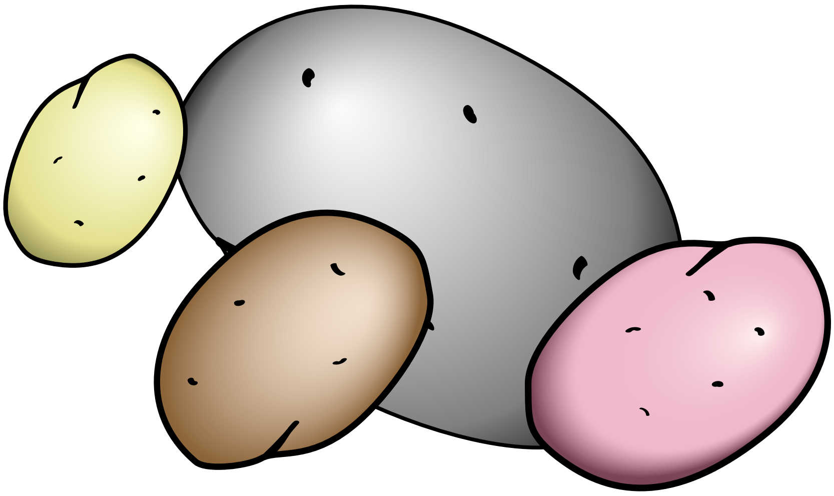
The aim of the research was to compare selected potato genotypes in terms of differences in the development of the above-ground parts of plants and roots in conditions of full water supply and in soil drought in the initial period of growth and, on this basis, to select genotypes with greater tolerance to drought stress.

Thirty-three potato genotypes from different group of maturity were selected for research. Pots were placed in a phytotron at a temperature of 22/15^{o}C (day/night) and a relative air humidity of approximately 70%. Half of the plants were watered to maintain optimal soil moisture, i.e. 65% of the field water capacity, and the other half was subjected to soil drought. Plants were grown for 21 days. After this time three plants from both combinations were harvested. After removing the plant from the pot, the above-ground part and roots were separated. The mass of both the aboveground and underground parts of the plant was determined, and the root/sprout ratio (root mass to sprout mass) and the share of roots in the total plant biomass were calculated. As a result, genotypes with distinctive root characteristics in the initial period of development were selected.

Significant differences between genotypes regarding the tested characteristics were demonstrated and genotypes with the best parameters determining higher tolerance to drought stress were selected. Diverse soil moisture conditions had a significant impact on all the studied features. The importance of the interaction of genotypes and humidity conditions has been proven in the case of the aboveground mass of plants and the share of roots in the total plant biomass.

Abstracts – Session 8

Post harvest



801

Towards smart potato storage: using CFD modeling and simulation to realize optimized and efficient ventilation within potato storage buildings

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Bulk potato storage technologies for preserving a quality product during about one year are becoming more advanced. The main determining factor for quality losses of stored products is the distribution and quantity of the preserving medium which is mostly air. Thus, ensuring homogeneous and optimal airflow distribution within the potato stack is of utmost importance. In this research, a numerical model for accurately determining airflow velocity at each point within a potato storage facility was developed. The model divides a storage building (26 m x 45 m x 10 m) into three main computational domains: pressure channel (from ventilation fans to slatted floor), potato stack (heap of potatoes of 4 m), and headspace (from the top of the stack to the ventilation fans). A representative geometry of a storage facility was used for building 2D and 3D discretization schemes. The two most common ventilation operations: open inlet-outlet (where the inlet and outlet hatches of the storage are open), and recirculation (where the inlet and outlet hatches of the storage are closed) were investigated. The geometry of the slatted floors are an integral part of the developed model with their details explicitly resolved. The model was validated by rigorous airflow velocity measurements carried out inside the pressure channels of a commercial storage facility. The results of the model simulation showed the airflow distribution within the storage building. Locations of large airflow rate and high pressure losses were identified: for example at the start of a ventilation channel there is an onset and development of huge airflow stagnation. Airflow passage ways where concreate walls and walk ways are present were demonstrated to create huge ventilation pressure losses. During both ventilation operations – open and closed inlet-outlet – the airflow distribution across the stack of potatoes was non homogeneous. On average there was around 7.5 % volumetric airflow difference between the closest (106 m^3 / hr. / m^3) and the farthest (114 m^3 / hr. / m^3) points (from the ventilation chamber) within the stacked potato. Also the pressure difference across the potato stack changed by around 15.5 % from the entrance (97 Pa) to the end (112 Pa) of the ventilation channel. The effect of this non uniform-airflow distribution will result in non-uniform temperature, humidity and respiration of the stored potato. High quality stored product can be obtained by optimizing this airflow within the storage facility. The geometry of the slatted floor was observed to affect the airflow distribution slightly. Ventilation optimization with controlled airflow and modification of airflow passages are the perspectives for ensuring energy efficient ventilation with quality stored potatoes all year round.

802

Developing automatic tools in the assessment of potato qualities

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With the increasing demand for efficient and accurate assessment of potato quality attributes, there is a growing need to develop digital tools suitable for measuring characteristics such as post-frying colouration of French fries and potato crisps, as well as evaluating disintegration and after-cooking darkening of steamed potatoes. These attributes are currently predominantly assessed through human visual notation carried by experts, introducing subjectivity and potential inconsistencies in the evaluation process.

In response to this issue, our research team works on a novel approach by leveraging machine learning techniques to automate the measurement of key quality parameters. Specifically, we already introduce a machine learning model designed for grading the post-frying colouration of both homemade and industrial French fries. This model aims to provide a standardized and objective evaluation, reducing the reliance on subjective human judgment.

Furthermore, we propose an image analysis model tailored for assessing the colouration of potato crisps. This digital tool enhances the precision of quality evaluation, offering a reliable alternative to subjective assessments as well as the tedious steps of the spectrometry measurement. The model is developed to analyse images of crisps, providing an automated and consistent measure of colour quality.

Currently, our team is actively working on extending this methodology to include a comprehensive approach for grading the quality of steamed potatoes, addressing attributes such as disintegration and after-cooking darkening. This ongoing development aims to provide a holistic solution for automating the assessment of various potato qualities, ensuring accuracy, consistency, and efficiency in the evaluation process.

In conclusion, our research contributes to the emerging field of digital tools for food quality assessment by proposing innovative machine learning models for the measurement of potato qualities. The presented models for French fries and potato crisps colouration, along with the ongoing work on steamed potatoes, exemplify our commitment to advancing automation in the evaluation of food quality, reducing reliance on subjective judgments, and fostering standardization in the industry.

803

Effect of water stress in potato crop on post-harvest sprouting

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Post-harvest storage of potato is increasingly challenging because of the recent non-renewal of the highly efficient anti-sprouting chemical, Chlorpropham (CIPC), by the European Union. In addition, climate change and more frequent extreme weather events affect potato crop in the field, which has repercussions for potato quality during storage. To evaluate the effect of water stress during the growing season on post-harvest quality of potatoes, we screened four potato varieties (Agria, Jule, Kennebec and Lady-Claire) for their sprouting response under two water conditions during the growing season 2022-2023: i) irrigated (control condition) and ii) non-irrigated (stress condition). Potatoes were stored at both 4°C and 8°C up to nine months to evaluate if storage at low temperature can mitigate the negative effect of water stress on potato sprouting. Sprouting evaluation was performed by measuring the sprout weight at three timepoints (after five, seven, and nine months of storage). In addition, the number of sprouted tubers was measured weekly to observe sprouting evolution kinetics.

Sprout weight was systematically lower in tubers stored at 4 °C compared to tubers stored at 8 °C and was reduced by 94%. This result was observed for all tested varieties and all timepoints ($p<0.001$). In addition, we observed a variety-dependent negative effect of water stress during the growing season on potato sprouting during storage. On average, sprouting was significantly higher in tubers of the variety Kennebec grown under water stress compared to the sprouting of tubers from the control condition ($p<0.001$), whereas sprouting of the three other varieties was not significantly different between the stress and the control condition ($p>0.05$).

Sprouting kinetic results showed that the increase of the number of sprouted tubers seems faster for potatoes grown under water stress compared to potatoes grown under control condition. Finaly, storage at low temperature seems to help to mitigate the negative effect of water stress by delaying the initiation and reducing the rate of sprouting.

These results demonstrate that the effect of climate change, and particularly of water stress, should be considered when choosing a variety for improved potato storage. In addition, storage temperature is a key factor to mitigate the negative effect of climate change on potato sprouting and to preserve post-harvest quality of potatoes.

804

OptiGERM : a French online Decision Support System to help the industry on tuber sprout control management in stores

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When approved in Europe, CIPC was considered as a very efficient molecule used as sprout suppressant on potato tubers, providing a low-cost protection during storage. Its non-renewal of approval now obliges producers and operators to optimize the use of preventive or curatives solutions to guarantee the delivery of unsprouted tubers to buyers (traders, manufacturers, consumers, etc.) even after several months of storage.

Even if they are few, the diversity of the current registered sprout suppressants obliges the operators of the potato industry to fine tuning their store management in relation with tuber qualities required by the markets and variety specifications. Considering this situation, ARVALIS saw the interest to build an online Decision Support System (DSS) to provide adapted advises on this issue. Called “OptiGERM”, this DSS is now being made operationally available for the operators of the sector. It provides a personalized approach which could be both prospective or curative with integration of a large number of storage parameters. For appropriate individual analysis and outlets, the frame of the DSS is articulated between, in one hand, a complete characterization of the stored batches (variety, production conditions and system, storage equipment, marketing objectives…), in a second hand, on the estimation of the risk of dormancy break before the store removal of the tubers and finally, on a third hand, an evaluated proposal of anti-sprouting program in relation with the storage period.

OptiGERM may be used in a curative situation, proposing program(s) of treatment when sprouts are present in relation with the market and the storage conditions. Meanwhile, used in a preventive way, OptiGERM provides firstly a diagnosis on the risk of tuber sprouting before the targeted date of pile removal. In a second stage, it advises one or more scenarios of sprouting control with integration of the marketing constraints of the potatoes and the equipment specificities of the store. A cost quotation of each proposal is given to allow the integration of a financial consideration on the choice on the treatment program.

Considering the facts that the storage period is often longer than the vegetation phase and that sprouting is one important issue after harvest, OptiGERM can deliver profitable advises to the different actors of the potato industry involved with storage management in both strategic and tactical approaches.

805

Sprout inhibitors combination for a better efficacy and rates modulations

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Since European chlorpropham (CIPC) withdrawal in 2020, sprout inhibitors programs have evolved and became more variable from one grower to another. The range of approved active ingredients has expanded and a program with different sprout inhibitors products can be favourable by combining both modes of action: preventive and curative. Trials were carried out to have a better knowledge on inhibitors products efficacy for a use alone or in combination.

Trials were carried out during 2021/2022 and 2022/2023 storage seasons, i.e. during two very different types of cultivation seasons in France. The first was quite cold, involving a slow sprouting pressure, while the second was the hottest summer ever seen in France, involving a strong and fast sprouting pressure. For this trial, different doses of curative active ingredient, mint oil, were tested to obtain the best efficacy. These doses were compared with each other, both as single applications or in combination with preventive treatments in the field using maleic hydrazide. Three varieties, with different dormancies, were used for these trials: Agata, Charlotte and Monalisa. These trials were carried out in experimental cells of 12 tons tubers capacity at the Arvalis research centre of Villers-Saint-Christophe, northern France. These cells were refrigerated with cooling unit which allowed the storage temperature to be maintained at 7°C during the trial.

The sprouting control is better with high dose of mint oil per application, for the same total amount applied over the storage season. This result is especially true for strong sprouting pressure. The doses can be more flexible for varieties with long dormancy. A treatment with maleic hydrazide during cultivation reduces the sprouting pressure, even for a long term storage, for all the mint oil doses.

The sprouting control depends on the conditions of the year and varieties dormancies. The results tend to show a better efficacy with the higher doses of mint oil, but greater flexibility appears possible when sprouting pressure is low or for varieties with a long dormancy. Sprouting control is easier and better with a preventive product treatment of maleic hydrazide applied during the cultivation phase, whatever the dose of curative product applied.

806

1,4-Dimethylnaphthalene performance in temperature-controlled shipping containers

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Various alternatives have been authorized since the withdrawal of Chlorpropham (CIPC) as a sprout inhibitor in potato storage in Europe. One of these registered active substances is 1,4-dimethylnaphthalene (1,4DMN), 1,4SIGHT®/DORMIR®: a product applied as a fog in stores to extend eco-dormancy, control sprouting and maintain quality of potatoes throughout the storage period. From harvest to the end of storage potatoes are also exported in refrigerated shipping containers from Europe to worldwide destinations. This transport phase over long distances can take weeks and due to the unavailability of CIPC exporters need an alternative, to ensure potatoes arrive at their destinations sprout-free. To gain an understanding of 1,4DMN within the export sector, different trials were conducted in refrigerated shipping containers over two seasons, to investigate the impact of various treatments on the uptake and sprouting efficacy. 1,4DMN distribution within the containers, held at 8C, and through various packaging materials, used within the potato export sector, was determined within the investigations, over a 30 to 41 days ‘transport phase’. Shelf-life assessments were also made 14 days after end of the ‘transport phase’. These trials demonstrated that 1,4DMN, as an alternative to CIPC, can maintain potato quality (sprouting & fry colour) for the potato export sector, under challenging conditions.

Acknowledgement:
Lars-Willem Köpp[2], Holger Thiesing[3], Bernhard Frings[1], John Hutchison[1]
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807

Transcriptomic changes induced by DMN exposure in dormant tubers of three potato cultivars

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Use of the sprout suppressant 1,4-dimethylnaphthalene (DMN) as a replacement for CIPC is of growing interest, as concerns increase regarding use of the latter. DMN is a desirable alternative due to its ability to effectively suppress sprout growth and maintain tuber quality over long periods. Its mode of action within tubers is unknown, however, and to date, studies assessing tuber response to exposure have been restricted to long dormancy cultivars. These studies indicated that DMN prolongs a dormant state by inducing a stress response and halting cell cycle progression, but description of the variability between cultivars remains undescribed. The goal of this study was to evaluate the response of multiple *Solanum tuberosum* cultivars, with varying dormancy lengths, to DMN treatment to identify the primary transcriptomic changes induced by the compound. Cultivars included La Chipper, Lamoka, and Colomba, which were harvested in 2015, 2021, and 2022, respectively. Tubers were exposed to either water or DMN for two days at two dormancy stages, after which all meristems were excised. Total RNA was extracted, and Illumina sequencing was performed. Differentially expressed genes were identified in Galaxy at a significance value of $q<0.05$ and a $\log_2$ fold change absolute value >1. The PlantGSEA was used to identify significant GO terms at $q<0.01$, and protein-protein interaction (PPI) networks with a confidence score >0.90 were visualized using Cytoscape. Response of the tubers differed by dormancy state with ecodormant tubers being most responsive to treatment. DMN suppressed genes related to cell cycle progression and cytokinin signaling and GO terms associated with morphogenesis and organ development, while inducing ethylene response genes and numerous stress response GO terms. Hundreds of genes were identified as exhibiting a similar response in all cultivars, but PPI networks, limited to interactions of two to four proteins, were only identified in the ecodormant state. Networks associated with cell cycle regulation and brassinosteroid and auxin biosynthesis were suppressed, and networks associated with ethylene signaling and response and lipid biosynthesis were induced. Together, these results suggest that although a global response is observed following DMN treatment, sprouts are suppressed primarily through induction of specific stress responses, changes to hormone perception and signaling, and the suppression of cell cycle progression.

808

Greening of potato tubers (*Solanum tuberosum* L.) in grocery stores can be reduced by appropriate storage and packaging

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In grocery stores, potatoes are usually exposed to light when stored at ambient temperature or under refrigerated conditions. Light exposure of potato tubers induces the formation of both chlorophyll (greening) and toxic glycoalkaloids (GAs). Greening leads to rejection by consumers and thus to food waste and economic loss. Nofima has, in collaboration with NIBIO and industry partners and through several projects, studied different aspects of potato greening. Among the investigated factors were the level of irradiance, type of illumination and storage temperatures used for potatoes in grocery stores. We also studied the susceptibility to greening for different cultivars, light transmittance in different packaging materials and the effect of storage temperature in combination with selected packaging materials. The mean temperatures in the examined grocery stores were 5.5 °C and 15.9 °C for cold and ambient temperature storage, respectively. The grocery stores used different fluorescent tubes and LED lights for illumination. Mean light irradiance was 5.5 for the fluorescent tubes and 7.8 W/m^2 for the LED light. Fiber materials generally had lower light transmittance than plastic materials, regardless of ink color, whereas dark inks (black, brown, dark blue, dark green) protected against light transmittance also for the plastic materials. The seven tested cultivars became unacceptable at different times (24-60 hours) and differed both in absolute color values and relative changes of values. The levels of total glycoalkaloids in cultivars with and without light exposure did not correspond well to the changes in color. Potatoes of cultivar Folva were packaged in commercially used plastic or fiber materials with different light barrier properties. They were then exposed to LED illumination for 4 days at 20 °C and 18 days at 6 °C. None of the tested packaging types provided sufficient protection from light. The greening rate was four times faster at room temperature (20 °C) than at cold storage (6 °C). Hence, placing the potatoes at cold storage instead of room temperature can quadruple the time needed to develop a green color, even for potatoes packaged in materials with limited light protection.

809

Glycoalkaloids in processing potatoes and fried potato products: formation and stability

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Glycoalkaloids (GA) are secondary plant metabolites in potatoes and act as a defence mechanism. Therefore, they are mainly formed when potatoes are exposed to stress. If consumed in high quantities, GA can lead to poisoning. A lowering of the threshold value in potatoes and products is currently being discussed. Furthermore, the European Food Safety Authority is requesting more data on the occurrence of GA in potatoes and products. This study therefore aims to analyse the sensitivity of different potato varieties to post-harvest stress factors and to investigate the stability of GA during the manufacturing of fried potato products.

Nine French fry potato varieties, one starch variety and ten crisps varieties were grown in a randomized design. Selected varieties were cultivated again in a second year. After harvest, sub-samples of each variety were subjected to various stress factors like light-exposure, mechanical damage and warm storage. Selected varieties were used to produce French fries and potato crisps in a pilot plant that represents an industry-like process. The GA contents in the raw materials were analysed for all varieties and treatments, and for the selected samples the GA contents in the products obtained will also be analysed. Samples were additionally taken during the manufacturing process in order to analyse the influence of individual process steps like peeling, blanching and frying on the GA content.

A cultivar effect on the GA content could already be shown in the untreated control. The sum of the main GA, α-solanine and α-chaconine, ranged from 45±1 to 258 ± 19 mg/kg in the raw and unpeeled potatoes. Of the stress factors applied, mainly the exposure to light led to an increase in GA in themajority of the varieties tested. Preliminary results of the products show a reduction of GA through the processing of up to 60% for French fries and 75 % for potato crisps in relation to the fat-free dry mass. As part of the ongoing project, further product samples will be analysed and the influence of different processing steps in the production of French fries and potato crisps will be investigated.

Since some raw potatoes already contain GA levels above the potential future threshold, unfavourable post-harvest treatments should be avoided. Furthermore, it is important to investigate the influence of individual steps in the manufacturing of potato products on the GA content in order to optimize the processing regarding a minimization of GA.

Poster list and poster abstracts

NO	Title	Author	Country	Day
1-01	Variety identification in the seed certification process using SSR markers– improvement of the official method in France	Sylvie Marhadour	France	Monday
1-02	Superior resistance to late blight in novel breeding clones – a helpful source for sustainable potato production	Thilo Hammann	Germany	
1-03	Preliminary assessment Ukrainian Potato Cultivars for Resistance to Potato Wart pathotypes spread in Ukraine and Georgia	Avrelia Zelya	Ukraine	
1-04	SustainPotato: Nordic-Baltic public-private partnership to breed more resistant potatoes for high latitudes	Muath Alsheikh	Norway	
1-05	Combining 11 genetic markers into three multiplex protocols for testing pathogen resistance in Estonian potato breeding material	Kai Ilves	Estonia	
1-06	Investigating key genes involved in potato anthocyanin biosynthesis and under stress conditions	Riccardo Aversano	Italy	
1-07	Understanding potato endodormancy to develop strategies for reducing waste during postharvest storage	Fabian Villamil	UK	
1-08	Expanding Late Blight resistance: characterization and functional analysis of a novel R3a homologue in wild potato species	Virkrant Singh	UK	Tuesday
1-09	Unveiling Potato Resistance: State-of-the-Art computational approaches for Identifying Resistance Genes against Diverse Diseases	Yuk Woon Cheung	UK	
1-10	Efficiency of molecular markers associated to H1, a major gene to control Globodera rostochiensis	Sylvie Marhadour	France	
1-11	Comparative analysis of R-genes expression and transcriptomic profiles in potato tubers of selected potato genotypes after inoculation with virulent and avirulent races of *Phytophthora infestans*	Jaroslaw Plich	Poland	
1-12	Establishment of an SNP catalogue for potato	Jose Ignacio Ruiz de Galarreta	Spain	
1-13	GWAS Analysis of resistance of potato to Common Scab using historical phenotypic values	Fatima Latif Azam	Ireland	
1-14	QTL discovery for agronomic and quality traits in a panel of diploid potato clones using PotatoMASH amplicon sequencing	Dan Milbourne	Ireland	
1-15	GBS and SPUD-SPET genotyping for advancing genetics and breeding applications in potato	Sanjeev Kumar Sharma	UK	
1-16	Modelling G x E interaction using unbalanced tetraploid Potato (*Solanum tuberosum* L.) data and pedigree information from Scandinavian and Mediterranean environment	Muhammad Farhan Yousaf	Denmark	Thursday
1-17	In vitro evaluation of host defense peptides for antimicrobial activity and successful introduction in *Solanum tuberosum* for disease resistance engineering	Nick Schimpf	Canada	
1-18	Gene editing in tetraploid potato to enhance PVY resistance	Jean Eric Chauvin	France	
1-19	PMR4 is a susceptibility gene for soft rot disease in potato	Pichaya Cheewapoonphon	NL	
1-20	Identification of duplicates in Nordic potato collections	Pawel Chrominski	Sweden	
1-21	Variance and covariance components of agronomic and quality traits assessed in tetraploid potato and implications on practical breeding	Kathrin Thelen	Germany	
1-22	Potato genetic resources at CGN	Lana de Bruijn	NL	

NO	Title	Author	Country	Day
2-01	Using the CRISPR-Cas system to localize plant viruses	Carl Spetz	Norway	Monday
2-02	Using the CRISPR-Cas system to localize plant viruses	Guro Bukaasen	Norway	
2-03	*Tobacco Rattle Virus* and Trichodoridae: building blocks of a systemic and sustainable approach to disease control	Roberto Miglino	NL	
2-04	Dynamics of potato virus Y infection pressure and strain composition in State of Colorado, USA	Mohamad Chich-Ali	USA	
2-05	Evolution of the prevalence of potato virus Y (PVY) and potato leafroll virus (PLRV) in Switzerland between 2016 and 2023	Cecile Thomas	Switzerland	
2-06	Mineral oil to control Potato virus Y transmission in seed potato production	Mounia Khelifa	France	
2-07	Potato & the French post-entry quarantine station	Lorene Belval	France	
2-08	Evaluation of a cryopreservation method for virus elimination in potato	Florence Esnault	France	
2-09	7-hydroxytropolone and analogs to control potato blackleg.	Euphrasie Munier-Lépinay	France	
2-10	Potato soft rot – as an economically important disease for Georgia	Maka Muradashvili	Georgia	
2-11	Detection of *Ralstonia solanacearum* in different environmental samples.	Włodzimierz Przewodowski	Poland	
3-01	Biofumigation with sorghum and brown mustard: a sustainable solution to control wireworm damage in Swiss potato production	Geoffrey Darbon	Switzerland	Tuesday
3-02	Trial results on wireworm control in potatoes using chemical, biological and arable methods	Michael Zellner	Germany	
3-03	Management tools to reduce wireworm damage in potatoes in Canada.	Christine Noronha	Canada	
3-04	Horizontal and vertical movement of wireworms, *Agriotes sputator* (Coleoptera: Elateridae) through soil in Canada	Christine Noronha	Canada	
3-05	Weeds control in potatoes under agro-climatic conditions of Barsa Country, Romania	Manuela Hermeziu	Romania	
3-06	Importance of soilborne inoculum of *Colletotrichum coccodes* and assessment of potato cultivar resistance to black dot and in France	Roman Valade	France	
3-07	Optimizing Fungicide Timing for Effective Management of *Colletotrichum coccodes* in Potatoes	Phillip S. Wharton	USA	
3-08	Potato black dot caused by *Colletotrichum coccodes* in Inner Mongolia of China	Limin Xu	China	
3-09	Inhibition of the development of *Rhizoctonia solani* by plant secondary metabolites – a laboratory study	Maximilian Koch	Norway	
3-10	Weeds as alternative hosts of *Spongospora subterranea,* the causal agent of potato powdery scab, in Finland	Lea Hiltunen	Finland	
3-11	The influence of a preparation based on hydrogen peroxide and silver colloids and a preparation containing grapefruit extract on reducing fungal and bacterial diseases of Gardena variety seed potatoes during storage	Aleksandra Bech	Poland	
3-12	High-resolution analysis of effector genes in 394 *Phytophthora infestans* isolates using amplicon sequencing	Simeon Rossmann	Norway	Thursday
3-13	Virulence and fungicide susceptibility of *Phytophthora infestans* isolates collected in Belgium in the years 2021-2023	Vincent Cesar	Belgium	
3-14	Diversity and complexity of virulence races of *Phytophthora infestans* in the Baltic Sea region	Helina Nassar	Estonia	
3-15	Long term changes in late blight development in Estonia	Mati Koppel	Estonia	

NO	Title	Author	Country	Day
3-16	Reaction of some potato genotypes to the action of *Phytophthora infestans* in different environmental conditions	Nichita Negruseri	Romania	Thursday
3-17	Insights into the metabolic responses of potato cultivars infected with *Phytophthora infestans*	Portia D. Singh	India	
3-18	Mutations conferring fungicide resistance in Alternaria from potato in South Africa	Elsie Cruywagen	S. Africa	
3-19	Mileos®, the French potato diseases DSS: a new module to control early blight.	Denis Gaucher	France	
3-20	Fusarium species causing potato dry rot in France: identification, pathogenicity and sensitivity to fungicides	Karima Bouchek-Mechiche	France	
3-21	Dryocrassin ABBA is an effective inhibitor against potato dry rot caused by *Fusarium oxysporum*	Wenzhong Wang	China	
3-22	Functional verification of endophytic *Bacillus subtilis* WZ10 and its control efficiency on potato Fusarium wilt of China	Yuanzheng Zhao	China	
3-23	Control effect of potato *Fusarium* wilt by co-culture of *Trichoderma asperellum* PT-29 and *Bacillus subtilis* S-16 and the comparative analysis of non-targeted metabolomics	Hongyou Zhou	China	
3-24	PATAFEST: Horizon Europe-funded Research Project Paving the Way for Sustainable Potato Protection and Postharvest Excellence	Amaia Ortiz Barredo	Spain	
4-01	Status of potato cyst nematodes in Norway	Solveig Haukeland	Norway	Thursday
4-02	Surveillance of *Meloidogyne chitwoodi* og *Meloidogyne fallax* in Norway (2019-2023)	Marit Skuterud Vennatrø	Norway	
4-03	Steaming as a tool to reduce the risk of spreading key nematode pests in infrastructure projects	Marit Skuterud Vennatrø	Norway	
4-04	Efficacy of *Bacillus subtilis* strain ZWZ-19 and associated volatile substances in inhibiting nematode of *Ditylenchus destructor*: an evaluation of control performance	Dong Wang	China	
4-05	Comparison of virulence of pathotype 38 (Nevsehir) isolates from different EPPO member countries	Jaroslaw Przetakiewicz	Poland	
4-06	Experiments in controlled conditions provide beneficial information on the applicability of biochar in potato production	Matti Salmela	Finland	
4-07	Exploration of plant growth-promoting rhizobacteria (PGPR) in potatoes	Rene Sutherland	S. Africa	
5-01	The effect of Smartblock, a sprout suppressant, on the physiological growth of potato (*Solanum tuberosum*)	Nomali Ngobese	S. Africa	Monday
5-02	Metabolomics – a promising tool to assess the physiological age of seed tubers of potato (*Solanum tuberosum* L.)	Chunmei Zou	Germany	
5-03	Assessment the suitability of potato breeding lines for cultivation in an organic production system	Krystyna Zarzyńska	Poland	
5-04	Variety and terms of potato planting in a summer seed production in the Republic of Moldova	Petru Iliev	Moldova	
5-05	Assessment of gene expression changes in relation to meristem position in eco-dormant tubers.	Michael Campbell	USA	

NO	Title	Author	Country	Day
5-06	Nitrogen uptake and partitioning in potato varieties of contrasting determinacy	Sarah Roberts	UK	Tuesday
5-07	Nitrogen use efficiency impact on several traits important for potato starch production	Inese Taskova	Latvia	
5-08	Potato tuber quality and nitrogen use efficiency responses to integrated nutrient management	Jubalani Ntuli	S. Africa	
5-09	Reducing Synthetic Fertilizer in Russet Burbank Production with Turkey Manure	Andrew Robinson	USA	
5-10	Improving tuber quality and vigour via the use of cover crops in organic and low input farming	Peter Dolnicar	Slovenia	
5-11	Smaller doses of hot water combined with mechanical flailing did not kill potato haulm sufficiently	Hanna Ellisiv Kringstad	Norway	
5-12	On how the cell cycle progression affects potato response to water shortage	Dorota Sołtys-Kalina	Poland	
7-01	Latest trends in climate-smart agricultural practices: a systematic review	Nomali Ngobese	S. Africa	Tuesday
7-02	Yield and quality assessment of potato varieties with 3 N-fertilization levels and different weather conditions in Middle East Norway	Jaroslaw S. Grodek	Norway	
7-03	Dissecting the cross-talk between cold tolerance mechanisms and tuberisation in potato	Beiyu Tu	NL	
7-04	Use of in-situ field chambers to quantify the influence of heat stress in potato	Mehmet Emin Çalışkan	Turkey	
7-05	Exploring factors influencing hybrid true potato seedling production	Olivia Kacheyo	NL	
7-06	Irrigation of seed potato in summer crop	Petru Iliev	Moldova	Thursday
7-07	From controlled environment to field: confounding factors in container trials	Karin I Köhl	Germany	
7-08	Responses of potato cultivars to water stress condition under greenhouse: Agronomical and Physiological parameters	Fadia Chairi	Belgium	
7-09	Influence of N fertilization, soil temperature, and moisture on gaseous N losses in the form of N2O in starch potato cultivation in Northern Germany	Dorothea Niemann	Germany	
8-01	Quantification of tuber damage with regard to the marketable quality of potato production in the Czech Republic	David Hajek	Czech Republik	Thursday
8-02	New strategies for sprout-free long-term storage of processing potatoes in Norway	Kristian Sæther	Norway	
8-03	Investigation of potato storage in Heilongjiang Province	Wenzhong Wang	China	
8-04	An improved method for introducing ethylene in stores with potatoes for processing	Adrian Briddon	United Kingdom	
8-05	Low temperature, reconditioning and CO2 levels in store during long-term storage of processing potatoes	Pia Heltoft	Norway	
8-06	Ethylene sensitivity and effects on potato storage and quality	Andreas Meyer	Germany	
8-07	Sustainable solutions to control potato dormancy – a mechanistic approach	M. Carmen Alamar	UK	
8-08	Improving Wound-Healing of Potato Tubers Using Natural Elicitors	Munevver Dogramaci	USA	

1-01

Variety identification in the seed certification process using SSR markers – improvement of the official method in France

Sylvie Marhadour[1,2], Amandine Méar[1,2], Natalie Laversin[3], Xavier Riquiez[3], Sophie Le Bechennec[4], Arnaud Barbary[4], Marion Flodrops[4], Flore Madruga[5], Céline Passeret[5], Géry Bronsard[6], Véronique Wambre[6], Florence Esnault[2], Marie-Laure Lesage[2], Yves Le Hingrat[1]

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[4] Bretagne Plants, Hanvec, France
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[6] Service Commun des Laboratoires, Villeneuve d'Ascq, France

Single sequence repeat (SSR) markers are essential tools to fingerprint varieties for their identification. Inov3PT, the technical institute of the French seed potato growers' organization, set up a method to check the initial material and the first generations of the multiplication process. Five coordinated French labs are using the same procedure which is officially used in the seed potato certification scheme, in case of doubt or fraud and also to manage genetic resources.

The kit has regularly been upgraded due to the increasing number of varieties to be checked. It is currently consisting in 8 markers. Nine ring tests have regularly been organized since 2003 to check the ability of the partners to use the method and the database named IdeAle. It currently contains 4122 profiles representing 2603 genotypes (1300 varieties). This is a secured internet platform with user authentication access. Data are updated in real time and can simultaneously be accessed by all users.

Between 2019 and 2023, we were supported by the French Ministry of Agriculture through a research project named IdEvol to improve the way of resolving the markers. We assessed the suitability of the Qiagen QIAxcel Advanced capillary gel electrophoresis to test the SSR markers routinely in use. The objectives were to simplify and reduce manual tasks, decrease the overall analysis time, minimize the exposure to hazardous substances for the laboratory staff, and reduce the waste treatment costs. An additional objective was to identify new SSR markers suitable for the procedure on the new instrument. One of the main issues was to check if the most resolutive cartridge was as resolutive as polyacrylamide gels to separate the different alleles of our markers. This was a requirement to continue using our database.

After minor adaptations of the PCR conditions, 326 varieties were divided among the partners and profiled with the 8 markers along with control varieties amplified in all labs. 6 markers could be confidently recovered on the new system *i.e.* the profiles read on the new system were highly concordant (94 to 97%) with the references contained in the database. An internal ring test confirmed these findings. Three new markers adapted to the new electrophoresis conditions were identified and tested across the network. We are now multiplexing the markers to further improve the overall efficiency of the method which, hence, will replace the official one.

1-02

Superior resistance to late blight in novel breeding clones – a helpful source for sustainable potato production

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[1]Julius Kühn-Institut, Federal Research Centre for Cultivated Plants, Sanitz, Germany

Potato contributes significantly to safeguarding global food security. A changing climate and expanding risks caused by more aggressive or new pathogens and pests as well as restrictions in chemical plant protection raise challenges to potato production, breeding and research. Novel races of late blight (*Phytophthora infestans*) exhibiting stronger aggressiveness, challenge potato growers and breeders. Former efforts to breed resistant potatoes by incorporating single resistance genes failed due to the high adaptability of the pathogen. Breeding for resistance based on stacking of different R-genes or QTL is the most promising way to prevent blight. Ultimately, plant genetic resources must be characterized and breeding clones selected combining improved levels of durable resistance plus acceptable agronomic and quality traits.

At Julius Kühn Institute (JKI), resistant breeding clones were developed in a long-term breeding program. Crosses with resistant accessions of wild species were made, subsequently backcrossed with cultivars to develop breeding clones expressing improved agronomic traits. The gene pool at JKI was proven for the presence of various R-genes from wild species. In total, eleven pairs of sequence specific PCR primers for seven resistance genes and one QTL allele are used. Reduced attack by foliage blight often correlates with late maturity; thus, maturation time was considered. Additional phenotypic characters and quality traits were evaluated.

A number of JKI breeding clones exhibited lower infestation than current varieties, demonstrating progress in breeding for foliage-blight resistance and resolution of the said correlation in these instances. Additionally, improved resistance against tuber-blight was found for some pre-breeding clones. In total 36 of 52 clones tested had PCR amplicons for one up to four resistance genes for the eight resistance genes tested. Amazingly, in the present study breeding clones were identified carrying only one or none of the analysed resistance genes, while showing high resistance levels. Some clones showed useful quality traits and high levels of tuber yields and starch contents. Yet other characters remain to be adapted.

The pre-breeding clones tested indicate potential as resistance donors and may be useful to genetically enrich potato breeding programs in order to enable sustainable potato production under reduced fungicide regimes. Late blight resistance of the gene pool under survey appears not solely based on individual major resistance genes, but also on quantitative effects.

1-03

Preliminary assessment Ukrainian Potato Cultivars for Resistance to Potato Wart pathotypes spread in Ukraine and Georgia

[1]Avrelia Zelya, [2]Zoia Sikharulidze, [1]George Zelya

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Potato is one of the most important crops in Ukraine and Georgia. Potato wart disease, caused by *Synchytrium endobioticum* is a very harmful quarantine disease. There are 11-Mizhirya, 13- Rachiv, 18-Yasynia and 22- Bystrets in Ukraine. The pathotype 38 is originated from Georgia. To prevent the disease spread, it is very important to test imported potatoes for the resistance to the wart disease before commercially releasing them in the fields. The potato varieties of Ukrainian breeding Bozhedar, Glazurna, Khortytsa, Slovyanka and Solokha testing provided in laboratory of quarantine pests and diseases UkrSRPQS IPP NAAS and in sources of wart aggressive pathotypes in 2021–2023. The Spieckermann test used in laboratory terms.Varieties Bozhedar and Glazurna had not defeated. Warts with size of 2–3 mm 18-Yasynnya pathotype determined on potato varieties Khortytsa and Solokha. Varieties Slovyanka defeated by all pathotypes. Warts types IV (8-10mm) were determined during causative agent defeating.The highest degree of disease damage was observed in the control variety Poliska rozheva susceptible to all wart pathotypes. The wart size was 46 mm. Varieties Bozhedar, Glazurna, Khortytsya, Slovyanka and Solokha determined in Institute of Phytopathology and Biodiversity. The preliminary assessment of potato cultivars for resistance to the pathotype 38 (Nevşehir) of potato wart was carried out using the pot test and the laboratory Spieckermann test.

All six tested cultivars were susceptible to the wart pathotype 38 as they showed wart formation with different classes. The warts with 2-3 mm observed on Glazurna and Slovianka. The warts type V (11–15 mm) were observed on tubers of Khortytsa and Bogedar. Big warts with 12-14mm were recorded on roots of Solokha. The warts with 4–5mm were developed on the remain tested cultivars. Varieties resistant to wart pathotypes proposed for improving in disease sources.

The new potato resistant varieties breeding to wart continues in spite of war situation in Ukraine. We hope that future research will identify new resistant varieties to wart.

1-04

SustainPotato: Nordic-Baltic public-private partnership to breed more resistant potatoes for high latitudes.

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This public-private pre-breeding partnership brings together four Nordic and Baltic potato breeding programs, public research institutions, and NordGen to use available tuber-bearing *Solanum* germplasm along with genomics and phenomics tools to develop potatoes with resistance to late blight and skin blemish. The outputs are bred germplasm together with new methods and tools to continue improving potato for Northern Europe. Late blight experiments were established in three locations (Sweden, Denmark and Norway) in 2022 and 2023. The experiments included 15 standard cultivars across sites and 87 breeding lines in each site. The 276 accessions were visually scored for leaf blight and genotyped with the 22K Solcap single nucleotide polymorphism (SNP) potato array. A two-stage genome-wide association study (GWAS) was carried out with best linear unbiased predictors (BLUPs) across years and environments. The BLUPs were the phenotypes from the tetrasomic inheritance analysis with software GWASpoly. Significant marker -trait associations (MTA) on multiple chromosomes were observed. Late blight incidence led to significant reduction of the drone-based traits chlorophyll content, ground cover, GRRI and VARI. Heritability estimates of these traits ranged from 0.53 to 0.81 (mean = 0.66). Genotypes with higher chlorophyll content, ground cover, GRRI, VARI and plant height exhibited enhanced total tuber weight across testing environments. Participation in the project gives NordGen the opportunity to establish a network with Scandinavian and Baltic potato breeders and researchers and to gain insights into their expectations concerning the potato genebank. This engagement also facilitated the deepening of NordGen's understanding of contemporary trends in potato breeding. The methods developed and employed for high-throughput phenotyping and genotyping are transferable to the characterization and evaluation of potato accessions at NordGen. The data derived from SNP genotyping holds potential utility in the identification of novel accessions slated for inclusion in NordGen's collection. Several genotypes investigated in the project exhibit prospective significance for NordGen and may be considered for long-term conservation in the future. The phenotypic and genotypic data could be disseminated to the public domain through incorporation into NordGen database.

1-05

Combining 11 genetic markers into three multiplex protocols for testing pathogen resistance in Estonian potato breeding material

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Potato is a staple crop with one of the most diverse distribution patterns. It is more commonly grown in the northern hemisphere, where the weather is unpredictable and favorable for various diseases to emerge and spread. Pesticides are costly and not always effective against pathogens damaging the plants. Reducing the use of pesticides is encouraged due to their off-target impact on environment and biodiversity. Therefore, using genetic markers for selecting breeding material with broad resistance is a preferred countermeasure for these pathogens.

In this study, we have combined 11 different pathogen resistance markers to be used as three multiplex PCR marker sets to screen potato breeding material for the presence of resistance genes against two potato cyst nematodes (*Globodera rostochiensis and Globodera pallida*), two viruses (Potato Virus X and Potato Virus Y) and an oomycete (*Phytophthora infestans*) commonly found in Estonia. These marker sets were used to analyse over 800 potato breeding clones from Estonian potato breeding program in 4 consecutive years starting with accessions from 2018. We observed that the resistance alleles for cyst nematodes were the most frequent in our sample set as at least one of the three different resistance genes were present in 92% of breeding clones. Over half (54%) of breeding clones tested positive for at least one virus resistance marker, whereas the resistance for *P. infestans* was only found in 12% of the tested breeding clones. 98 different potato clone accessions previously fingerprinted with SSR markers by Ivanova-Pozdejeva *et al.,* 2022 were also tested for the presence of these molecular markers. This selection includes older potato cultivars and fewer resistance markers were found compared to the breeding clones.

In Estonia, potato breeding began in 1920 and during this time, 49 potato varieties have been registered. However, marker assisted selection has only been applied since 2017. Therefore, all resistance alleles recorded during this screening have been introduced to the breeding material through traditional breeding: plant crossing and phenotypic selection. The three-set multiplex PCR analysis has now been implemented as a valuable tool in the selection process of Estonian potato breeding material. Breeding clones with favorable phenotype are evaluated on the amount of resistance genes present to confirm their further potential.

*Ivanova-Pozdejeva *et al.,* Potato Res., Vol. 65: 153-170 (2022)

1-06

Investigating key genes involved in potato anthocyanin biosynthesis and under stress conditions

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Anthocyanins are bioactive pigments synthesized by plants in response to abiotic and biotic cues that constitute a crucial component of the plant stress defense mechanism. An in-depth comprehension of the regulatory framework governing anthocyanin biosynthesis is imperative to elucidate their role in stress responses. This study assesses the allelic composition of key regulatory genes orchestrating anthocyanin production and their transcriptional activation under abiotic stress conditions in potato (*Solanum tuberosum*). Toward this goal, we analyzed the main biosynthesis activator gene R2R3 MYB *StAN1*, which requires functional alleles (StAN1-r1 and StAN1-r2), alongside the repressor gene R3-MYB *StMYBATV*. PCR analysis and subsequent sequencing of amplified products provided a detailed characterization of these genes. Furthermore, we examined their expression levels in leaves using qPCR. The results allowed discrimination of different *StAN1* alleles in 19 potato genotypes and highlighted the presence of SNPs in the *StMYBATV* sequence in anthocyanin-rich genotypes, indicative of potential functional alterations. Under conditions of stress imposition, the purple cultivars Blue Star and Violet Queen proved to be tolerant with high expression of *StAN1*, in agreement with the presence of functional alleles r1 and r2. Unexpectedly, the acyanic cultivar Agata – susceptibile to the imposed osmotic stress – displaying elevated expression of *StAN2* (a paralogous gene of *StAN1*) and *StDFR* (encoding a structural gene in anthocyanin biosynthesis), but not of *StAN1* presumably to the presence of non-functional alleles (r0). This observation implies a distinct stress-responsive transcriptional profile in Agata. In conclusion, our findings contribute to the scientific understanding of the interplay between genetic regulation, anthocyanins biosynthesis, and stress response mechanisms in potato.

1-07

Understanding potato endodormancy to develop strategies for reducing waste during postharvest storage

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Potato (*Solanum tuberosum*) ranks sixth globally in terms of agricultural production surpassed only by sugar cane, maize, rice, wheat, and oil palm. Due its importance, potato remains a focus of breeding programs emphasizing pathogen resistance, climate resilience, and tuber quality enhancement (Alamar *et al*., 2017; Ravikiran *et al*., 2023). However, a less explored yet critical aspect contributing to wastage is dormancy break. In the UK, potato tubers are stored for up to 9 months to ensure year-round availability. During storage, a cascade of events begins in the tuber, leading to changes in metabolism and physiology, which result in the resumption of growth. These factors subsequently lead to losses due to a reduction in raw material quality. Therefore, effective control and management of potato dormancy are crucial for the sustainability of the potato industry.

Most of the studies of potato dormancy extension have focused on analyzing ecodormancy under storage. although preharvest factors, such as genetic background, are known to affect potato quality, less studied and understood is how preharvest environmental factors affect the length of endodormancy of potato tubers.

This research aims to understand the effect of *CYCLING DOF FACTOR 1* (*CDF1*)*,* a gene known to regulate tuberization, on the time to endodormancy break. To assess the impact of various *CDF1* alleles on the time to endodormancy break, potato tubers from 47 diploid hybrids, including hybrids homozygous for early or late tuberization, were stored at 15°C for 50 days. Eye movement was assessed twice a week, categorizing tubers into the following stages: dormant; pre-eye movement; dormancy break; sprout < 1 mm; 1 mm < sprout < 2 mm; sprout > 2 mm.

Different segregation patterns within the two different homozygote classes were identified to elucidate two potentially dependent physiological processes: early tuberization and dormancy break. Preliminary results suggest that hybrids exhibiting early tuberization have a shorter time to endodormancy break, whereas those exhibiting late tuberization experience an extended time to endodormancy break. However, comprehending the effects of other genes within the regulatory network requires the development of additional mapping populations. Our findings establish initial steps toward understanding and elucidating the genetic control of this complex trait.

Disclaimer:
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1-08

Expanding Late Blight resistance: characterization and functional analysis of a novel R3a homologue in wild potato species

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The identification of disease resistance genes *R1-R11* in *Solanum demissum* has revealed that introducing these *R* genes into cultivated potatoes can confer resistance to blight. Among these genes, *R3a*, located on the short arm of chromosome XI, is well-characterised. It possesses N-terminal coiled-coil (CC), a central nucleotide-binding site (NBS), and a C-terminal leucine-rich repeat (LRR) domain, placing it in the NLR class of *R* genes. Studying the deployment of R3a in extant potato cultivars has shown that this gene is widely utilised in breeding programs.

In this study, we identified a functional *R3a*-like gene in the diploid wild potato species *S. bulbocastanum*. Compared to the *R3a* gene from *S. demissum*, the homologue from *S. bulbocastanum* displays a high level of conservation for the CC-NB domains, whereas the LRR is significantly diverging. Cloning and functional analysis of this *R3a* homologue (*R3a*-blb7645) revealed that the gene not only recognises Avr3a^{KI} but can also weakly recognise the Avr3a^{EM} variant, which typically evades recognition by the wild-type gene. However, functional assays in late blight did not consistently reveal broader disease resistance spectra but highlighted the naturally occurring diversity of *R3a*, which has never been identified before.

1-09

Unveiling Potato Resistance: State-of-the-Art computational approaches for Identifying Resistance Genes against Diverse Diseases

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Potatoes (*Solanum tuberosum*) represent a vital global crop, providing sustenance to billions and contributing significantly to agricultural economies and food security. However, the potato faces numerous threats from diverse pathogens including viruses, wart diseases, nematodes, and late blight. To address these challenges, we have embraced cutting-edge association genetics techniques for the identification of resistance genes, aiming to enhance crop resilience and food security.

Functional nucleotide-binding, leucine-rich repeat (NLR) disease resistance (*R*) genes play a pivotal role in controlling various diseases in potatoes and have been the focus of much research. Our approach utilises *R*-gene enrichment sequencing (RenSeq), specifically the SMRT-AgRenSeq-d workflow developed by Adams et al. (2022) and adapted for tetraploid potatoes by Wang et al. (2023). This innovative combination incorporates PacBio HiFi long-read RenSeq assembly (SMRT-RenSeq), *k*-mer-based Association genetics RenSeq (AgRenSeq), and diagnostic RenSeq (dRenSeq). To further this, we have shown in independent experiments that despite limited phenotype penetration, this approach robustly identifies candidate *R*-genes for viruses, oomycetes, fungi, and nematodes.

Next generation sequencing, such as PacBio HIFI technologies, are used in our investigations to provide high accuracy long reads allowing us to unravel complex genomic regions which has aided in the advancement in the association genetics approaches and in the development of high accuracy markers for over 15 functional NLRs. This research represents an innovative exploration of tetraploid potatoes, emphasising the identification of resistance genes against diverse pathogens. By integrating next generation sequencing technologies, we revolutionise our ability to dissect the genetic foundations of potato defence mechanisms, paving the way for more effective and efficient breeding strategies.

1-10

Efficiency of molecular markers associated to H1, a major gene to control *Globodera rostochiensis*

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The *H1* gene has long been used to breed potato varieties resistant to *G. rostochiensis* and several markers diagnostic for *H1* have been published. The *H1* gene has long been used to breed potato varieties resistant to *G. rostochiensis* and several markers diagnostic for *H1* have been published. The aim of this study was to test the efficiency of markers from literature linked to resistance to *Globodera* nematodes, especially to *G. rostochiensis*.
In addition to published markers, markers identified by association mapping in INRAE breeding stocks were tested. This work was performed within the French research project Geconem entitled "How to collectively manage genetic resistance to potato cyst nematodes?" which lasted between 2019 and 2023.

Overall, 6 markers were tested including 57R and TG689, the markers traditionally used for the *H1* gene. Different genotyping methods were used such as: PACE (equivalent to KASP), HRM and standard PCR. Two panels of genotypes were used, both characterized for their phenotypic resistance. The first panel consisted of 16 genotypes and was used for the markers technical set-up. The second consisted of 284 genotypes representing breeding stocks of 3 breeding companies (Bretagne Plants Innovation, SIPRE and Grocep). It was used to detect reliable associations between markers and resistance.

The HRM markers (TG689_1P and 57R_1P published by Meiyalaghan, S., et al.) required some tests to identify the best commercial kit to reveal the polymorphism. One kit performed better than the two others. H1_KASP and solcap_snp_c2_55239 (Geconem project) performed efficiently using PACE chemistry.

Results obtained on the 284-panel showed that markers solcap_snp_c2_55239 and 57R outperformed the other markers in characterizing the presence of the *H1* gene. Both markers flanked the gene and can be confidently used in markers assisted selection.

1-11

Comparative analysis of R-genes expression and transcriptomic profiles in potato tubers of selected potato genotypes after inoculation with virulent and avirulent races of *Phytophthora infestans*

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Late blight is the most important and destructive potato disease which leads to reduction of global potato production by ~16% annually. The disease is caused by the oomycete pathogen *Phytophthora infestans* (Mont.) de Bary, which may infect the entire potato plant, including stems, leaves, fruits and tubers. The most effective way to reduce this negative impact is growing of potato cultivars that are resistant to late blight. Resistance breeding is based mainly on the resistance genes (R-genes) identified in various wild *Solanum* species. These R-genes encode proteins that directly or indirectly detect effector proteins produced by the pathogen This leads to the activation of effector triggered immunity (and results in typical hypersensitive response (HR)

Relationship between resistance of tubers and foliage against *P. infestans* remains unclear and foliage resistance does not guarantee tuber resistance. In the case of interaction with compatible races of the pathogen some R genes provides effective protection of foliage and tubers while other fails in tuber resistance. One of the hypothetical explanation of this phenomenon are differences in level of expressions of particular R-genes. As a part of our study, we compare level of expression of two selected R-genes (*Rpi-phu1* and *R2*) in leaves and tubers of potato clones/cultivars inoculated with compatible and incompatible isolates of *P. infestans*. The level of R genes expression was measured before inoculation, and in five time-points (24, 48, 72, 96 and 120 h) post inoculations. As plant maerial we used cultivar Bzura (*R2*), potato clones TG 97-411 (*Rpi-phu1*) and their progeny clone DC-69 (*R2* and *Rpi-phu1*).

In addition to differences in the level of expression of the R-genes themselves, more general differences in the defense response of individual potato genotypes can be also expected. Therefore, we performed comparative analysis transcriptome of tubers above mentioned potato genotypes 48h after inoculation with compatible and incompatible races of *P. infestans*. On the poster preliminary results of these analysis are presented.

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1-12

Establishment of an SNP catalogue for potato

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Single Nucleotide Polymorphisms (SNP) are useful for genetic studies including association between a phenotype and a functional variant. Potato SNP were published by Hamilton et al (2011 SolCAP 69K SNPs), Uitdewilligen et al (2013 PotVar GBS SNPs 135K) and by Caruana et al (2019 183K). Part of them (40K) are included in the Illumina Potato GGP V4 chip. However SNPs from different sources are cross referenced to distinct genome assemblies and sometimes do not have annotations. Recently an updated long-read genome assembly (DM6.1) for the doubled monoploid potato *S. tuberosum* Group *Phureja* was produced and annotated representing the current reference. The aim of this study was to compile all currently available potato SNP map them to the DM6.1 genome, retrieve the annotations and integrate them in the DM6.1 GFF3 File for downstream applications. First the potato Chip SNP were processed, mapped and the annotations were integrated. They consisted of SolCAP SNP, PotVAR SNP, ST4.03 SNP and some miscellaneous SNP. Then the potato NON-Chip SNP were processed in an analogous way, mapped and the annotations were integrated. They consisted of SolCAP SNP and PotVAR SNP not included in the chip and Caruana SNP. For the final processing all available potato SNP, Chip SNP and non-Chip SNP were combined and integrated in the GFF3 File. In this way we have processed a total of 30,946 Chip SNP and 320,196 non-Chip SNP, retrieved their annotations and integrated them in the DM6.1 GFF3 File. With respect to Chip SNP all are integrated, 9,688 Chip SNP are INTERGENIC. Only 10,306 genes out of 40,652 are targeted by the 30,946 SNP, including a total of 105 disease resistance genes (out of 697), targeted by 237 SNP. After filtering for duplicates a total of 343,445 Chip and NON-Chip SNP remained. Among them were 28,701 Intergenic SNP. Only 18,974 genes out of 40,652 are targeted by the 343,445 SNP. A total of 1,390 SNP target 227 disease resistance genes. The final results are integrated in an Excel workbook with a total of 826,369 records containing all 343,445 SNP Chip and NON Chip records with annotations, as well as all other GFF3 records such as Genes, CDS, Exons and mRNA.

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1-13

GWAS Analysis of resistance of potato to Common Scab using historical phenotypic values

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Common scab, caused by *Streptomyces* spp., is worldwide one of the most important skin blemish diseases in potato, leading to a significant reduction in economic value. Resistant varieties are the most effective way of dealing with this disease. Earlier studies on the genetics of the resistance of this disease resulted in minor-effect QTL.

The first aim of the study was to explore historical phenotypic values on scab resistance available from a vast array of sources, such as scientific literature, breeding companies' booklets, national trials for VCU, webpages, etc. We observed that heritable differences in resistance were rather consistent across different datasets, albeit with exceptions which may hint towards interactions with different pathotypes.

The second aim was a genome wide association analysis (GWAS) to identify any single locus or multiple small-effect QTL that could explain this trait to some degree. GWASpoly was used to carry out the analysis with 281 different varieties for which we had the SNP array genotypic data available. Different GWAS models were tested, naïve, K and K+P for the additive model. Using the most stringent characteristics with the K+P model, we found two new SNPs on the south arm of chromosome *1*.

This study is a contribution to the list of putative alleles that could be involved in the common scab disease resistance.

1-14

QTL discovery for agronomic and quality traits in a panel of diploid potato clones using PotatoMASH amplicon sequencing

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Fixation-Restitution Breeding is an innovative potato breeding approach allowing accumulation and fixation of favourable alleles via self compatible diploids, which are subsequently used to rapidly transfer and fix the traits into tetraploid breeding populations by virtue of the ability to produce unreduced diploid pollen. We genotyped a population of 630 diploid potato clones, from six independent commercial potato breeding programmes, that form the foundational germplasm for this approach. The diploids were phenotyped for 23 traits over three years, and genotyped with PotatoMASH (Potato Multi-allele scanning haplotags), a pooled amplicon-based genotyping-by-sequencing approach based on GT-Seq. PotatoMASH scans allelic variation at 339 loci evenly spread at 1Mb intervals throughout the gene-rich euchromatic portion of the genome and, combined with SMAP software, combines multiple SNPs across each read to generate multi-allelic short-read haplotypes (haplotags) that better reflect the true allelic composition of the locus than the constituent bi-allelic SNPs. We performed Genome-Wide Association Studies (GWAS) for all the traits with the primary SNP set and the SMAP-derived short read haplotags derived from this SNP set and tested their performance in QTL detection. In this study, We found a total of 41 unique QTLs across both marker types. A core of 13 of the QTLs were detected with SNPs and haplotags, 14 were found only using haplotags and 14 QTLs were detected only using the SNPs. We conclude that short-read haplotags can improve QTL discovery in GWAS, but that they should not be used to the exclusion of analyses utilizing the bi-allelic SNP data.

1-15

GBS and SPUD-SPET genotyping for advancing genetics and breeding applications in potato

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Sequence-based genotyping (SBG) has become the preferred approach for high-throughput cost-efficient genotyping as compared to array technologies due to the several advantages it provides. This includes greater flexibility, scalability, and capability to scan polymorphisms without prior knowledge, characteristics of an 'open system' genotyping platform. We are deploying these advance genotyping technologies to mine diverse potato collections for identifying novel alleles affecting key production, agronomic and processing traits including insights on other important aspects of potato biology. Mainly two kinds of high-throughput marker-dense genotyping platforms have been developed viz. non-targeted (genotyping-by-sequencing, GBS) and targeted (Single Primer Enrichment Technology, SPET).

GBS procedure employs methylation-sensitive restriction enzyme for genome complexity reduction and reduced-representation sequencing. Although GBS is a non-targeted genotyping approach, SNPs discovered are largely confined (~90%) to genic or gene-associated regions of the genome demonstrating the utility of the approach developed. Our novel SPUD-SPET targeted genotyping design spans the entire gene-space and includes SNPs detected through whole-exome capture sequencing for all 39k potato genes. SPUD-SPET is scalable and provides a very robust and efficient enrichment system circumvening some of the limitations encountered in non-targeted reduced representation sequencing by combining array-like SNP targeting strategy along with the random sampling of variants of traditional SBG methods.

Performing GWAS (Genome-wide association studies) using SBG and fixed array SNPs demonstrated the effectiveness of marker-dense de novo genotyping platforms in overcoming ascertainment bias and identifying significant marker-trait associations (MTAs) with higher precision and resolution. GWAS also detected QTL 'hotspots' for several traits at previously known as well as newly identified genomic locations. Due to the genome-wide genotyping and de novo SNP discovery performed simultaneously on a large tetraploid panel representing a greater diversity of the cultivated potato gene pool, the identified MTAs are likely to have higher transferability across a wider range of potato germplasm and increased utility for expediting genomics-assisted breeding for the several complex traits studied. Overall, advances in next-generation genotyping technologies have enhanced precision and resolution of genetic studies previously not achievable in potato with the increased ability to saturate any population of interest with thousands of markers without their a priori knowledge providing a much-needed boost for potato research and breeding. GBS and SPUD-SPET approaches have been applied in a range of potato genetic studies and insights from this undertaking will be presented.

1-16

Modelling G x E interaction using unbalanced tetraploid Potato (*Solanum tuberosum* L.) data and pedigree information from Scandinavian and Mediterranean environment.

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Analysis of genotype-by-environment interactions (G x E) is critical for cultivar selection and identifying suitable environments. Various methods measure its effects (G x E) on plant traits. Mixed models using the REML-BLUP procedure with random genotype effects have been suggested as advantageous amongst them. Since they make it possible to obtain precise breeding values (BV); especially when the dataset is unbalanced over time and space. The purpose of this research was to develop a mixed model for G x E interaction using unbalanced data of potato breeding program. Specifically, determine the performance of genotypes in Scandinavian and Mediterranean environments, using a unique dataset and pedigree information and predict new genotypes by borrowing information from other environments modeling the correlation matrix across environments. A set of 13197 potato breeding lines and varieties with phenotypic data spanning 17 years were evaluated across Denmark, Spain and Morocco using a mixed model approach with the pedigree based additive relationship matrix to model covariance among, was fitted to predict genotypic performance of all genotypes in all the environments for yield (YD), tuber size (TS), and scab (SC) disease traits. Cross-validation (CV) analyses were carried out using the 5-fold (CV1) and leave-one-breeding-cycle-out (CV2) approaches. Our study evaluated variance components and heritabilities in potato breeding across different traits and environments. Additive genetic variance and residual variance were substantial contributors to phenotypic variance, notably in YD and TS, but G x E interaction variance played an important role in both characteristics. In contrast, for SC traits, residual and G x E variance were key contributors. Furthermore, moderate heritabilities for YD and TS suggest that genetic factors play a substantial role in determining their phenotypic expression across environments. Conversely, the lower heritabilities for SC traits indicate a greater influence of environmental factors or genetic complexity. CV analyses revealed that modeling G x E significantly improves prediction accuracy under unbalanced data. The predictions were typically good, all the accuracy ratios were > 0.5 for Pearson's correlation. Notably, the accuracy ratios obtained by CV1 was better than CV2. The model presented here can be applied to genotype performance, selection for target environments, and genetic merit prediction.

1-17

In vitro evaluation of host defense peptides for antimicrobial activity and successful introduction in *Solanum tuberosum* for disease resistance engineering

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As global environmental conditions continue to worsen, the need to improve food production becomes evermore important. Despite current plant disease control methods, one-third of the global harvest is lost to disease. The ineffectiveness, costs, and hazards of these techniques warrant the investigation of alternatives. Short cationic proteins of the innate immune system called host defense peptides (HDPs), can allow for long-lived resistance against a broad range of microorganisms without toxicity to mammalian and plant cells. Herein, plant HDPs were investigated *in vitro* for antimicrobial and cytotoxic activities. The most promising candidates were subsequently introduced in *Solanum tuberosum* for disease-resistance engineering. Fungal spores were incubated with various concentrations and combinations of five plant HDPs for 24 h to assess antifungal activity by quantifying germinated spores. Antibacterial activity was assessed by measuring the absorbance (600 nm) of challenged cultures. Cytotoxicity was studied by challenging mesophyll protoplasts and mammalian kidney cells in colorimetric viability assays. Following the introduction of HDP coding sequences into plants by *Agrobacterium*-mediated transformation, successful integration events were identified by PCR analysis, gene copy number was investigated by qPCR and transcription by Northern analysis. Singly, HDPs SM-985, Ib-AMP 1Q, shepherin 1, and P4650 were active against bacterial and/or fungal pathogens. P4650 and BnPRP1 interacted synergistically in combinations with other peptides, decreasing minimum inhibitory concentrations (MICs) by ≤83%. Although P4650 and several combinations were toxic to protoplasts at concentrations of 60-100 µM, no single HDP or combination was toxic to mammalian cells. Three three-peptide combinations inhibited the growth of all tested fungi at 20-50 µM concentrations and bacteria at just 2.5 µM. The combination of SM-985, Ib-AMP 1Q and shepherin 1 was selected for plant transformation because of high antimicrobial activity and complete lack of cytotoxicity. Coding sequences of single peptides and combinations of two were likewise introduced to study the effect of HDP stacking in disease resistance engineering. Transgenic plants will be challenged by pathogens in future research to assess disease susceptibility. This study identifies novel HDPs for engineering disease resistance in crops and contributes to improving food security.

1-18

Gene editing in tetraploid potato to enhance PVY resistance

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Plant scientists have rapidly adapted New Genome editing Tools for crop improvement, to complement traditional breeding approaches. The current technical challenge is to efficiently induce precise and predictable targeted point mutations valuable for crop breeding purposes. Several base editing tools such as the CRISPR/Cas9 system and its derivate Base Editors, have demonstrated their utility in plant breeding. However, such technologies proved their limits with non-predictable mutations introduced, resulting in difficulty in transferring known mutations between cultivars or species. New technologies of precise base editing currently in development such as the Prime Editing, support the possibility to obtain expected DNA substitution in different species, without having to characterize large populations of mutants. In combination, new varieties can be created without requesting bacterial DNA insertion, with established protoplast transfection and regeneration protocols. In this lecture, the objective will be to explain the application of genome editing tools to transfer well-characterized mutations involved in PVY resistance, isolated from diploid *Solanaceae* such as pepper and tomato, to the tetraploid potato. A presentation of the application of the different generations of genome editing tools and their results on plants will be introduced and the advantages and disadvantages of each of them will be pointed out.

1-19

PMR4 is a susceptibility gene for soft rot disease in potato

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Bacterial soft rot affects a large number of economically important plant species, and is characterized by the breakdown of plant tissue into a soft, watery mass. In potato, soft rot is predominantly caused by *Pectobacteriaceae* bacteria including *Pectobacterium* and *Dickeya* species. Infections can lead to significant losses in storage and during cropping in downgrading and rejection of seed lots due to blackleg. In order to diminish the susceptibility to soft rot diseases, we set out to identify and eliminate susceptibility (*S*) genes. Seventeen *S* genes from *Arabidopsis* were selected for targeting the potato orthologs via RNAi in transgenic Desiree. Plants in which *Powdery Mildew Resistance 4* (*PMR4*) was targeted, showed strongly reduced lesions in leaves upon inoculation with *Pectobacterium* and *Dickeya* species. This suggested that potato *PMR4* could serve as a *S* gene in potato. To confirm this hypothesis, we generated *PMR4* CRISPR/Cas9 mutants in potato variety Desiree. After sequencing of transformants, we identified different mutant alleles in the different events. One of the mutants with large deletions in all four alleles showed reduced lesion size as compared to non-transgenic Desiree after leaf inoculation. Also, after stem inoculation, smaller lesions were observed. After root inoculation, a delay in colonization was found. In addition, we found a 2.5 fold induced expression of *Pathogenesis Related Protein 1* (*PR1*) in the leaves of the mutant, and 2 fold in stems, suggesting a role of SA-induced resistance in the reduced susceptibility. It is concluded that *PMR4* functions as a susceptibility gene for soft rot disease in potato. Our future investigations aim to uncover allelic variation in *PMR4* to identify breeding material for soft rot resistance.

1-20

Identification of duplicates in Nordic potato collections

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The potato arrived in the Nordic countries approximately 300 years ago and subsequently became a staple food in the region. In the early 1980s organized conservation efforts for potato genetic resources were initiated within the Nordic countries. Today potato landraces, improved varieties, and breeding lines cultivated in the Nordic region are conserved in genebanks at the Nordic Genetic Resource Center (NordGen) in Alnarp, Sweden, and the Norwegian Genetic Resource Centre (NGS) in Norway. Furthermore, potato breeding companies in Denmark, Norway, and Sweden maintain collections of potato germplasm for their own breeding purposes. All these collections contain a substantial number of potato genotypes associated with diverse local names and cultivation histories. However, the presence of duplicates and varied names has occasionally resulted in confusion. Morphological identification alone was found to be insufficient, prompting the use of molecular fingerprinting methods as a more reliable tool for identifying duplicates within and across potato collections. In this study, 198 cultivated potato (*Solanum tuberosum* L.) accessions were genotyped using 62 microsatellite markers.

The analyzed accessions come from three collections: 43 from the Danish Potato Breeding Foundation in Vandel (LKF-Vandel), 90 from NordGen, and 65 from NGS. The molecular fingerprinting unveiled the presence of 31 duplicate groups within the examined material, with the most extensive group comprising ten accessions bearing distinct names. Accessions from all three collections were included in this group. The results indicate that certain accessions with different names are the same genotype, suggesting widespread distribution across the entire Nordic region and subsequent local naming over the years. Additionally, the study identified cases where improved varieties from early potato breeding efforts in other countries were mistakenly considered Nordic landraces. The study also confirmed that accessions in different collections sharing the same name, indeed corresponded to the same genotype. The results will be used to improve the management practices for potato collections at both NordGen and NGS. The newfound knowledge will be useful for potato breeding, as well as enable the dissemination of more accurate information to users of the collections and other stakeholders interested in potato diversity.

1-21

Variance and covariance components of agronomic and quality traits assessed in tetraploid potato and implications on practical breeding

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Potato is a versatile food crop and major component of human nutrition worldwide. Model calculations and computer simulations can be used to optimize the resource allocation in potato breeding programs. For such approaches, quantitative genetic parameters are needed. The objectives of our study are to (i) estimate quantitative genetic parameters of the most important phenotypic traits in potato breeding programs, (ii) compare the importance of inter- vs. intra- population variance, and (iii) quantify genotypic and phenotypic covariances among phenotypic characters. Here, variance components of 26 potato traits were assessed using linear mixed model approaches, and the genotypic and phenotypic correlations between these traits were calculated using 1066 clones from three breeding companies. The examined traits showed an overall high to medium heritability, and variance analysis revealed trait-specific differences in the influence of the genotypic, environmental, and genotype-environment interaction effect. Accounting for heterogeneity in the residual variances between the 15 environments led to an improvement of the variance parameter estimation. An important choice to be made by breeders is the number of crosses vs. the size of individual crosses, when the total number of progenies is limited. Therefore, segregation variance was estimated, which showed high trait specific differences for the amount of inter- vs. intra-population variance. The herein presented results can be used as base for further simulation studies and, thus, help to optimize the resource allocation in breeding programs.

1-22

Potato genetic resources at CGN

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The Centre for Genetic Resources the Netherlands (CGN) is the Dutch genebank focusing on preserving genetic resources of crops, farm animal breeds, autochthonous trees and aquaculture species. CGN plant genetic resources maintains more than 23.000 accessions from 31 crops, with a focus on vegetables. Since 2022 it receives additional funding from the Ministry of Agriculture to expand its current collections.

CGN's potato collection consists of almost 1500 potato samples, stored as botanical seeds. This includes 15% Andean cultivars (landraces) and 85% wild species: 113 species according the taxonomy of Hawkes, which would be reduced to 73 species when using GRINTAX. The germplasm originates from twelve countries in mainly South America, gathered between 1930-1998 during several collecting missions. The collection at CGN does not contain any clonal material like for instance heritage or modern cultivars.

The germplasm is available for research, breeding and educational purposes. Access is facilitated through a webpage, in which signing an SMTA agreement under the ITPGRFA's Multilateral System is obligatory for receiving the germplasm. The wild potato species can contain important traits such as tolerances or resistances against pests and diseases. Evaluation data on the accessions can be downloaded for 25 traits or searched online. The available traits include e.g. nematodes, late blight, wart and Erwinia, but the evaluation results are far from complete, so unfortunately large gaps exist. Users are encouraged to share their results with CGN.

Phytosanitary measurements are required by EU Directives to prevent the spread of new potato pathogens from South America into the European Union. After phytosanitary checks by the NVWA (Netherlands Food and Consumer Product Safety Authority), true seed multiplications are carried out by several Dutch potato breeding companies. Challenges such as genetic bottlenecks or inadequate seed production from wild accessions can complicate propagation efforts. Still, most propagations are successful, ensuring availability of potato genetic resources for current users and next generations to come.

Homepage CGN-plant:
https://www.wur.eu/cgn/pgr

2-01

Using the CRISPR-Cas system to localize plant viruses

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The CRISPR-Cas system is a powerful tool that enables simple and easy gene editing of plants. This system is based on the Cas9 protein, which enables modification of the DNA. Nevertheless, other Cas proteins are available that target RNA instead, such as the Cas13 proteins. In my laboratory, we have developed a protoplast-based system, that allows intracellular localization of viral RNA. This system is based on Cas13 proteins fused to fluorescent markers that allow visual localization of the targeted RNA using a simple fluorescent microscope or a more advanced confocal microscope. Intracellular localization of viral RNA can be useful to determine if plants are truly resistant to viruses (i.e. no replication of the viral RNA), determine the site of viral replication and to understand the life cycle of the virus. The system we have developed is based on the model plant *Nicotiana benthamiana*, which is a close relative of potato and one of the most widely used plants to study potato-infecting viruses.

2-02

Occurrence of tobacco rattle virus and its trichodorid vectors on four locations in Norway

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Potato (*Solanum tuberosum*) is an important agricultural crop in Norway. The crop is susceptible to a variety of plant viruses, which could lead to loss of quality and reduction of yield. Corky ringspots caused by tobacco rattle virus (TRV) make the tubers less appealing to the consumer. The aim of this study was to study occurrence of tobacco rattle virus (TRV) and its associated vectors in Norway.

To conduct a comprehensive investigation, soil samples were collected from four distinct locations, namely Lyngdal, Klepp, Bodø and Våler (Innlandet county). These samples have been divided into three each and underwent the following testing process: First, bait plants were used to capture the virus from nematodes that feed on plant roots. Subsequently, the roots were tested by a bioassay using inoculation to test plants, followed by molecular testing for TRV by RT-PCR and Sanger sequencing. Second, nematode extraction was conducted using a Seinhorst elutriator, with the extracted nematodes subjected to measurement and classification. At last, a portion of the soil was dried to explore the potential seed transmission of TRV in different weed species.

The use of bait plants proved to be a successful strategy, as TRV was effectively isolated from the roots of bait plants grown in soil from all locations. The isolates were obtained by sap inoculation from bait plant roots to *Chenopodium quinoa*. RT-PCR, utilizing TRV-specific primers, confirmed that the observed local lesions were indeed a result of TRV infection. Sanger sequencing results further demonstrated that isolates from the four locations exhibited close genetic relatedness. These findings strongly suggest that nematodes in the soil samples served as vectors, transmitting TRV to bait plants during the feeding process.

The extraction of nematodes revealed different nematode genera and quantities of nematodes across the four locations. Notably, *Paratrichodorus pachydermus,* a member of Trichodoridae family known to vector *Tobraviruses*, was identified consistently in all locations. Interestingly, the examination of dried soil ruled out the possibility of seed transmission of TRV in weed seedlings germinating from the samples in our study.

In summary, this study has substantiated the presence of TRV and its nematode vector, *P. pachydermus*, in all four locations studies. Consequently, the research contributes significantly to our understanding of the occurrence of TRV and and trichodorid nematodes in Norway.

2-03

Tobacco Rattle Virus and Trichodoridae: building blocks of a systemic and sustainable approach to disease control

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Tobacco rattle virus (TRV) is widespread in many countries around the world and is transmitted by root-feeding trichodorid nematodes (Trichodorus spp. and Paratrichodorus spp.), and in some plant species is also spread by infected seeds. In potato TRV is causal agent of “spraing” disease, also known as “corky ring spot” (CRS), which is characterized by necrotic rings in the tuber flesh and affects the marketability and value of potato seed lots. This is a relevant problem for the potato processing industry that demands a minimum of damage in the tubers.

Restriction in the use of current synthetical nematicides and active farming on sandy soils is increasing the spread of both virus and vector, which translates in increasing economic importance of this disease. Following the call for a sustainable and resilient agriculture (FAO Sustainable Development Goals) we have started a multidisciplinary non-chemical approach for this disease management.
The approach is based on Integrated Crop Management (ICM), which includes the choice and order of crops in the rotation, the availability of resilient crops, soil management, monitoring and targeted control. We focus on four building blocks: 1) Breeding for new potato cultivars that are fully resistant to TRV; 2) Breeding for resistance to TRV in green manure crops; 3) Knowledge of the host plant status for trichodorid nematodes and TRV and 4) Implementation into the farmer’s practice. This will decrease dependency on and emission of synthetic crop protection agents.

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2-04

Dynamics of potato virus Y infection pressure and strain composition in State of Colorado, USA

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The San Luis Valley (SLV), Colorado, is the second-largest fresh potato growing region in the United States, which accounts for about 95% of the total production in Colorado. Potato virus Y (PVY) is the leading cause of seed potato rejection in the SLV, which has caused a constant decline in seed potato production over the past two decades. To help potato growers control PVY, we monitored the dynamics of PVY infection pressure over the growing seasons of 2022 and 2023 (May through August) using tobacco bait plants exposed to field infection weekly. PVY infection dynamics were slightly different between the two seasons, but July and August had the highest infection in both years. The first PVY infection was detected in the second half of June which coincides with the emergence of potato crops in the valley. PVY infection increased toward the beginning of August and then declined toward the end of the season. Three PVY strains were identified in tobacco bait plants and potato fields, namely, PVY^{O}, $PVY^{N\text{-}Wi}$ and PVY^{NTN}. Unlike other producing areas of the United States, PVY^{O} is still the major strain infecting potato crops in Colorado comprising ~40% of total PVY strain composition. This could be explained by the prevalence of the potato cultivar Russet Norkotah, that lacks any identified *N* genes, including the Ny_{tbr} that controls PVY^{O}, which imposes no negative selection against this strain. The current study demonstrated the usefulness of bait plants to understand PVY epidemiology and develop more targeted control practices of PVY.

2-05

Evolution of the prevalence of potato virus Y (PVY) and potato leafroll virus (PLRV) in Switzerland between 2016 and 2023

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Potato virus Y (PVY) and Potato leafroll virus (PLRV) are the two most damaging viruses for the seed potatoes production. They lead to significant yield losses and have a major economic impact worldwide. Numerous species of aphids transmit these viruses respectively in a nonpersistent and in a persistent manner. PVY and PLRV are monitored each year in the fields and in the laboratory during the seed potatoes certification process to guarantee the sanitary quality of seed potatoes and to limit virus spread. These data allowed to assess the prevalence of these two viruses in Switzerland over the last eight years.

Since 2016, and each year, 250’000 tubers are collected out of 1’000 lots, with an average of 200 tubers per lot. Then, qRT-PCR are performed on the tuber samples to detect the presence of PVY and PLRV.

The data indicate that, since 2016, PVY infections increased in Switzerland. The lowest prevalence of PVY was observed in 2016 for 28% of the lots, although the highest prevalence was observed in 2020 for 61% of the lots. PLRV infections also increased since 2016. Only 9% of the lots were infected by PLRV in 2016, and a maximum of 30% of the lots were infected in 2020. Mixed infections with PVY and PLRV are relatively low and also increased since 2016. They affected only 2% of the lots in 2016 and a maximum of 21% of the lots in 2020. Moreover, the rejected area of seed potatoes increased since 2016, with a minimum of 1 ha rejected in 2016 and a maximum of 110 ha rejected in 2023.

Given the increasing prevalence of PVY and PLRV, which could rise further in the context of climate change, improved protection and new control strategies must be developed to limit viral infections.

2-06

Mineral oil to control *Potato virus Y* transmission in seed potato production

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Mineral oil is the main alternative treatment identified to limit the spread of *Potato Y virus* (PVY) in seed potato production, this plant protection product is a part of the biocontrol list according to the French plant health authorities. Because there are currently no exact recommendations for its use, the mineral oil is commonly spread by farmers on potato plants every 2–3 days during the active plant growth and every 7 days when the vegetation is stabilized.

Our main objective is to better understand the duration of the oil protection and understand which fraction of oil was involved in the protection against the virus transmission by the vector.

High resolution mass spectrometry using an electrospray ionization source (ESI-HRMS) was selected to detect the mineral oil with a high sensitivity and an experimental protocol was developed to distinguish the fraction of oil which penetrates the leaf from the surface fractions.

The results of kinetic study demonstrated that oil persists on treated leaves surface after 7 days. The relationship between this persistence and the oil ability to protect the leaves against virus transmission by aphids will be discussed. The aim of this work is to give recommendations to farmers with regard to the frequency of applications for optimal performance against virus transmission.

2-07

Potato & the French post-entry quarantine station

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The ANSES Quarantine Unit (QU) holds the national reference mandates regarding potato quarantine viruses, citrus quarantine viruses and plum pox virus. These mandates ensure the proper operation of the official analysis system which serves to guarantee plant health safety in France. QU is also involved in plant pest surveillance in the national territory and hosts the only French post-entry quarantine station which is an official, multi-species and public station. Over a recent period (09/2021-10/2023), 4 public bodies and 13 private companies (French and other European establishments) have benefited from the French quarantine system to introduce diverse plant genetic resources into the European Union (EU).

According to Regulation (EU) 2016/2031, the introduction into the European territory of plants of potato and other stolon/tuber-forming *Solanum spp.* is prohibited. However, the EU legislation provides for conditions under which they may be introduced for testing, research or varietal selection purposes. To this end, QU receives every year potato samples/varieties for the implementation of a quarantine scheme, adapted to the EU and French regulations, and including analyses targeting regulated quarantine pests. QU relies on its qualified staff, level security 2/3 containment facilities, pest conservatories and scientific and technical partnerships to carry out cultivation operations, sanitary monitoring, biological indexing and laboratory analyses (ELISA, PCR and more recently high-throughput sequencing (HTS)). QU's ISO/IEC 17025 accreditation guarantees the quality of its analyses reports. It notably includes the detection of all *S. tuberosum* viruses by ELISA and of *Xylella fastidiosa* by rt-PCR.

Samples already received belong in particular to the following species: *Solanum alandiae*, *S. albicans*, *S. chacoense*, *S. chaucha*, *S. demissum*, *S. fendleri*, *S. oplocense*, *S. polyadenium*, *S. polytrichon*, *S. trifidum*, *S. tuberosum* and *S. stoloniferum*. The vast majority of these samples were released to their owners (as vitroplants) at the end of the quarantine period. Nevertheless, the French quarantine station acts as a sanitary filter and has already been responsible for the interception of potato pests, notably viruses such as APLV, APMoV, PBRSV, PLRV, PVA, PVM, PVS, PVY, PVX, PYV, TRV, TRSV and TSWV.

Find out more about our activities by visiting our poster and by viewing our service offer via this link: https://www.anses.fr/fr/system/files/Offre_LSV_Clermont.pdf.

2-08

Evaluation of a cryopreservation method for virus elimination in potato

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The BrACySol BRC maintains and characterizes genetic resources of different crop species that are economically important at the national and international level, including tuber-bearing *Solanum* species (potato and related species).

The *Solanum* collection contains around 12 000 accessions, composed of wild species originating from South America, potato varieties representing worldwide diversity, and scientific material harboring traits of interest like resistance to different pathogens or tuber quality traits. These accessions are maintained by vegetative propagation in the form of tubers planted each year in fields or greenhouses, of *in vitro* plantlets or of cryopreserved shoot tips. Even if different measures are applied during the growing season to avoid pathogen development, vegetative multiplication favors in particular viral dissemination. About 3% of this collection is infected by one or a mixture of viruses. This work aims at assessing if the cryopreservation method that is used routinely in the BrACySol BRC may efficiently eliminate the main viruses that are present in the genetic resources of the BRC.

This study was performed on 18 clones infected with one of the 5 following viruses : PVY, PVX, PVS, PVA or PVM. The cryopreservation method used is a PVS2-droplet-vitrification method (Kim et al, 2006). The average survival and recovery rates obtained for *Solanum tuberosum* accessions are 98% and 89% respectively.

Three different treatments were tested: 1. the complete cryopreservation method, 2. all the steps of the cryopreservation process except immersion in liquid nitrogen, 3. shoot tip isolation only. The experiment was carried out on 30 shoot tips for each treatment and each clone. Two ELISA tests were then performed: first on the *in vitro* plantlets recovered from the shoot tips after applying the different treatments, then on the same plantlets that were afterward grown in a greenhouse if they were negative at the first test. To confirm the results, a third test is planned on these plants after they have produced tubers.

We obtained virus-free plants from 17 of the 18 tested clones. The efficiency of virus elimination depends on the virus tested. The complete process is needed to eliminate some virus, whereas shoot tip isolation only allowed to obtain virus-free plants for others. The results obtained will be presented in this poster.

Kim et al, 2006, Cryoletters, 27, 4, 223-234

2-09

7-hydroxytropolone and analogs to control potato blackleg

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Blackleg affects seed potato growers by reducing tuber yield and quality. For this disease caused by several Soft Rot Pectobacteriaceae (SRP), there is no pesticide commercially available in Europe to control the infection. A previous study described the potential antagonistic effect of 6 bacteria against *Dickeya solani* and other SRP (Cigna et al., 2023). Among these antagonists, *Pseudomonas* PA14H7 was evaluated as having the broadest spectrum of activity. We have shown that this activity was correlated to the production of 7-hydroxytropolone (7-HT) (Munier-Lépinay et al., 2023). In this study, we demonstrate that this activity is due to the ability of 7-HT to chelate iron. Unfortunately 7-HT is not commercially available and its obtention requires environmentally unfriendly synthesis and is time-consuming. In order to develop a biocontrol tool against potato blackleg, a screening of potential analogs of 7-HT easily accessible was conducted. The search for alternative molecules was based on analogs having the same elemental composition as 7-HT ($C_7H_6O_3$) and bearing functional groups able to chelate iron, such as catechol, phenol or carboxylic acid. Among the potential commercially available molecules, we selected those able to complex iron, as confirmed by LC-MS analyses. Then, biological tests were conducted to compare their activity against *Dickeya solani* versus the 7-HT one. Among the chosen analogs, two of them have shown promising results.

2-10

Potato soft rot – as an economically important disease for Georgia

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The control of strategic crop diseases remains one of the topical problems worldwide, especially when the disease is widespread and causes significant economic losses. Potato is an important food crop in Georgia. It has a main agricultural value especially for farmers in mountainous regions. In recent years, a significant spread of potato bacteriosis in Georgia has been observed. This is caused by introducing the infected planting material into the country, climate changes favorable for the overwintering of bacterial pathogens and their vectors and by the lack of effective control measures. The lack of awareness about the diversity of these pathogens often makes it impossible to choose the right strategy for selecting protective measures. Potato soft rot was first detected in 2008 in Georgia, Akhalkalaki region. The research conducted in 2019–2022 has revealed the high incidence of potato soft rot in many agro-ecological potato growing zones: upper Adjara (Khulo municipality), Samtskhe-Javakheti (Akhaltsikhe and Akhalkalaki municipalities), Kvemo Kartli (Marneuli, Dmanisi municipalities) and Kolkheti lowland (Kobuleti municipality). The infected samples were collected from potato fields and warehouses. As a result of microbiological, biochemical and molecular analysis, sixty-eight isolates were identified as *Pectobacterium* spp. and *Dickeya* spp. among them, thirty-two isolates belonged to the species *Dickeya solani*. Survey of potato fields reveled that the soft rot of potatoes turned out to be an important obstacle to the potato harvest.

To isolate and study the main properties of phages active against *Pectobacterium* spp. and *Dickeya solani,* thirty-six enriched samples, including thirty soil samples and six water samples, were prepared and screened for ten test strains. Thirteen bacteriophages with an overlapping spectrum were saved for further research, which allows the creation of a phage drug active against the target bacterial strains.

This research is being continue within grant #FR-21-1778 of Shota Rustaveli National Science Foundation of Georgia (SRNSFG).

2-11

Detection of *Ralstonia solanacearum* in different environmental samples

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Quarantine bacteria *Ralstonia solanacearum* (Rs) (Smith) Yabuuchi et al., the causal agent of potato brown rot, is one of the most troublesome pathogens of potatoes. Because of its pathogenicity, the bacteria pose a serious phytosanitary risk to the European and Mediterranean Plant Protection Organization (EPPO) region.

One of the greatest dangers in the uncontrolled spread of the pathogen is the asymptomatic (latent) form of the disease, often associated with low cell concentration in potato tissue, increased tolerance of potato varieties to the presence of bacteria in the infected tissue, as well as the varied degree of virulence of strains infecting potato tissue. The occurrence and severity of disease symptoms depend on many factors, such as the number and virulence of bacterial cells, the plant species/variety, the type of infected tissue, as well as the existing environmental conditions. These factors cause a relatively high risk of uncontrolled spread of these bacteria in the environment.

In the absence of effective methods of direct control in potato tissues, the most effective way to protect against the spread of *R. solanacearum* is by planting healthy seed material and applying hygiene throughout the entire potato production and storage process. In both cases, reliable diagnostics are necessary to confirm the phytosanitary purity of the seed potato material and the place of production. Since the effectiveness of the diagnostic methods recommended by EPPO for monitoring the health of potatoes is largely dependent on the presence of various types of contaminants in the tested environmental samples, the EPPO PM 7/21 standards (3) require the use of appropriate diagnostic methods to verify the obtained result.

To improve the diagnosis of *R. solanacearum* in environmental samples, our team in this work evaluated different methods for isolating these bacteria in the presence of components of various environmental samples. The presented solutions allow not only to improvement of the effectiveness of currently used tests but also to development of new and simple methods aimed at minimizing the risk of uncontrolled spread of this quarantine pathogen in the environment.

3-01

Biofumigation with sorghum and brown mustard: a sustainable solution to control wireworm damage in Swiss potato production

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Wireworms pose a growing threat to potato cultivation. In Switzerland, reports from farmers highlight the severe impact of wireworm tuber drilling, often resulting in dramatic or complete harvest losses. The economic costs for the Swiss potato market are substantial, estimated at several thousand euros annually. Alarmingly, this trend is not unique to Switzerland, as wireworm infestations are increasing across Europe following the setback of fipronil, a previously relied-upon pesticide. Despite the urgency of the issue, there is a notable absence of direct means to control wireworm infestations in Swiss agriculture. Our research investigates the potential of biofumigation as a sustainable strategy to mitigate wireworm damage in potato production. Biofumigation is an agricultural technique where specific crops like brassicas or sorghum are shredded and incorporated into the soil. These plants release biocidal compounds that suppress soil pests and pathogens. In summer 2023, we set up a field experiment to test the effect of biofumigated brown mustard and sorghum on wireworm damage in the following potato crop. We first surveyed the wireworm populations of our experimental site. We captured 198 wireworms, and were able to determine that 92% of individuals belonged to the *Agriotes sputator* species. Brown mustard and sorghum were sown, before being shred and integrated into the soil 10 weeks later. Both crops were sampled at 7 and 10 weeks after sowing (+7 and +10WAS) for the assessment of biomass production, and dhurrin or glucosinolates content, in stems and leaves separately. Sorghum total biomass was 3.93 times higher at +10WAS, but dhurrin content per surface was almost two times higher at +7WAS. This was due to higher dhurrin concentration in leaves, which also made up a higher percentage of the aboveground biomass. In brown mustard, aboveground biomass was only 5.6% higher at the second timepoint and stem and leaf glucosinolates concentrations were respectively 234% and 127% higher at +7WAS which corresponded to full bloom of the plants. These results allow to unfold the trade-out between biomass and biocidal molecules concentration in field conditions. In addition, the monitoring of these molecules in plant leaves and stems permits to adjust the ideal time of shredding and burrowing. By harnessing the natural bioactive compounds present in these crops, our research offers a promising avenue for sustainable wireworm management.

3-02

Trial results on wireworm control in potatoes using chemical, biological and arable methods

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According to our observations, the damage caused by the larvae (wireworm) of the *Agriotes* spp. is steadily increasing in agricultural practice, especially in maize and potatoes. Scientific studies have shown that soils with a large supply of organic matter, such as peat soils, set-aside soils, mineral soils after several years of forage cultivation or after ploughing up grassland, generally have a higher wireworm population in the soil. However, according to our observations, the trend towards reduced tillage and the increased cultivation of catch crops, which has been recognisable in recent years, also promotes the survival rate of egg clutches and young larvae in the soil and thus the number of wireworm larvae in arable soils. In addition, climate change contributes significantly to an increase in wireworm damage. One reason for this is that the larvae in the soil no longer go through a 4 to 5-year development cycle but only need 2 to 4 years from egg to beetle. On the other hand, wireworm species that are actually native to southern Europe and only have a 1- to 2-year development cycle are becoming increasingly common in Germany. In both cases, the pest reproduces much faster and the damage increases as a result.

Extensive field trials have been carried out in Bavaria for several years with the aim of developing a practical solution to the wireworm problem for the arable farmers affected. As it will be very difficult to obtain registration for chemically synthesised plant protection products in Germany, we are focusing our research work on biological and arable approaches to reducing wireworm damage. For example, we have been carrying out trials with entomopathogenic fungi such as *Beauveria bassiana* and *Metarhizium* spp. for several years. According to the results of our trials to date, this approach to controlling wireworms is also a viable option in maize. However, in order to find its way into widespread agricultural practice, its efficacy must be further improved.

According to our scientific work, a promising and easy-to-implement measure to reduce wireworm damage in practice is to mechanically tillage the crop stubble four times (4-8 days apart in dry conditions) within the first four weeks after harvest. This dries out the soil in the top layer and with it the egg clutches and the still early larval stages of the pest. In our field trials, this measure reduced the damage caused by the wireworm in potatoes is reduced 62 %. Even with the best chemical-synthetic agents, this level of control success has hardly been achieved in the past. The sowing of a cover crop following the four-time mechanical cultivation of the cereal stubble did not result in an increase in wireworm damage to potatoes.

3-03

Management tools to reduce wireworm damage in potatoes in Canada

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The cryptic nature of wireworm larvae, combined with its wide host range and scarcity of efficacious insecticides makes control of this pest exceedingly difficult. Potatoes are the important economic crop and severe wireworm damage can potentially cause million in losses or even crop failure. In Prince Edward Island, a province of Canada, tuber losses due to wireworms reached seven million in 2013. *Agriotes Sputator* was identified as the main species causing damage. Because of the lack of viable control options we embarked on a research project from 2008 to 2010 to study the use of rotation crops, brown mustard (*Brassica Juncea* var. Duchess), buckwheat (*Fagopyrum esculentum* var. Mancan) and Alfalfa (*Medicago sativa* var. AC Brador); each crop grown for two years in a heavily infested fields prior to a potato crop; Barley (*Hordeum vulgare* var Chapais) was grown as the standard crop for comparison. The study was conducted on three different commercial fields. Results showed an 80% reduction in tuber damage and an increase in marketable tuber yield following brown mustard and buckwheat crop when compared with alfalfa and barley crop. In this trial two crop were planted per year for two years with the first crop plowed down as green manure. However, subsequent studies showed that planting these crops for one year prior to potatoes was sufficient to reduce tuber damage. Adoption of this strategy was slow at first but increasing wireworm pressure and movement into new uninfected area, resulted in the widespread adoption of these two rotation crops. As more farmers adopted this practice reported incidence of damage started to decrease in fields planted with these crops. To track the efficacy of control strategies and infestation into new areas, in 2009, we began to survey populations every 3-4 years in eighty-five fields across the island using pheromone traps. Results showed a population increase during the initial years (2009-2016) which reached record levels in 2016. A gradual decline in populations was noted between 2019 to 2022. The adoption and planting of rotation crops brown mustard or buckwheat prior to potatoes began in 2015 and was the main strategy used to reduce populations over this time span. Our survey results showed a 50% decrease in click beetle numbers in 2022 in all regions of the province when compared to 2016 numbers, we also noted a decrease in number of heavily infested fields. Detailed research results will be presented and discussed.

3-04

Horizontal and vertical movement of wireworms, *Agriotes sputator* (Coleoptera: Elateridae) through soil in Canada

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The larvae of the click beetles (Coleoptera: Elateridae), wireworms, are identified as a major pest of potatoes and other vegetable crops worldwide. A steady increase in the population of an invasive species *Agriotes sputator* in Prince Edward Island (PEI), Canada, resulted in its spread into un-infested crop land. Severe winters conditions in Canada requires elaterid species to enter diapause during this unfavourable period. In Quebec, elaterid larvae were found to overwinter below the frost line during the winter months. However, information on the timing of wireworm movement within the soil profile is required to ascertain the correct time for installing bait traps to monitor populations. We investigated the horizontal and vertical movement of the wireworms in the soil. Studies have shown that wireworms responded to soil moisture by moving lower down in the soil profile during the summer months. But there was a dearth of information on the wireworm's response to bait traps and time spent at a food source. Using 5cm diameter tubes, we studied the time required and distance traversed by a wireworm, through the top layers of the soil, towards a food source and time spent feeding. Results show that 15 and 20% of medium and large size wireworms respectively moved a distance 3.6m in 24 hours to find a food source. Results also show that if a food source is found some wireworms will feed for a short duration before moving in search of another food source. This information is critical for determining the time required from bait instillation to removal to obtain an accurate representation of the population. To study vertical movement, 5cm diameter tubes were used to take soil cores to a depth of 80cm. Wireworms 10/tube were placed at the top of the tube and the bottom was sealed with mesh cloth to prevent wireworms from escaping. Each tube was reinstalled into the same location where the core was collected. Once a month from November to June, tubes were removed and the number of wireworms at different depths was recorded. Results show that wireworms can move down to a depth of 80cm in the spoil profile. We found that the majority of wireworms spend the winter months at a depth just below the frost line until April when they begin to move up as the soil temperature rises. All wireworms were at the surface by end of May – beginning of June.

3-05

Weeds control in potatoes under agro-climatic conditions of Barsa Country, Romania

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Potato (*Solanum tuberosum*) is one of the most intensive field crops, which requires permanent care. Weed control is considered to be an important factor for successful yield. The number of registered herbicides has been limited and in most cases their efficacy greatly depends on precipitation. It is important to conduct location specific experiments on weed management because the efficiency of a given chemical is limited only to controlling certain weed species and it can vary with the weed density, time of weed emergence, cropping system and the environmental conditions under which the crop is grown. The present study was carried out in 2022–2023 to National Institute for Research and Development for Potato and Sugar Beet Brasov and to a farmer in Codlea, Romania. The experiment was laid out in randomized complete block design with four replications. The study determined the degree of damage to crops and weeds, fresh and dry weight of weeds, their number and floristic composition. Two factors were tested: factor I – potato varieties: Brasovia variety to NIRDPSB Brasov and Ultra variety to Codlea; factor II – four different combination of herbicides to control weeds + the untreated plot (V1: Control; V2: metribuzin; V3: metribuzin + metribuzin fractional doses; V4: aclonifen + metribuzin; V5: aclonifen). In the period of examination were registered a predominant number of 6 weed species *(*Green foxtail, Lamb's quarters, Redroot pigweed, Field bindweed, Birdeye speedwell, Cleavers*)*. The measurement of weeds was made by using a metric frame (4 x 0.25 m2 quadrats), recording the number of weeds per square meter. The result from the control variant (V1) represents the first level of infestation, while the results from the variants V2-V4 represent the effects of the used herbicides. Metribuzim applied fractional or in combination with aclonifen gave very good control of broadleaf weeds and the highest marketable potato yields. Chemical weed control has proven high efficiency in reducing the number and biomass of weeds.

3-06

Importance of soilborne inoculum of *Colletotrichum coccodes* and assessment of potato cultivar resistance to black dot in France

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Black dot, caused by *Colletotrichum coccodes*, is a tuber blemish and foliar disease of potato which is one of the most important diseases affecting pre-packing potatoes in France. The disease is characterized by presence of black microsclerotia on the tuber surface which can also be found on stolons, roots and stems both above and below ground. Microsclerotia of the pathogen, which has a wide host range, are released in the soil and can survive at least 8 years and act as an effective source of inoculum. Disease management can be effective by using resistant varieties for many pathogens. Nevertheless, very few data are available in France about cultivar susceptibility for black dot and the assessment is complicated by soil inoculum heterogeneity.

In this study, we characterized the susceptibility of 12 French potato cultivars over three years in dedicated trials and conducted a one-year survey across 93 fields. A real-time PCR was developed to quantify levels of soilborne and seedborne inoculums to take account the interaction between cultivars resistance, inoculum density and technical factors such as fungicide applications in fields survey. After harvest, tubers were washed and assessed visually for black dot incidence and severity. Additionally, qPCR analysis were performed on a sub-sample of 20 tubers per repetition and per cultivar for specific trials and for commercial fields.

The results showed significant and consistent differences between cultivar's susceptibility even if no cultivars were totally resistant to black dot. The use of qPCR methods to quantify soilborne and seedborne inoculums is beneficial to avoid bias due to inoculum heterogeneity. We also showed a good correlation between visual assessments and qPCR method. The adoption of this protocol could enhance the systematic evaluation of French commercial potato cultivars. Given the widespread presence of black dot in French soils (more than 95% of surveyed fields) and, to some extent, the correlation between disease severity inoculum, soil inoculum and agronomic factors, control strategies will be discussed.

3-07

Optimizing Fungicide Timing for Effective Management of *Colletotrichum coccodes* in Potatoes

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Colletotrichum coccodes, the causal agent of black dot, is an economically important pathogen of potato causing stem blights and tuber blemishes, which the latter is primarily an issue in storage. Tuber infection is typically characterized by barely visible small black spots and dark sooty lesions, which can lead to rejection of the crop by processors, supermarkets, and consumers. Although stem blight symptoms usually occur late in the season or after vine kill, infection is thought to occur early in the growing season. To investigate the optimal timings for management of black dot randomized complete block fungicide spray trials were carried out over 2 years from 2021–2022 with several different fungicides. Disease incidence and severity on stems was rated towards the end of the growing season using qPCR, and tuber black dot was rated after harvest using qPCR. Results showed that the optimal timing for fungicide applications was when plants were 15–20 cm tall. Finally, to determine when tubers are the most susceptible to *C. coccodes* infection*,* tubers were inoculated at different times before and after skin set and visually rated for disease one-week post-inoculation. Results demonstrated that tubers were the most susceptible before skin set. Results from these studies increase our understanding of the epidemiology of black dot and may be useful for future disease management.

3-08

Potato black dot caused by *Colletotrichum coccodes* in Inner Mongolia of China

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Potato black dot became an increasingly severe disease in Inner Mongolia, mainly infecting tubers, causing silvery to brown lesions on tuber skin with poorly defined margins and forming black sclerotia later as a sign of skin blemish diseases which significantly affected the yield and fresh market. Pathogens isolated from symptomatic tubers were identified as *Colletotrichum coccodes* by morphological and molecular identification. The occurrence rate of this disease companied with the fruiting phase of potato was 30~35% in Harqin and Dalate counties of Inner Mongolia by field investigations. Tubers showing silver or brown scurf and black dot on skin were consistent with symptomatic samples collecting from the field in pathogenicity test. The colony was initial white mycelia and later developed with numerous rounded dark sclerotia by ring arrangement in vitro culture after 10 d. Conidia were cylindrical, hyaline, aseptate with obtuse apices. The dural culture method was conducted with three biocontrol Bacillus strains and showed significant effect on *C. coccodes* with inhibition rate all over 50% indicating potential control strategy of this disease. This was first report of potato black dot caused by *C. coccodes* in Inner Mongolia, while the efficient control strategies are still unknown. The pathogen causing potato black dot has been ascertained in our result which will led a light to further research of disease control.

3-09

Inhibition of the development of *Rhizoctonia solani* by plant secondary metabolites – a laboratory study

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Black scurf and stem canker on potatoes, caused by the destructive soil-borne pathogen *Rhizoctonia solani* Kühn are a major problem for potato growers worldwide. Biological control agents such as plant leaf extracts can influence the severity of *R. solani* infection and help to reduce the risks to human health and the environment associated with the use of chemical fungicides. In this study, the inhibitory effect of the secondary plant metabolites aucubin, catalpol (iridoid glucosides) and acteoside (phenylethanoid glycoside) from methanolic extracts of *Plantago lanceolata* (Ribwort plantain (en), Smalkjempe (no)), a native plant in the Nordic countries, on the growth of *R. solani* mycelium on potato dextrose agar growth medium will be tested for the first time. Plant extracts will be obtained from plants of different age classes and metabolic profiling will be performed with LC-(HR)MS analyses and the concentrations of identified metabolites will be determined. To analyse whether the inhibitory interactions on fungal growth originate from the known secondary metabolites or are caused by the bulk plant extract, we will first expose the fungus to different concentrations of extracts, redissolved in aqueous solution and added to the growth medium, and in a further step we will carry out the same approach with the isolated secondary metabolites as pure substances. The fugus will be incubated for 5 days and the mycelium growth radius will be measured every 24 hours during incubation. Thereafter a suppression index will be calculated and compared to the untreated control. The results are pending at the time of submission of the abstract but will provide a good initial understanding to determine whether extracts of *P. lanceolata* can be used as a natural biological control agent as an additional component of a more sustainable strategy to manage the risk of infection of potato with *R. solani* and to reduce the severity of the disease caused by this pathogen.

3-10

Weeds as alternative hosts of *Spongospora subterranea*, the causal agent of potato powdery scab, in Finland

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Potato powdery scab, caused by *Spongospora subterranea* f. sp. *subterranea* (*Sss*), and the potato mop virus it vectors, are a growing problem in Finnish potato production. However, very little is known about the factors influencing their occurrence in the northern conditions of Finland, for example, the role of weeds as alternative hosts is not clear. Furthermore, several weed species belonging to the *Solanaceae* family appear to be spreading more widely, probably due to both global warming and human activity, and more information is needed on their potential risks.

In 2019 and 2020, weed samples were collected from twenty potato field plots with a previous history of powdery scab. The samples consisted of 31 plant species belonging to 17 plant families. The most common weed species was *Chenopodium album* followed by *Fallopia convolvulus*, *Matricaria matricarioides* and *Viola arvensis*. No root galls were observed on any of the sampled plants. However, the pathogen was detected in plants of 19 weed species from 11 families when the roots were analysed by PCR using species specific primers. Infections by *Sss* were most common in weeds of the families *Brassicaceae* and *Polygonaceae* and of the species *C. album*.

The results suggest that many common weeds are alternative hosts of powdery scab in Finland, but they do not develop root galls under northern Finnish conditions, so they do not directly increase the disease pressure in the soil. However, zoospore production from the infected roots may lead to a short-term build-up of an inoculum and act as a source of additional infection for potato roots and tubers. This emphasises need for timely and careful weed control, which should also be considered as an integral part of effective management of powdery scab.

The work is underway to map the prevalence of solanaceous weeds in Finnish potato production areas and to investigate their role as alternative hosts for potato powdery scab.

3-11

The influence of a preparation based on hydrogen peroxide and silver colloids and a preparation containing grapefruit extract on reducing fungal and bacterial diseases of Gardena variety seed potatoes during storage

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The Gardena variety is the result of a strategy adopted recently for breeding potato varieties, which involves obtaining genotypes with both high tuber utility value and increased resistance to pests. It was selected using molecular markers.

This is the first variety of this type bred in Poland. Therefore, activities were undertaken as part of the project: Innovative solutions in cultivation, storage and introduction to the market of a Polish potato variety highly resistant to *Phytophthora infestans*, aimed at developing detailed agrotechnics in various production technologies (conventional, ecological).

The experiments were conducted in various locations in Poland. Two field experiments and two storage experiments were located at the Hodowla Ziemniaka Zamarte. One of the storage experiments was the identification of the effectiveness and technologies of using environmentally friendly preparations limiting the development of fungal and bacterial diseases of seed potatoes during storage. Tubers intended for storage came from a plantation that was protected in accordance with the IOR recommendations. The plants were dug with a single-row combine harvester and then poured into pallet boxes. They were then stored for drying. After the ripening period and healing of the skin, two preparations were applied to the tubers: Huwa San (hydrogen peroxide and srepra colloids), Biosept (grapefruit extract) in various concentrations and combinations. Designed to limit the development of fungal and bacterial diseases during storage. After the storage period, the storage stability was assessed.

The Gardena variety stimulates quite quickly during storage. It is necessary to constantly monitor the conditions in the storage chamber and maintain 2–3°C throughout the storage period. After using Huwa San and Biosept at a concentration of 2.5% and 5%, the sprout weight was higher than in the other variants. A reduction in the formation of etiolated sprouts was observed when higher concentrations of Biosept or its mixture with Huwa San were used. The use of Biosept at a concentration of 2.5% effectively eliminated tubers with symptoms of dry and wet rot of potato tubers and inhibited premature maturation of tubers.

3-12

High-resolution analysis of effector genes in 394 *Phytophthora infestans* isolates using amplicon sequencing

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Phytophthora infestans causes late blight of potato by secreting a variety of effector proteins. These effectors are targeted to the host apoplast or to the interior of the plant cells to overcome the host's defense responses and establish infection. Variation and composition of the effector set in a *P. infestans* strain drive differences in virulence and aggressiveness.

Two amplicon sequencing (AmpSeq) approaches optimized for the Illumina MiSeq and PacBio HiFi platforms were developed in this project. AmpSeq was used to investigate sequence variation in effector genes, primarily from the RXLR family, in Norwegian and Polish isolates of *P. infestans*. In total, we targeted more than 80 genes, of which approximately 90 % were effectors. For Illumina MiSeq, amplicons were limited to about 350 bp in length, while we aimed for amplification of the full coding regions for PacBio HiFi sequencing. These over 80 targets were amplified and sequenced from nearly 400 *P. infestans* isolates from Polish and Norwegian collections. We implemented and developed various bioinformatics tools to build a customized, fully open-source and reproducible analysis pipeline. This largely automates the initial data processing and generates several tabular and figure outputs that guide deep exploration of the data. We found several instances of effector variation between isolates that were previously classified as the same SSR-genotype (Lim Rossmann et al., 2023). Some of this variation corresponded to previously described alleles, while some represented novel alleles. On average, only approximately five alleles were observed per individual gene, however, no isolates contained identical effector sets. Together with the data processing tools, the AmpSeq approaches we developed have the potential to greatly accelerate the assessment of virulence potential in *P. infestans* strains. Information on effector diversity could be used to develop resistant potato cultivars and predicting disease outcomes by matching effector variants and host resistance genes.

Reference: Lim Rossmann, S et al. (2023). Effector gene variation in Polish and Norwegian *Phytophthora infestans* strains. 2023 IS-MPMI Congress, Providence, USA. https://doi.org/10.5281/zenodo.8369743

3-13

Virulence and fungicide susceptibility of *Phytophthora infestans* isolates collected in Belgium in the years 2021-2023

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A total of 363 isolates of *Phytophthora infestans* were sampled from naturally infected potato (dumps, volunteers and crops) in the years 2021-2023. Single-lesion isolates were obtained by placing pieces of infected tissue on tuber slices of a susceptible potato cultivar (Bintje). Pure cultures were obtained by transferring small pieces of mycelium growing on the upper side of the potato slice on pea agar medium.

Genotyping: The isolates were analyzed using standardized 12 plex Euroblight SSR genotyping. Genotypes were determined by comparing fragment sizes with isolates previous genotyped (Euroblight monitoring).

Virulence profile: virulence was determined using Black’s differential set of potato clones, each having one of the R1-R11 resistance genes. Virulence was also determined by detached leaf assay on several commercial varieties which have a good rating about resistance in field.

Fungicide susceptibility: the floating leaf disk method (leaf of potato cv. Bintje) was used to assess Metalaxyl and Mandipropamid sensitivity. Leaf discs were floated abaxial side up in Petri dishes containing water or fungicide at concentrations of 0 to 100 µg/ml. Each disc was inoculated with a 10µl droplet of sporangial suspension. Fluazinam susceptibility was assessed on potato leaf discs by mixing the fungicide at different concentrations (0.1 – 1 – 10 and 100mg/L) with the sporangial suspensions. The susceptibility of Dimetomorph was measured using the radial growth method on culture medium. Isolates susceptibility was tested at each of the 9 concentrations of the fungicide: 0, 0.39, 0.78, 1.56, 3.13, 6.26, 12.5, 25 and 50 ppm. The diameter of the colonies (mm) was measured after 7 days of incubation in the dark at a temperature of 18°C.

In 2023, 2 clonal lineages dominated in Belgium. The most prevalent was EU_36_A2 clone which made up 50% of the population. The second most widespread clone is the EU_43_A1. The proportion of EU_43_A1 increased from 4% in 2021 to 24% in 2023. The proportion of EU_13_A2 decreased from 12% in 2021 to 2% in 2023. Two other genotypes, EU_37_A2 and EU_6_A1 were found in very few cases. A new genotype EU_45_A1 appeared in 2022, representing 3% of the population

EU_13_A2 were resistant to Metalaxyl, EU_37_A2 were resistant to fluazinam and EU_43_A1 were resistant to Mandipropamid and Dimetomorph.

All known virulence genes were found in belgian isolates. EU_ 13_A2 and EU_43_A1 had a more complex virulence profile than other genotypes. Significant differences were observed between genotypes regarding their virulence on resistant varieties.

3-14

Diversity and complexity of virulence races of *Phytophthora infestans* in the Baltic Sea region

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Potato late blight is destructive disease for potato production globally, including Baltic Sea region. In this study virulence with Black's differentials (R1–R11) studied among 931 isolates of *Phytophtora infestans*, collected from potato fields of Estonia (358), Latvia (229), Lithuania (142) and Pskov region in Russia (202). Late blight samples were collected during five years in Estonia (2010–2014), nine years in Latvia (2010–2013, 2017–2020 and 2023) and four years in Lithuania and Pskov region (2010–2013). All 11 differential factors found among four different populations from all studied years. The most frequent differential factors were R1, R2, R3, R4, R7, R10 and R11. Less frequent virulence factor was R9 with 15%, beaning lower among Estonian (9%) and Pskov populations (12%), and extremely high in Latvian 2017–2023 population with 57% ($p < 0.001$). Another less frequent virulence factor was R5 (16%), but varied from 6% in Pskov region to 26% (2010–2013) and 29% (2017-2023) in Latvia ($p < 0.001$).

The average number of virulence factors per isolate was 6.8 and varied strongly between studied countries and years. The number of virulence factors per isolate was higher among Latvian population in 2010–2013 (7.4) and later period 2017–2023 (8.3) compared to other studied populations. One of the most common phenotype 1.2.3.4.5.6.7.8.9.10.11 in Latvia (2010–2013, 2017–2023) and Lithuania, is not frequent in Estonian and Pskov region populations. Complex races appeared in all studied populations and years, however the most prevalent in the Latvian populations in 2010–2013 and 2017–2023. Unique pathotypes were more often among both Latvian and Lithuanian *P. infestans* populations (73%, 75% and 68% respectively) compared to Pskov region (59%) and Estonian (63%) populations. Also the racial diversity with Shannon diversity index showed higher values in Latvian populations ($Hs = 0.72$ in 2010–2013; $Hs = 0.88$ in 2017–2023) and in Lithuania ($Hs = 0.72$). However, among 931 isolates (2010–2023), the racial diversity (Hs) decreasing in time was noticed. The racial structure of the *P. infestans* population in the Pskov region has never been characterized before.

3-15

Long term changes in late blight development in Estonia

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The establishment and development of potato late blight caused by oomycete *Phytopthora infestans* in potato varieties with different resistance levels have been recorded at Jõgeva Plant Breeding, Estonia since 1922. The same methodology has been used during the 100-year period where several varieties have been tested during the longer period. The late blight infection has been assessed in the replicated untreated small plot trials once or twice a week from the onset of the infection until the end of the growing period. The time of first symptoms, delay of infection compared to the most susceptible variety, and speed of infection development (apparent infection rate) are calculated for tested genotypes. The obtained long-term time series enables the analysis of the changes having took place at the beginning of the infection and in the speed of the epidemic. The long-term data illustrate a clear trend in the earlier establishment of late blight infection, but also an increased variability in the time of detection of first symptoms during the last 30 years. There are indications of increased speed of development of late blight infection in some varieties and the shorter period between the establishment of infection in susceptible and more resistant varieties is characteristic for the later years. The possible roles of changes in pathogen biology and changing climate for late blight development are discussed in the presentation.

The increased variability at the beginning of infection and breakdowns of race-specific resistance increase the need to use decision support systems for the timely beginning application of fungicides for late blight control.

3-16

Reaction of some potato genotypes to the action of *Phytophthora infestans* in different environmental conditions

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Potato late blight caused by the pathogen *Phytophtora infestans* (Mont.) de Bary is the most widespread and the main limiting factor in production. It occurs in all areas of potato cultivation, from the mountainous regions to the south of the country, under irrigated conditions.

More than 175 years after the appearance of late blight in Europe, late blight remains a disease that most growers constantly face due to the frequency and aggressiveness with which it manifests itself on all organs of potato plants. In this paper, a series of observations on the behavior of four potato genotypes to the attack of the fungus *Phytophtora infestans* (Mont.) de Bary, under natural infection conditions, can be found. The experiments were located in two different locations from a pedo-climatic point of view within the plant protection laboratory at S.C.D.A. Suceava in the period 2021-2022, the experience placement method being that of randomized blocks. The Temerar variety records the highest production values for all treatment schemes applied in both years of research, the highest value being recorded in 2021 for the B1 variant, the first treatment being applied when closing the rows (preventatively) with systemic products. In this case, the production difference compared to the untreated control variant is 13.9 t/ha in Suceava, and 26% in Pojorâta. As for the treatment, it is applied when the first symptoms of hand on the foliage are noticed (B2) production losses between 3-7 t/ha are observed compared to the variants in the care of the treatment applied preventively, and the increase in production compared to the untreated control variant is between 6-18%. Due to the type of soil on which the experience at Pojorâta was located and the climatic conditions that were conducive to the installation of late blight, the differences in production between the two locations are significant. The highest value being recorded for the Temerar variety.

3-17

Insights into the metabolic responses of potato cultivars infected with *Phytophthora infestans*

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Integrating high-throughput biochemical and metabolic data into smart farming is envisaged to assist in precision agriculture. As a component of the Indian smart agriculture initiatives FarmerZone and SaIAfarm, these projects focus on potato smart farming. These initiatives seek to give small-holding Indian farmers advice based on a variety of data (soil, disease, irrigation, marketing, etc.). Potato, being a major staple food crop globally, needs continuous research attention in the wake of the biotic and abiotic stress it encounters. Among the biotic stresses, the late blight disease caused by *Phytophthora infestans* significantly limits potato productivity. According to a USDA report, this disease leads to an estimated $6.7 billion in yield losses annually worldwide. Our current study aims to identify biomarkers that could be used in the future to integrate smart farming by analysing the metabolic responses of potato cultivars infected with *Phytophthora infestans*. This research could provide insight into the pathways linked to pathogenesis and aid in disease control.

In this work, a nontargeted metabolic profiling of resistant (*Kufri. Girdhar*) and susceptible (*Kufri. Jyoti* and *Kufri. Chandermukhi*) Indian potato cultivars using gas chromatography-mass spectrometry (GC-MS) was applied to elucidate the metabolic resistance mechanisms against *P. infestans*. The GC-MS-based profiling detected ~93 metabolic signatures, including organic acids, sugars, amino acids, and secondary metabolites. Putative pathogenesis-related (PR) metabolites, which are identified through up-and-down regulation, were mainly fatty acids, polyamines, and organic acid profiles throughout the infection progression. Multivariate analysis facilitated effective sample discrimination between control and infected leaves. This adjustment of metabolites can correlate with the activation of defence signalling pathways and the accumulation of defence compounds in potato leaves. Overall, this study unraveled *P. infestans*-driven metabolic changes in potato leaf tissues.
The potential biomarkers identified could be considered to further develop low-cost assays or real-time monitoring systems for the diagnosis of late blight in potato fields.

3-18

Mutations conferring fungicide resistance in *Alternaria* from potato in South Africa

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Foliar diseases of potato, caused by *Alternaria* species, are a serious constraint to potato production world-wide. These diseases are mainly controlled by the application of fungicides; however, the development of fungicide resistance is a growing problem in agriculture. *Alternaria alternata* is classified by the Fungicide Resistance Action Committee (FRAC) as a high-risk pathogen for development of resistance, while *A. solani* is classified as medium risk. Both species have developed resistance to various classes of fungicides, including the QoIs, SDHIs and to a lesser extent DMIs. Early blight on potatoes in South Africa are caused by *A. grandis* and *A. solani* while and brown spot is caused by *A. alternata* and *A. arborescens*. Various isolates of these four species from different potato production regions in Sout Africa were tested *in vitro* against dicarboximide (FRAC 2), DMI (FRAC 3), QoI (FRAC 11) and SDHI (FRAC 7) fungicides. A total of 31 isolates (both sensitive and tolerant) were selected for whole genome sequencing to investigate mutations conferring loss of sensitivity to these fungicide classes. Assembled genomes revealed the well characterised G143A and F129L mutations conferring QoI resistance to small-spored and large-spored *Alternaria* species, respectively. Various mutations were present in the *Sdh*-subunits, however, the most common mutation (I280V) in *SdhB* has not previously been reported from *Alternaria*, but only from *Corynespora cassicola*. Loss of sensitivity to dicarboximide fungicides is due to mutations in the histidine kinase gene and were due to two mutations in the small-spored species (A98E & P94A) and two different mutations in the large-spored species (Q262L & S45A). *Alternaria alternata, A. arborescens, A. grandis* and most *A. solani* had the same G462S mutation in the *cyp51* gene conferring resistance to DMI fungicides, however, one *A. solani* isolate had a different mutation, G153C. Further studies to characterize the fitness of isolates with loss of sensitivity to different classes of fungicides is underway as well as development of rapid molecular methods to detect mutations leading to loss of sensitivity in large populations. The results of this study will enable continued monitoring of mutations in the populations which will enable farmers to rapidly adjust their spraying programs when resistance is identified in an area.

3-19

Mileos®, the French potato diseases DSS: a new module to control early blight

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Early blight caused by *Alternaria* species from section *Porri* is a secondary foliar disease in French potato-growing regions. This is a weakness disease strongly linked to plant physiology, with rare yield damage, which can be controlled mainly by prophylaxis measures to reduce plant stress. However, the challenge lies in the potential confusion of symptoms with abiotic stresses, often leading to unnecessary fungicide applications. Consequently, our objective was to develop a Decision Support System (DSS) to optimize fungicide usage, ensuring judicious application only when imperative.

To achieve this field experiments were conducted from 2018 to 2021 in Northern France. The experiments were carried out with the starch and late maturity cultivar Amyla and the processing and mid-late maturity cultivar Fontane, on natural conditions, with or without irrigation according to the site and the year. The experimental design involved testing different initiation dates for the initial treatment, spanning from early August to mid-September, with a subsequent renewal two weeks post the initial treatment. qPCR analyses were performed to confirm the presence of *Alternaria* section *Porri*. The evaluated model includes two parts, each addressing distinct phases of decision-making. The first, one is a physiological model named P-Days to determine the date when the crop sensitivity begins. The second one is an epidemiological model named DSV to determine the days with at risk of contamination following the initial phase.

Results showed that early blight like symptoms on the leaves occurred prior to the DNA detection of *Alternaria*. This confirms that early blight symptoms are prone to being misdiagnosed. When *A. solani* is detected by molecular analysis, the P-Days threshold is 600 for Amyla cultivar and 500 for Fontane linked with cultivar precocity ratings. The disease development on leaves is well correlated with the daily risk identify by the epidemiological model DSV. Treatments dates recommended by the DSS Mileos® achieved effective protection and significantly reduced the Treatment Frequency Index. Finally, we demonstrated the importance of also considering the future of the crop in treatment decision-making, such as yield projections, expected tuber size, date of haulm killing. Sometimes, a treatment is not necessary if the crop's stage is too advanced. This study not only enhances our understanding of early blight dynamics but also provides a practical tool, the DSS Mileos®, for growers to optimize fungicide application on potato crops.

3-20

Fusarium species causing potato dry rot in France: identification, pathogenicity and sensitivity to fungicides

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Fusarium is the most important pathogen causing tuber dry rot during storage worldwide. Until now, seed treatment after harvest or before planting by efficient fungicides have allowed to control the development of the disease in storage and have limited the spread of the pathogen from seed during growing season. However, in the last decade, European regulations have banned several effective fungicides because of their potential harmful effects on the environment and to human health (e.g. pencycuron against *R. solani*, mancozeb against *H. solani*) and other are threatened with removal (e.g. imazalil against *Fusarium* spp. and fludioxonil against *R. solani and H. solani*) without efficient alternative solutions. In France the last studies on Fusarium causing potato dry rot date from 1980s (Tivoli et al, 1987) , therefore in 2022 in order to anticipate a possible withdrawal of current efficient fungicides we have set up a new project named MC STOCK in order 1) to update our knowledge on the current Fusarium species responsible of potato dry rot in France, 2) to identify the inoculum sources in storage and 3) to assess alternative methods (prophylaxis, biocontrol products, ozone, luminotherapy, etc…). In this poster, we will focus on some studies: identification of the species associated with Fusarium potato dry rot in France, assessment of their pathogenicity in controlled conditions, and finally evaluation of the sensitivity of isolates belonging to different species to the available fungicides. The occurrence of *Fusarium* spp. was determined by collecting isolates from 113 seed potato lots with tuber dry rot symptoms, originating from different areas in France between 2021 and 2023. The 122 isolates collected belonged to twelve different *Fusarium* species, according to phylogenetic analysis of the rDNA ITS and Tef1 regions. *F. sambucinum* was the main species isolated but *F. avenaceum*, *F. arthrosporioides*, *F. cerealis* and *F. culmorum* were also frequently recovered from different lots. The first results under controlled conditions showed that the five species are able to produce dry rot on tubers and their level of aggressivity depends on the potato varieties used. The less common species were either not pathogenic or weakly pathogenic. The sensitivity of isolates of different species to the available fungicides (imazalil, fludioxonil, thiabendazole) is currently under investigation.

3-21

Dryocrassin ABBA is an effective inhibitor against potato dry rot caused by *Fusarium oxysporum*

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Fusarium oxysporum is an important plant pathogenic fungi. It can cause potato dry rot during postharvest and storage. Yield reduction can reach 25%, and with up to 60% in some cases. Dryocrassin ABBA is a phloroglucinol compound extracted from *Dryopteris crassirhizoma*, which has many pharmacological activities. However, little is known about the effect on potato dry rot caused by *F. oxysporum*. Mycelial discs (6 mm in diameter) were placed in the centre of the Petri dishes with 10 ml of PDA containing dryocrassin ABBA (2.0 mg/ml) and then incubated at 25°C. PDA containing only DW was used as the control. In this study we investigated whether Dryocrassin ABBA treatment could inhibit *F. oxysporum*. We found that:

1. The mycelial growth of *F. oxysporum* was inhibited. Scanning electron microscopy observations showed that abnormal, tightly twisted morphological changes in hyphae.

2. Compared with the control group, the MDA content of *F. oxysporum* spores decreased with 0.5 mg/mL treatment, but increased 1.64 and 1.96 times after 1.0 and 2.0 mg/mL treatment, respectively. The CAT activity of spores decreased by 5.54%, 59.9% and 70.0% with 0.5, 1.0 and 2.0 mg/mL treatment, respectively.

3. 1,244 differentially expressed genes (DEGs) were found, including 594 up-regulated and 650 down-regulated DEGs. KEGG top20 enrichment analysis showed that there were 17 significant KEGG enrichment pathways, and mainly related to carbohydrate metabolism.

4. The down-regulated DEGs were related to amino acid metabolism, carbohydrate metabolism, energy metabolism and lipid metabolism in *F. oxysporum*. It was also found that the expression levels of cell wall degrading enzymes (PCWDEs) and stress were negatively affected, including pectin, cellulose, hemicellulose and MFS transporters.

5. 5 DEGs were selected for qRT-PCR to verify RNA-seq data. The control and treatment groups were completely consistent with the sequencing results, indicated that the sequencing data were accurate and reliable.

In summary, Dryocrassin ABBA can regulate the expression of PCWDEs genes, inhibit mycelial growth and change hyphae structure. Amino acid metabolism, lipid metabolism and MFS transporters are effective pesticide targets. Using Dryocrassin ABBA is a possible biological agent to be used to control potato dry rot caused by *F. oxysporum*.

3-22

Functional verification of endophytic *Bacillus subtilis* WZ10 and its control efficiency on potato Fusarium wilt of China

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For study the growth promotion function of *Bacillus subtilis* WZ10 and its control efficiency on potato Fusarium wilt, growth promoting ability of strain WZ10 was tested by Salkowski's colorimetric and spectrophotometry methods and pot experiment, biocontrol effect was determined by pot experiment and physiology and biochemistry measure, phosphorus and kalium degradation abilities were tested by transparent zone method. The results showed that *Bacillus subtilis* WZ10 could produce IAA and degrade inorganic phosphorus, and showed significant control efficiency on potato Fusarium wilt. Compared to the control ones, the plant height, root length and fresh weight of plants were significantly increased by 14.34%, 19.75% and 77.07%, respectively and the activities of PPO, POD, SOD and soluble protein amount of plants were significantly increased after strain WZ10 inoculation. Meanwhile, the control effect of strain WZ10 on potato Fusarium wilt was 80.65%, which was significantly higher than that of 30% metriaxalin treatment. In this study, strain WZ10 had strong growth promotion ability and significant control effect on potato Fusarium wilt, which will lay a foundation for the subsequent functional development and potato Fusarium wilt control.

3-23

Control effect of potato Fusarium wilt by co-culture of *Trichoderma asperellum* PT-29 and *Bacillus subtilis* S-16 and the comparative analysis of non-targeted metabolomics

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In this study, the inhibitory effects of the fermentation broth of *Bacillus subtilis* ZWZ-19 (B) and *Trichoderma asperellum* PT-29 (T) on *Fusarium oxysporum* were compared under single-culture and co-culture conditions. The control effects of co-culture fermentation broth of two strains on potato wilt and related defense enzyme activities of potato were tested by pot experiment. The results indicated that two strains and three proportional co-culture broth all showed inhibition effect on *Fusarium oxysporum*, and the combination of PT-29 and S-16 co-culture broth(B1T1, ratio1:1) showed the best inhibition effect. In addition, the control effect of fermentation broth of S-16 single-culture on potato wilt was 60.09%, that of fermentation broth of PT-29 single-culture was 54.85%, but B1T1 was up to 73.44%. The activities of CAT, SOD, POD, and PAL in potato leaves treated with B1T1 were significantly higher than control treatment. Metabolomic analysis showed 134 metabolites were determined and classified into different types of amino acids. And 10 metabolic pathways had the most significant variations, and 12 were related to amino acid metabolism in the KEGG analysis. A correlation analysis of the 79 differential metabolites generated through the comprehensive comparison between B, T, and B1T1 was conducted, and the results showed that highly abundant amino acids in B1T1 were correlated with amino acids in B, but not in T.

3-24

PATAFEST: Horizon Europe-funded Research Project Paving the Way for Sustainable Potato Protection and Postharvest Excellence

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Potato is a key crop in Europe supporting economies and providing a crucial food source. However, the potato crop faces ongoing threats from pests and soil-borne pathogen diseases, resulting in substantial economic losses and food wastage. One of the most important pests is caused by bacteria *Candidatus* Liberibacter solanacearum (CLso), causing a disease known as zebra chip (ZC). The introduction of CLso bacterium on potato is mainly linked to the presence of the vector psyllid *Bactericera cockerelli* (BC) causing severe damage, both in terms of yield losses and quality. Besides, potato postharvest storage is also affected by the presence of soil-borne pathogens as *Fusarium sambucinum, Colletothricum coccodes, Helminthosporium solani* responsible for diseases such as dry rot, black dot, and silver scurf. The European regulatory framework for potato's imports has implemented phytosanitary requirements to protect the sector. However, globalisation, climate change, economical drivers, as well as the political context (EU Green Deal target of 50% pesticides reduction) are threatening the entrance of emerging potato pests and the incidence of soil-borne pathogen disease in postharvest storage. PATAFEST project involves 18 partners from 9 countries including researchers on agri-food sector, technology providers, agricultural cooperatives, experts on innovation management, and citizens.

This collaborative effort aims: 1) to research at molecular level the main resistance potato varieties against CLso and postharvest pathogens, 2) to develop sustainable and effective preharvest plant and soil treatments against the CLso vector and soil-borne pathogens combined with other innovative technological tools, including mobile app image analysis and AI predictive models that allow the early detection of pest threat and 3) to develop and validate postharvest technologies like biocontrol coating solution, controlled atmosphere storage technologies and high-performance volatile organic compounds sensors to control the incidence of soil pathogens and maintain the quality of potato tubers stored. These strategies will be integrated into an Integrated Pest Management approach, validated in key European potato-producing countries. PATAFEST will ensure a long-term strategy for tackling future potato pest threats by carrying out strong dissemination, communication, and exploitation plan, with an overarching multi-actor approach and citizen of science activities.

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4-01

Status of potato cyst nematodes in Norway

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Potato cyst nematodes (PCN) were first detected in Norway 1955 and have been under strict quarantine regulation since then. Systematic surveys have been conducted regularly so that the distribution of the two PCN species *Globodera rostochiensis* and *G. pallida* is rather well documented. Until the mid-1970s PCN was only detected in a few counties in the southern and western part of the country, with *G. rostochiensis* the dominating species. From about the mid-80s PCN surveys indicated a slow spread to counties further north (Trøndelag). Between 2009 and 2016 a countrywide survey of all ware potato production areas showed that only 5% were positive for PCN of which 98% were *G. rostochiensis*, additionally no spread to new counties were observed. The Food and Safety Authorities have now developed an open register of farms infested with PCN.

Obligatory use of certified seed is a key strategy to prevent spread of PCN and was initiated as early as 1958. Every year NIBIO receives between 1000 to 1500 soil samples from certified seed potato producers for PCN testing. Until today PCN has not been detected amongst the certified seed producers. Import of seed potato is illegal, another key aspect preventing introduction and spread of the pest.

4-02

Surveillance of *Meloidogyne chitwoodi* and *Meloidogyne fallax* in Norway 2019–2023

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Root knot nematodes (*Meloidogyne* spp.) are a large group of globally distributed obligate plant parasites. They are considered a key nematode pest, causing significant damage that affects both crop yield and quality. The two species *M. chitwoodi* and *M. fallax* are considered a serious threat to European potato and carrot production. Their broad host range makes them especially difficult to control once established. They are known to be present in several European countries and have recently been reported in Sweden and Denmark. If introduced to Norway, there is a likely risk of establishment, and consequently a risk of extensive damage to Norwegian potato and carrot production.

The surveillance project "Quarantine pests in potatoes" was therefore initiated by the Norwegian Food Safety Authorities in 2019, with the aim to determine status and presence of *Meloidogyne chitwoodi* and *M. fallax* in Norwegian potato production. Since then, 1,648 samples of ware and commercial potatoes, representing all potato growing areas, have been analyzed for presence of *M. chitwoodi* and *M. fallax*. Thus far, the surveillance of *Meloidogyne fallax* og *Meloidogyne chitwoodi* concludes that both species have status as «absent, pest not recorded».

4-03

Steaming as a tool to reduce the risk of spreading key nematode pests in infrastructure projects

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Potato cyst nematodes (PCN) *Globodera rostochiensis* and *G. pallida,* and the root-knot nematode (RKN, *Meloidogyne hapla*) are key pests of potato and vegetable crops, respectively. PCN and RKN are very difficult to combat or control once established due to the absence of permitted chemical nematicides, highly specialized farming, the short Norwegian growing season restricting the implementation of crop-rotations, and the long-term viability of PCN cysts in untreated soils. To avoid spread to uninfected fields, PCN are regulated by strict requirements for management of infected farmland, including handling of infected soil. Today, PCN infected soil for infrastructure projects is deposited as contaminated waste and represents a significant loss of resources. In contrast to PCN, RKN is not regulated in Norway, but poses a similar risk to carrot production.

In this study we investigated the survival of the selected nematode pests after exposure to soil steam. We examined the thermal sensitivity of *G. rostochiensis*, *G. pallida* and *M. hapla* under controlled conditions using a stationary soil steaming prototype and exposure to soil target temperatures ranging from 60 to 90 °C for three minutes. After treatments, the survival (hatching) of eggs and juveniles was recorded after exposure to potato root exudate for six weeks (PCN) and after extraction of *M. hapla*. To investigate the ability of the surviving nematodes to infect roots we inoculated the nematodes onto host plants in pot experiments. We present results from the survival (hatching) experiments and the infection trials.

4-04

Efficacy of *Bacillus subtilis* strain ZWZ-19 and associated volatile substances in inhibiting nematode of *Ditylenchus destructor*: an evaluation of control performance

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The application of endophytic bacteria presents significant potential for managing nematode of *Ditylenchus destructor*. Herein, we evaluated the inhibitory capabilities of eight biocontrol bacterial strains against *D. destructor* using direct contact and fumigation techniques. Strain ZWZ-19, exhibiting substantial contact and fumigation efficacy against *D. destructor*, and the adjusted mortality rate of the nematodes reached 86.94% and 72.79%, respectively after 72 hours. The strain was characterized based on its colony morphology, physiological and biochemical attributes, as well as 16S rDNA sequencing, and was identified as *Bacillus subtilis*. Field and pot trials demonstrated that *B. subtilis* ZWZ-19 effectively suppressed *D. destructor* with efficiency exceeding 48.10%. GC-MS analysis identified 18 volatile substances in strain ZWZ-19, each with a concentration exceeding 1.34%. Among these, hexamethylcyclotrisiloxane displayed strong inhibitory activity against the nematode, achieving an adjusted mortality rate exceeding 60.74% after 72 hours. Given its low toxicity and high safety profile, this compound is considered a promising candidate as an effective new nematicidal fumigant for controlling *D. destructor*.

4-05

Comparison of virulence of pathotype 38 (Nevsehir) isolates from different EPPO member countries

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Synchytrium endobioticum (Shilb.) Perc. is an obligate biotrophic, soil-borne fungus which causes the potato wart disease. *S. endobioticum* originated from Andean zone in South America and is currently present almost all over the world. The thick-walled winter sporangia are the dormant structures of the fungus and can survive for more than 40 years in the absence of host even under adverse environmental conditions. Since the discovery of pathotype 2(G1) in Germany, more than 40 pathotypes have been reported in Europe. The most relevant pathotypes in West Europe are: 1(D1), 2(G1), 6(O1) and 18(T1). Recently pathotype 38 (Nevsehir) was detected in Turkey, Georgia and The Netherlands. There is a significant risk that this pathotype will also spread to other countries.

In this study, isolates of pathotype 38 (Nevsehir) isolates from Turkey, Georgia and the Netherlands were compared on a much larger assortment of differentiating cultivars compared to the EPPO PM 7/28 standard (2). Results show that there are differences in virulence profile between individual isolates. Isolates from Turkey and Georgia are very similar. The isolate from the Netherlands seems to be more different from the others.

Correct assessment of virulence is extremely important in the search for sources of resistance to particular pathotypes/isolates of *S. endobioticum*. Studies have shown that, for example, the Otolia cultivar is extremely susceptible to all tested isolates. Eurodelta, on the other hand, is resistant to Dutch isolate and susceptible to other ones originating from Turkey and Georgia.

4-06

Experiments in controlled conditions provide beneficial information on the applicability of biochar in potato production

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Char products from organic side-streams and waste biomasses may be suitable for soil improvement in agriculture, promoting carbon sequestration and sustainable bioeconomy. Physical and chemical properties of char products are dependent on the feedstock material and processing conditions, and one goal of our study was to examine whether differing char products can be utilised in potato cultivation. We used a series of short-term growth chamber experiments to investigate the potential phytotoxity of different treatments in three indicator species: barley, radish and rape. Bio- and hydrochars were produced by pyrolysis or hydrotermic carbonation from different materials, and they were applied at three different rates (5, 10 or 50 t/ha). Subsequently, we established a multi-year field trial testing effects of three biochars, applied at the rate of 10 t/ha, on crop growth, tuber yield and disease occurrence in the potato variety Innovator.

In the chamber experiments, chars and their application rates affected abiotic soil conditions, including pH, total nitrogen and organic matter. A principal component analysis showed that variation in 13 soil variables could be summarised by three groups of correlated characteristics. Two traits (emergence and biomass) and the three species were differently affected by the treatments (planting time, char treatment, application rate); for example, planting immediately after the char application had a negative effect on the trait averages only in barley. Few treatment combinations had detrimental effects on the plants, and various treatment interactions were found particularly in barley and rape. As expected, char treatment did not affect crop growth and development, tuber yield or the occurrence of diseases in the first year of the potato field trial.

Our observations that the three indicator species exhibited marked variation in their responses to the treatments and that no effects of biochar were found in a single growing season in the field highlight the importance of longer-term evaluations of plant performance where multiple species or varieties are closely monitored in agriculturally relevant environments (e.g., ideal *vs.* stressful conditions, varying growing seasons).

4-07

Exploration of plant growth-promoting rhizobacteria (PGPR) in potatoes

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Potato is not only contributing to food and nutritional security but is the largest vegetable commodity in South Africa. The crop is grown by subsistence and emerging farmers, while also having considerable commercial value. The exploitation of plant growth-promoting rhizobacteria (PGPRs) to improve crop production has immense potential in the industry. In addition, these PGPRs may further enhance tolerance against several destructive diseases. One hundred and seventy six endophytic and rhizospheric bacteria have been isolated from potatoes roots and rhizosphere from various locations in Gauteng, South Africa. More than 27 of these isolates showed the ability to solubilize inorganic phosphorus from insoluble compounds. Improving availability of phosphorus in soil will not only reduce application of inorganic phosphorous but also increase yields. In addition, 47 isolates showed the ability to produce siderophores which will enable potato plants to grow in soil with low iron availability. *In vivo* trials showed that 10 isolates triggered increase stem length, 15 isolates caused increase root length, while three isolates led to increased total dry weight of the plants. The resulting growth promotion of potato, e.g. increase in root and shoot weight, and total root length, may enable farmers to produce crops of good quality with higher yields, leading to improved food security and improved nutrition. Field trials will be conducted to verify the results of the greenhouse trials.

As knowledge of PGPR to subsistence and emerging farmers is limited, several training events were held to increase their basic knowledge. The training workshops created awareness among smallholder potato farmers on PGPR, while at the same time focusing on management strategies to reduce soilborne diseases. This had led to a better understanding of PGPR and assist the subsistence and emerging farmers in implementing effective strategies to reduce the spread of soil-borne diseases.

5-01

The effect of Smartblock, a sprout suppressant, on the physiological growth of potato (*Solanum tuberosum*)

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SmartBlock is a new sprout suppressant proposed as an alternative to Chlorpropham (CIPC), whose long-term effect on seed potatoes is unknown. The objective of this study was to determine the effect of its dosages on the emergence rate and growth of potatoes cultivated in a controlled environment. Mnandi and Vanderplank cultivar seed potatoes with sprouts not greater than 3 mm were stored in 9 L plastic containers and treated with two levels of SmartBlock (0.100 and 0.135 µL/kg) compared to a control. The pot experiment was arranged in a completely randomized design with three replicates. Emergence rate, plant height, number of stems, stem diameter, leaf area, stomatal conductance, CO_2 assimilation, chlorophyll content and transpiration rate were recorded. 100% emergence was reached in both the control and 0.100 µL/kg SmartBlock applications. Only 88% of potatoes treated with 0.135 µL/kg SmartBlock emerged. Results indicate SmartBlock application can delay and reduce emergence. The delay did not hurt the plant height, stem diameter and leaf area of the plants. The treatments significantly reduced the stomatal conductance and CO_2 assimilation of both cultivars. However, transpiration and chlorophyll content were not significantly affected. The higher concentration (0.135 µL/kg) resulted in higher stomatal conductance compared to the lower concentration in both cultivars, 335 and 479 mmol H_2O m^{-2} s^{-1} respectively. Both dosages (0.100 and 0.135 µL/kg) resulted in lower CO_2 assimilation in Mnandi when compared to Vanderplank cultivar, with Vanderplank having 17 and 18 µmol CO_2 m^{-2} s^{-1} while Mnandi having 15 and 7 CO_2 m^{-2} s^{-1}. The differences observed between cultivars might be due to genetics. The results suggest SmartBlock may negatively affect potatoes' yield capacity since it tempered with net photosynthetic indices such as stomatal conductance and CO_2 assimilation within cultivars.

5-02

Metabolomics – a promising tool to assess the physiological age of seed tubers of potato (*Solanum tuberosum* L.)

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The physiological age of seed tubers represents their physiological status that evolves progressively with increasing chronological age, depending on conditions during production and storage. Physiological age of seed tubers strongly affects the performance of the subsequent crop. A major challenge lies in developing a reliable and rapid diagnostic tool capable of assessing physiological age across various developmental stages of seed tubers and across cultivars differing in physiological responses to seed tuber conditions.

This study employs modern metabolomics platforms and gas and liquid chromatography–mass spectrometry methods to identify biochemical indicators of physiological age. Seed tubers of four modern, contrasting cultivars were produced under uniform conditions. Different storage temperatures were applied to create variation in rate of physiological ageing. Monthly assessments from harvest to planting were conducted on tissue-specific samples to examine changes in metabolomics profiles caused by storage duration and cultivar-specific and/or tissue-specific physiological responses to storage temperatures.

Principal component analyses unveiled cultivar-specific metabolite compositions, collectively displaying a consistent progression from early in time to late in time and from cold storage to warm storage, suggesting physiological ageing. Examining individual metabolites revealed intriguing patterns, with some metabolites prevalent throughout cold storage, others emerging solely at the end of storage. Certain metabolites exhibited strong interactions between storage duration and temperature, displaying increases or decreases over time, particularly at warm storage. Tissue-specific variations were also observed, with peaks or troughs in the contents of the apical eye or non-apical eyes compared to other tissues.

Subsequent analyses will identify these metabolites and correlate their patterns with concurrent sprouting behaviours in sprouting tests, linking biochemical changes within seed tubers to visible physiological transitions from dormancy to various sprouting stages.

5-03

Assessment the suitability of potato breeding lines for cultivation in an organic production system

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The proper selection of varieties for organic cultivation is crucial. There is still a lack of varieties with the characteristics of being suitable for organic cultivation. The aim of our research was to evaluate breeding lines in terms of their suitability for organic cultivation and further breeding.

The research was carried out in 2022-2023 at the Institute of Plant Breeding and Acclimatization-NRI in Poland. The research material included new potato genotypes which were breeding materials from two Polish Potato Breeding Stations. The breeders initially selected those lines that, had features useful in organic cultivation, and the detailed selection was carried out under organic cultivation conditions. To assess the interaction between the genotype and environmental conditions, field experiments were set up in two localities with different soil conditions (Jadwisin – light soil and Radzików – heavy soil). During the growing season, plant development was assessed by measurements the morphological and physiological characteristics of plants, and after harvesting, the parameters of agrotechnical value and tuber quality were assessed.

The following features were assessed: phenological phases on the BBCH scale, LAI index, occurrence of fungal diseases during the growing season: early blight, late blight, tuber yield and tuber size distribution, occurrence of external and internal defects of tubers: common scab, black scurf, deformations, cracks, greening, damage by pests, rusty spots on the flesh, hollowness, culinary value (darkening of the cooked flesh, taste), storability (length of the tuber dormancy period, weight losses, storage diseases). Several lines were examined during two years. The studied lines differed significantly in terms of the examined characteristics. Most features were found to interact with soil conditions. The lines that performed best on both lighter and stronger soil were selected for further breeding.

5-04

Variety and time of potato planting in summer seed production in the Republic of Moldova

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Quality of seed potatoes is one of main constraints in potato production in the Republic of Moldova. The traditional sources of seed tubers are the North European countries with their efficient system of seed potato production. However, the global climate and economical changes often affect the traditional seed potato production areas. One of the ways of reducing the dependence on imported seed is local seed potato multiplication in summer planting.

On the basis of many years of research it was established that early and medium early varieties are more adapted to summer planting, as these produce a fairly good yield before the first autumn frosts kill the vines. Taking into consideration the different lengths of the vegetation period among varieties, the planting period for each variety is established by the following formula:

$Pp = DffC^{o} - (Pv + Eup)$ where:

Pp – planting period;
$DtmC^{o}$ – time of the first air temperatures below 0 °C with a probability of 10%, (dates from a regional meteo station);
Pv – variety-specific vegetation length, in days;
Eup –planting – earthing up period, days (8...15 in case of using last year tubers and 15...30 in case of using fresh harvest tubers after breaking dormancy). So in case of using fresh harvest tubers (after breaking dormancy) for planting, planting should start one to two weeks earlier.

The results show that the quality of the seed produced in a summer crop meets the farmer requirements. This local seed production can substantially reduce seed shortage. We also observed that because of lower virus presure and better climate conditons for tuberization, the percentage of plants affected by viruses and ecological degeneration was substantialy reduced, resulting in higher phytosanitary and physiological quality after storage.

5-05

Assessment of gene expression changes in relation to meristem position in eco-dormant tubers

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Tubers of many cultivars of potato exhibit apical dominance upon sprouting. How sprout regulators, such as 1,4-dimethynaphthalene (DMN), alter the process of apical dominance is unclear. In this study single meristems of ecodormant tubers of *Solanum tuberosum* cv. Lamoka were examined for changes in gene expression using RNA-seq. Tubers were harvested in the fall of 2022, then stored until ecodormant as denoted by peeping following one week of incubation at approximately 22°C. Ecodormant tubers were exposed to either water (control) or DMN for a period of two days, then single meristems were collected from four positions from apical to stolon end. Following Illumina sequencing of RNA extractions, differentially expressed genes were identified in Galaxy using DESeq2 at a significance value of $q<0.05$ and a $\log_2$ fold change absolute value >1. Fourteen days after treatment, signficant spatially different gene changes were found in mersitems along the apical-distal positions of the control tubers reflecting apical dominance. Tubers treated with DMN did not exhibit significant gene changes based on meristem position at fourteen days after exposure. DMN did alter gene expression compared to untreated controls and it also changed gene expression associated with apical meristem dominance.

5-06

Nitrogen uptake and partitioning in potato varieties of contrasting determinacy

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Ammonium nitrate and other fertilisers represent one of the largest sources of GHG emissions from potato crops grown on mineral soils. In anticipation of likely future legislation mandating reduced farm GHG emissions—which will restrict the amount of nitrogen (N) that growers can apply—it is important to understand N uptake patterns under different fertiliser regimes and across varieties. Varietal determinacy (a description of growth habit) strongly influences optimum N rates which for determinate varieties can be double that required by indeterminate varieties for the same season length. This fundamental understanding how N uptake and partitioning differs with determinacy under conventional fertiliser regimes will also provide baseline data to evaluate how alternative sources of N (with lower associated GHG emissions) affect N uptake and N use efficiency.

Innovator (determinate) and Royal (indeterminate) were planted at a range of N rates (Innovator; 0, 180, 220, 260 and 300 kg N/ha, Royal; 0, 90, 130, 170 and 210 kg N/ha) in Cambridge in 2023. Plots were sampled at *c.* 23, 37, 45, 54 and 144 days after emergence (DAE) to collect fresh and dry weights of haulm and tubers; N content was quantified by Dumas combustion.

When fertilised, there was little difference in either the rate of, or timing of, fastest N uptake either between N rates or between varieties (fastest uptake was 0.12 and 0.15 kg N/ha/day for Innovator and Royal, respectively, and occurred 29 DAE for both), despite large differences in total N uptake. In Royal, harvest index (HI) decreased with increasing N rate at 54 DAE in Royal, but by the end of the season there was no difference. There was no variation in HI between fertilised Innovator treatments during or at the end of the season.

Under fertilised conditions in both varieties *c.* >90 % of total N uptake occurred by 50 DAE, but during the same period only *c.* 65 % was taken up in the unfertilised plots, highlighting differences in uptake pattern with differences in supply.

The agronomic optimum N application for Innovator was 180 kg N/ha (71 t tuber FW/ha) and for Royal was 130 kg N/ha (81 t/ha). The greatest varietal differences in biomass partitioning were observed mid-season, highlighting the risk of harvesting an indeterminate crop grown under high N rates early in the season, before resource reallocation from haulm to tubers was maximised.

5-07

Nitrogen use efficiency impact on several traits important for potato starch production

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The enhancement of nitrogen use efficiency (NUE) in potatoes (Solanum tuberosum L.) has the potential to reduce the necessary nitrogen input. This, in turn, can lead to increased economic benefits and a decrease in environmental pollution resulting from nitrogen loss. The objective of this study was to assess the NUE of various potato genotypes and to examine its relationship with tuber yield, starch yield, and starch content under different nitrogen availability in soil.

Over a two-year experiment, the performance of 19 potato genotypes was assessed using diverse farming practices, incorporating varying levels of nitrogen fertilizer rates. These practices included the integrated farming (IF) system with three distinct nitrogen fertilizer rates and the organic farming (OF) system without nitrogen fertilization. Nitrogen fertilization in both farming systems was quantified as plant-available nitrogen in the soil and nitrogen added through fertilizer. A significant impact of genotype and farming system on the tested traits was observed. The correlation between potato genotype tuber yield and NUE was consistently high or moderate in the farming system with different nitrogen availability across both years. Tuber yield in potatoes cultivated in a system with higher nitrogen availability typically did not exhibit a significant increase, leading to a detected decrease in genotype NUE. The correlation between starch yield and NUE was high and strong in both farming systems, although a moderate to strong correlation was also identified between tuber yield and starch yield. NUE demonstrated a weak correlation with starch content in potato tubers, indicating that genotype characteristics and growing conditions had a more significant impact on this trait.

An elevation of nitrogen fertilization did not result in an increase in starch yield due to a decrease in starch content and a insignificant increase in tuber yield. Nonetheless, genotypes with higher NUE consistently produced higher tuber and starch yields compared to genotypes with relatively lower NUE, even within farming systems with varying nitrogen fertilizer rates over both experimental years.

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5-08

Potato tuber quality and nitrogen use efficiency responses to integrated nutrient management

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Tuber quality and nitrogen use efficiency (NUE) in Limpopo potato growing areas is limited by poor soil fertility, which is caused by soil degradation, poor fertilizer application and management, and high temperatures that increase soil water evaporation and nitrogen volatilization. This study aimed to assess the potential of integrating cultivar selection, mulch and fertiliser application in improving tuber quality and NUE. The experiment was carried out as 3 x 2 x 4 factorial, arranged in a completely randomized design (CRD) at University of Limpopo. Integrated nutrient management (INM) treatment factors were: three N fertilizer application rates (control, 50%, and 100% of recommended N rates), two soil cover levels (grass mulch and no mulch), and four potato cultivars (Mondial, Sababa, Panamera and Tyson). Crop data collected included tuber grading based on tuber size, tuber dry matter content and NUE. NUE was calculated as a percentage of N taken up by the crop per soil total N. Tuber dry matter content and tuber size were not significantly affected by INM. However, planting a late maturing cultivar (Panamera) indicated to produce significantly higher dry matter accumulation, proportion of medium and large tubers compared to other potato cultivars. Furthermore, the percentage of large tubers tended to increase with an increase in fertilizer application rates and mulch application. Integrating 50% of recommended application rate with organic mulch resulted in significantly higher NUE of the cultivars compared to full fertilizer recommendation rate. However, the control treatment indicated significantly higher NUE than 50% of recommended fertilizer application rate treatments particularly when a late maturing cultivar was integrated with 0% of recommended fertilizer application rate and mulching. NUE significantly decreased linearly with increasing N application rate. High tuber quality and NUE associated with Panamera was linked to its extended period of nutrient, water uptake and dry matter accumulation that supported the development of tubers. Low NUE under 100% fertilised conditions suggest that fertilizer saturated states tend to lose more nutrients than unsaturated states. Incorporating reduced fertilizer application with organic mulch and planting a late maturing cultivar can be recommended for improving NUE while optimising tuber quality.

KEYWORDS: potato cultivars, fertilizer rates, mulching, poor soil fertility, tuber quality, NUE

5-09

Reducing Synthetic Fertilizer in Russet Burbank Production with Turkey Manure

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There are concerns of increasing nitrates in water because of high amounts of synthetic fertilizers used in potato production. Utilizing a natural and local source of fertilizer, turkey manure compost can be used to provide a sustainable option for potato production that could benefit soil health. The aim of this study was to compare different amounts of turkey manure compost with and without Environmentally Smart Nitrogen (ESN) on Russet Burbank potato production in Minnesota, USA. Treatments included a no nitrogen check, grower standard of 280 kg N ha^{-1}, 6.8 tons turkey manure ha^{-1}, 11.3 tons turkey manure ha^{-1}, 6.8 tons turkey manure ha^{-1} + 56 kg N ha^{-1}, 6.76 tons turkey manure ha^{-1} + 112 kg N/ha^{-1}, 11.3 tons turkey manure ha^{-1} + 56 kg N ha^{-1}, and 11.3 tons turkey manure ha^{-1} + 112 kg N/ha^{-1}. Tubers sized between 170 to 284 g, total yield, marketable yield, and the percent of tubers >170 oz were similar to the grower standard, except the no nitrogen check and 6.8 tons turkey manure ha^{-1} treatment which were less. Tuber number echoed the results found by tuber yield. Based on these results and previous work, turkey compost has proven to be a suitable option for potato fertilizer, but variety, soil type, turkey compost all should to be taken into consideration. This work has found that turkey compost with the addition of reduced amount of ESN can benefit total yield and increase tuber size and allow potato growers to rely less on synthetic fertilizer.

5-10

Improving tuber quality and vigour via the use of cover crops in organic and low input farming

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Abstract: In the ECOBREED project (grant agreement no. 771367) we tested the influence of cover crops on the subsequent potato crop in organic fields. A cover crop trial was conducted at the Agricultural Institute of Slovenia in the seasons 2020/21 and 2021/22. 7 treatments were used: 5 individual cover crop species, i.e. black mustard (10 kg/ha), oil radish (15 kg/ha), lucerne, black oat and vetch (all three 25 kg/ha), a sixth treatment was included, i.e. a mixture of the 5 individual species, and number 7 was the uncovered control. After overwintering, the field was ploughed and planted with 4 potato varieties: Alouette, Carolus, KIS Kokra and KIS Tamar. In autumn, yield, tuber size, number of tubers and dry matter were evaluated. The influence of cover crops on tuber quality was evaluated. Visual observations of tubers for regularity of shape, depth of eyes, tuber uniformity, skin finish, secondary growth, growth cracks, rhizoctonia, silver scurf and common scab were made after harvest in the store. The results show that cultivar choice influenced yield and yield components, dry matter and most of the quality traits. Cover crops influenced yield, tuber size and dry matter, as well as shape regularity, eye depth and skin texture.

5-11

Smaller doses of hot water combined with mechanical flailing did not kill potato haulm sufficiently

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EU's ban of the herbicide diquat (e.g. in the product Reglone) to kill potato haulm, has left the producers and scientists in need to find alternative measures. Alternatives should be both convenient and cost-efficient enough to be an adequate substitute for the growers. This experiment was made as part of a more comprehensive project, testing various chemical, thermal and mechanical methods. Five different doses of hot water, combined with mechanical haulm flailing, were tested as a means for killing of potato haulm in an open field in Innlandet, Norway. Remaining fresh stem and leaves, and number of plants with regrowth, were measured visually 7 times over 14 days following the hot water treatment. The potatoes were also harvested and analysed for quality. Although there were differences in how fast desiccation and amount of regrowth occurred among the doses, the variations were small and took many days to manifest. The experiment showed that higher doses of hot water than the ones tested in this experiment would be needed for sufficient haulm killing.

5-12

On how the cell cycle progression affects potato response to water shortage

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High yield and quality are the most important characteristics of potato production. Significant increases in global average temperatures are leading to longer periods of soil drought, extreme heat waves, rainfall and flooding, forcing a shift in the timing and location of potato planting and contributing to yield reductions. Potato is sensitive to drought. Due to the quantitative nature of drought tolerance and the lack of a clear determinant of this tolerance, there is still a great need to identify factors/processes responsible for this tolerance.

One of the most visible responses of plants to drought is growth inhibition, which is initiated by the inhibition of both cell proliferation (decrease in cell number) and/or cell expansion (enlargement of cells to their final size). Both processes are coordinated by the cell cycle.

Katahdin-derived potato cultivars grew in the tent in three randomized blocks design. The control plants were watered continuously. The second half of the plants were subjected to drought. Potato leaves and tubers were collected. Potato drought tolerance was calculated as yield quality (average tuber weight per plant). In potato leaves, cell cycle progression (flow cytometry), and expression of the cell cycle-related genes (RNA-seq) were evaluated.

Two cvs. were chosen for cell cycle analysis. Sensitive cultivar characterized a 26% decrease in yield quality and tolerant cv. with no yield quality losses. Cell cycle progression was different in tolerant and sensitive cultivars. The tolerant cultivar modulated cell cycle progression expressed as decreased cell frequency in the S phase and increased cell frequency in the G0/G1 phase. Such cell cycle arrest can be interpreted as an adaptation of the plant to drought. The observed delay in cell cycle progression allows the avoidance of unfavorable changes in progeny cells in response to stress treatment. The global gene expression profile suggests that among the differentially expressed genes, those directly involved in cell cycle regulation, such as cyclins and cyclin-dependent kinases, were also responsible for the shift in cell cycle progression. Of particular interest is *retinoblastoma-related protein 901 (RBL901)* gene, which was overexpressed in the tolerant cultivar and is a negative regulator of cell cycle progression.

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7-01

Latest trends in climate-smart agricultural practices: a systematic review

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Climate-smart agriculture (CSA) ensures maximum food production under the threat of climate change. The adoption of CSA practices is necessary to improve food production to meet high population demand. This study assessed the latest trends in CSA research and the determinants for the adoption of CSA practices. The literature sources used in this review were retrieved from Web of Science, Scopus, and Google Scholar. Popular keywords used are climate change, climate-smart agriculture, technology, and adoption. This review synthesized literature from 2000-2022. The charting method used was preferred reporting items for systematic review and meta-analysis (PRISMA). VoSviewer software was used to map out the most used keywords, the number of studies conducted, and the countries' collaboration in CSA research. In this review, it is shown that the adoption of CSA practices is hampered by factors such as lack of knowledge, lack of financial support, lack of extension services, land size, household resources, and location. Other studies showed that awareness and training enhance farmers' knowledge, leading to increased adoption. The mapping results showed that most of the CSA studies are conducted in Kenya, the United States of America, and the Netherlands. The results of this study can be useful to researchers and farmers to aid their understanding of climate-smart agriculture.

7-02

Yield and quality assessment of potato varieties with 3 N-fertilization levels and different weather conditions in Middle East Norway

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As a crop with a relative limited root system, potato plants are susceptible to shortage in water and nutrients supplies. A limited content of water in soil may restrict plant development and promote pathogen with a destructive influence on the plant and tuber quality, i.e., common scab. Periods with the extent of water over time may promote powdery scab and bacterial diseases that reduces yield and quality before and after harvest. The global warming and extreme weather episodes may have a negative impact on crop production and lead to challenges in economy, foods supplies and trade on the national and international arena. Poor weather conditions during the growing season may lead to significant yield and quality losses, both for fresh and stored potatoes. In this experiment meteorological data was used to analyze growing conditions and response of table potato varieties to weather and fertilizing in three different years. In the year 2023 the extreme weather "Hans" occurred in August, with high rainfalls and flooding in Innlandet county, resulting in both direct and in-direct damages in the potato fields and post-harvest.

This poster presents results from the three years of study: 2020, 2021 and 2023, with the three table varieties Nordlys, Celandine and Undset. The experiments were randomized variety trials with the three nitrogen levels of 70, 130 and 190 kg N/ha with two repetitions. Fields were supplied with irrigation when needed in dry periods. During 3 years of experiments the mean air temperature in June was higher than normal for the period 1991-2020. Rainfall distributions were also different for each of analyzed years with dry period in June in 2023, almost normal rainfall in 2021 and over normal rainfall in 2020. Weather conditions in July and August also varied, with the most of rainfall occurrence in July/August in 2023, long above normal in mentioned period. July and August where dry months in 2020, in 2021 precipitation in July was above normal but August was dry with approximately 20% of normal rainfall during all three years of experiment. Accumulated rainfall in 2023 in period 25.04 to 24.09 was 620 mm against 268 and 284,9 mm in 2021 and 2022, respectively.

Analysis of yield data for the seasons 2020, 2021 and 2023 has shown differences in total and marketable yield, tuber size distribution and total amount of dry matter produced pr area among years of trials. Mean weight of tubers > 40 mm was in season 2023 reduced by approximately 30 %. There was more green tubers and skin blemishes in 2023 than in 2020 and 2021. There was also more green haulm by the time of haulm killing in 2023. This work will continue to compare following years and climate data on chosen varieties. The global radiation, air and soil temperature, total rainfall and rainfall distribution on site can be used to calculate harvest index of different varieties.

7-03

Dissecting the cross-talk between cold tolerance mechanisms and tuberisation in potato

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Potato cultivation faces challenges with cold stress, particularly during the (tuber) seedling stage in late spring. Although late planting can mitigate this stress, early planting with enhanced cold tolerance holds significant potential advantages. Genes in the tuberisation pathway like *StCDF1 (CYCLING DOF FACTOR 1)* and *StSP6A (SELF PRUNING 6A)* were reported to directly affect drought and heat responses in potato and their homologues in Arabidopsis were suggested to be involved in cold tolerance through the *CBF-COR (C-REPEAT BINDING FACTOR – COLD RESPONSIVE)* pathway. These results indicate a possible link between cold response and tuberisation and offers promising avenues for enhancing cold tolerance in potato varieties.

This study investigates the interplay between tuberization regulators and cold response in potato. Specifically, it explores the impact of *StCDF1* overexpression and knockdown in two diploid potato genotypes (CE3027 and CE3130) under cold treatment (1°C for ~3 days) and subsequent recovery (~3 days).

Results show differential *StCBF1* expression under cold treatment, with StCDF1 likely repressing *StCBF1* expression by binding to its upstream region. Allelic variations in the upstream and coding sequences of *StCBF1* were observed, impacting the binding site of StCDF1 in CE3027, yet maintaining *StCBF1* downregulation by StCDF1. Interestingly, both overexpressed and knockdown *StCDF1* lines exhibited increased susceptibility to cold stress compared to the wild type. The downregulation of *StCBF1* by StCDF1 might contribute to reduced cold tolerance in *StCDF1* overexpressed lines.

This investigation sheds light on the complex relationship between tuberization regulators, such as *StCDF1*, and their impact on cold response in potatoes. These findings hold promise for the development of markers and mechanisms to breed cold-tolerant potato varieties without compromising tuber yield, vital in the face of escalating environmental challenges driven by climate change.

7-04

Use of in-situ field chambers to quantify the influence of heat stress in potato

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Food security and sustainability are threatened by heat stress due to global warming. The effects of elevated temperature on potato are expected to be more drastic in many parts of the world due to its sensitivity to supra-optimal temperatures. Hence, developing climate-resilient potato cultivars is needed to sustain potato production. However, the selection of heat-resilient potato genotypes under field conditions is challenging due to difficulties in creating warmer environments in an open field. This study tested the usability of open-sided clear polyethylene greenhouses (22.5 m x 14.0m x 4.6 m) constructed in the field to create a warmer environment in the selection of heat-resilient potato genotypes in two seasons. Previously selected 29 putative heat-tolerant and heat-susceptible genotypes were planted with four replications both in the greenhouse and in the open field next to the greenhouse. The greenhouse was created around 6–10 °C warmer environment than the open field from planting to harvest depending on the date and time of the day. Some morphological, physiological, biochemical, and agronomical traits of potato genotypes were determined during the growing period and after harvest. All traits evaluated including tuber yield and tuber dry matter contents were significantly affected by the heat environment. The results demonstrated that creating a warmer environment in the field could be a very effective strategy for selecting heat-resilient potato genotypes under field conditions. We will share and discuss our results in this poster.

7-05

Exploring factors influencing hybrid true potato seedling production

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Seedling production is a critical aspect in the success of field transplanting cropping systems for hybrid potato. We assessed the contribution of various factors including light, temperature as well as substrate and plug properties including water scheduling and nutrient application levels to seedling growth and development through various climate room studies. Additionally, we explored the possibility of defining and enhancing critical seedling vigour attributes to improve plant performance as well as plant response and adaptation to field conditions after field transplanting. Moreover, additional attributes besides leaf number and stem length were defined to design selection criteria for “transplantability” of TPS seedlings. To achieve this, seedlings of hybrid genotypes were raised under contrasting daylengths, light intensities and temperature regimes, and combinations of these factors, and the effects of these factors on seedling vigour were quantified. Increased light intensity and daylight integral enhanced leaf parameters and increased biomass under long-day conditions. Seedlings did not show conclusive responses under short-day conditions in most attributes. Higher temperatures increased biomass and constant day and night temperatures enhanced compaction of shoot architecture as did higher light intensities — to a greater extent. Moreover, we assessed the effects of increased plug volumes — and consequent decrease in seedling densities — as well as effects of increased watering intervals and of nitrogen and phosphorus on seedling vigour attributes. Increased seedling densities through decreased plug volumes causes significant reductions in seedling vigour by lowering seedling biomass, stem length and root:shoot ratios. Longer watering intervals reduced seedling vigour and led to stress phenotypes in seedlings as opposed to nutrient treatments where presumably, a more prolonged exposure to treatments would have led to significant stress in seedlings. Even so, increased nitrogen significantly influenced seedling growth while seedlings showed no response to increased phosphorus. These results will inform protocols for seedling production in greenhouse nurseries for true-potato-seed-based production systems. Additionally, the results provide a starting point for further research on optimizing hybrid seedling production for field transplanting.

7-06

Irrigation of seed potato in a summer crop

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Given the climate conditions in the Republic of Moldova, irrigation is one of the decisive factors in obtaining a high potato yield of good quality. The objective of this study was to evaluate and improve irrigation methods in seed and ware potato production, based on scientific insight in how the summer crop develops. Specifically, we aimed to create and maintain optimal moisture level in the 0-40 cm soil layer, where most of the potato roots are concentrated.

Two methods of potato irrigation were studied: sprinkler irrigation and drip irrigation. To maintain the moisture level in the 0–40 cm soil layer at 75–80 % field capacity, the amount of irrigation water varied from 1080 to 2100 m^3/ha. The total amount of the water varied from 1770 m^3 in the variant without irrigation to 3870 m^3/ha in the variant with sprinkler irrigation. As a result, the yield in the variants with irigation was three-four times higher than in the variants without irrigation. This means that seed potato production without irrigation is not efficient and therefore not recommended. Drip irrigation showed higher efficiency because less water was lost through direct evaporation or seepage into the deeper soil layer than with sprinkler irrigation. With drip irrigation we obtained a yield of 26.8 t/ha, using for planting freshly harvested tubers (after breaking dormancy) and 38.5 t/ha using seed tubers from last season, which is 5–6 t/ha more than with sprinkler irigation. We also observed that with drip irigation fewer green tubers occurred, because sprinkler irrigation sometimes caused ridge damage, exposing the tubers to direct sunlight.

During crop monitoring, we assessed that an optimal water supply in July guaranted a uniform and rapid earthing up, it enabled a uniform growth and development of the plants in August, while in September it guaranted the tubers to grow well. Atmospheric precipitation in October in small quantities made a harvest easier due to better soil separation. Precipitation beyond 25 mm in that stage led to complication of the harvesting process because of increased tare.

7-07

From controlled environment to field: confounding factors in container trials

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Global climate change models predict an increase of extreme weather events, among them drought and heat. Potato, one of the big five food crops globally, produces a high amount food calories per volume of water used by the plant. But, potato is drought sensitive. Maintenance of agricultural yield thus requires breeding of resilient cultivars. The bottleneck in drought tolerance breeding is the phenotyping in managed field environments. Power analysis indicated that a minimum of three drought stress trials under field conditions are required to get a stable tolerance ranking of the genotypes (DOI:10.3390/agronomy11050865). This is a significant amount of work. Thus, fundamental research on drought tolerance resorts to container-based test systems in controlled environments as a proxy. However, breeders debate the portability of results from these systems to performance under field conditions. Thus, we analysed the effects of climate conditions, container size, starting material, and substrate on yield and drought tolerance assessment of potato genotypes in pot trials compared to field trials. The tolerance ranking in the field was obtained from seven multisite-multiyear trials. The tolerance ranking in controlled environments was highly reproducible, but weakly correlated with field performance. Changing to variable climate conditions, increasing container size and substituting cuttings by seed tubers did not improve the correlation between pot and field results. Replacing horticultural substrate by sandy soil resulted in yield and tuber size distributions similar to those under field conditions. However, as the effect of the treatment × genotype × substrate interaction on yield was low, drought tolerance indices that depend on relative yields can be assessed on horticultural substrate too. Realistic estimates of tuber yield and tuber size distribution, however, require the use of mineral soil-based substrates.

7-08

Responses of potato cultivars to water stress condition in greenhouse: Agronomical and Physiological parameters

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Due to the effects of climate change, conditions tend to be increasingly extreme, with water availability being one of the main limiting factors in potato production. The objective of this study was to analyze the differential response of physiological and yield components in eight potato varieties under water deficit conditions. For this purpose, a greenhouse trial was carried out with the varieties Bintje, Montis, Sevilla, Lady Jane, Louisa, Dior, Acoustic and Tentation. Varieties were submitted to a moderate (MS) and severe (SS) stresses from 23 days after planting (DAP) until 55 DAP and compared to well-watered (WW) condition. Data were collected on morphological traits such as plant height and root length and weight. As well as the physiological traits such as stomatal conductance (gs), chlorophyll and Flavonoid content, relative water content (RWC), water use efficiency (WUE) and carbon isotope composition. At 55 DAP yield components were determined. Variation of all parameters (Δ) in comparison with control were calculated and contrasted with a drought tolerant index (TDI). Δ Gs, Δ WUE and Δ δ^{13}C explained 31-66%, 0-91% and 0-88% of DTI linear variation under MS and SS, respectively. The results showed that the genotype that maintain a better water status are more tolerant to water stress.

7-09

Influence of N fertilization, soil temperature, and moisture on gaseous N losses in the form of N_2O in starch potato cultivation in Northern Germany

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The strong impact on the environment and the high greenhouse gas potential of nitrous oxide (N_2O) underline the need to reduce its emissions in crop production. Avoiding gas losses during nitrogen (N) fertilization proves to be a strategy to improve N use efficiency and comply with sustainable fertilization practices in accordance with good professional standards.

The aim of the study, as part of the POTENZIO^N project (Potentials for increasing nutrient efficiency and reducing nitrogen emissions in starch potatoes), is to identify factors that influence gaseous N losses in the form of N_2O in potato cultivation. Next to N fertilization, soil moisture and temperatures were also examined.

In 2023, a field trial was carried out with the Eurotonda potato variety on sandy soil in Northern Germany at the Suderburg site. The study investigated the impact of type (Calcium ammonium nitrate, pig manure) and intensity (144 kg N ha^{-1}, 180 kg N ha^{-1}, unfertilized control) of N fertilization on N_2O emissions in the period from April to August. Soil moisture and soil temperature were measured for different variants using sensor data.

The Suderburg site had very low cumulative emissions (ranging from 0,03 to 0,25 kg ha^{-1}). The results show that the variant with organic fertilization on demand has the highest cumulative N_2O emissions. Despite the lack of significance, the results indicate that organic fertilization could possibly lead to higher N_2O emissions compared to mineral fertilization. This may be caused by higher carbon content in the soil as a result of manure application.

The organically fertilized variant has significantly higher N_2O emissions compared to the unfertilized control variant. Fertilization is therefore an important factor on the extent of N_2O emissions.

Another effect of the fertilization is that the soil temperatures in the fertilized variants as required are about 1 °C lower than in the control. This is partly due to the fact that some of the solar radiation is intercepted or reflected by the plant canopy, which leads to a reduction in the radiation absorption by the soil. While increased NO_3^- substrate availability leads to higher N_2O emissions, lower temperatures counteract lower N_2O emissions due to increased plant growth and shading.

The results highlight the interaction of environmental factors such as N availability, soil temperature, and soil moisture in different soil types which significantly influence N_2O emissions in potato cultivation.

8-01

Quantification of tuber damage with regard to the marketable quality of potato production in the Czech Republic

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In the 2022/2023 season, the downward trend in potato production in the Czech Republic continued, with an estimated 738 000 tonnes of potatoes produced. The total consumption in the country was estimated at 1 104 000 tonnes, with total losses, either from storage or tubers in the form of waste, estimated at 127 000 tonnes. At least 653 000 t of potatoes were stored in the country in different types of storage and in different types of storage.

In the context of a research on tuber damage in a 3000 tonnes potato storage facility, we focused on bulk potato storage. We addressed the quantification of damage occurring in the placed samples with respect to the marketable quality of potato production. The methodology evaluated quality parameters in three tuber size categories 0-35 mm, 35-55 mm and above 55 mm. Based on the quality parameters of ware potatoes, four basic categories were identified – no defects, mechanically damaged, affected by storage diseases and affected by pests. The samples were placed at different distances from the fan of the storage box, which uses a sub-grid ventilation system. All this took place in a farmer storage in the Bohemian-Moravian Highlands. With regard to the varieties stored by the commercial producer, the DALI variety was chosen.

The results of the research indicate that mechanical damage of tubers, which contributes to the development of storage diseases, is still the biggest cause of tuber quality degradation on post-harvest lines.

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8-02

New strategies for sprout-free long-term storage of processing potatoes in Norway

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The Norwegian potato industry is working towards being able to supply the Norwegian market with potatoes during the entire year. To fulfill this, the industry must be able to store potatoes for up to 9-10 months. Long-term storage requires optimal storage conditions, and processing potatoes needs a storage temperature above 6 ⁰C to avoid the accumulation of reducing sugars and elevated acrylamide content in the end product. Sprout suppressants are needed to avoid sprouting during the long storage season. As a result of CIPC getting banned in Norway and the rest of Europe in 2020, the need to test new antisprout agents arose. In this ongoing study, which is part of the project "Antigro 2021-2025", the focus is to do develop new, robust and sustainable strategies for long-term storage of processing potatoes under Norwegian conditions. Looking into alternatives with reduced doses, fewer applications or no use of sprout suppressants is the end goal. Possibilities for strategies with no sprout suppressants is mainly tested through the development of new cultivars/breeding lines which accumulate less sugar during cold storage temperatures.

Small-scale experiments were carried out during the storage season of 2021-22 and 2022-23. Six different treatment strategies were tested including two different sprout suppressants: 1,4-sight and Biox-M in the varieties Innovator, Peik, Fontane, Oleva, Lady Claire and Kiebitz. Climatic conditions including temperature and relative humidity and CO_2 and ethylene were logged during the storage season. The first season the stores had a setpoint of 8⁰C, while the second season the stores had a setpoint of 7 ⁰C. Small-scale experiments investigating the potential for cold temperature storage were carried out in the same time period. 3 different temperatures and 5 different varieties were included in the experiments. Sprout development was followed visually with weekly registrations and via a camera taking photos every three hours from mid storage season to the end of the storage season (January to June). Storage related quality measures such as sprout development, weight loss, glucose, frying color and other were registered three times during the storage season (March, April/May and June).

All treatment strategies with different sprout suppressors had good effect on the varieties included. Under Norwegian conditions, which has a shorter growing season and colder climate, the tubers are less mature at harvest. This may result in the possibility to reduce the total dosage of the sprout suppressant. Experiments for reduced chemical storage showed that some of the processing varieties can be stored at temperatures <6 ⁰C without developing darkening, sugar accumulation and acrylamide above the acceptable value.

8-03

Investigation of potato storage in Heilongjiang Province

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Potato is one of the four major food crops in China. Heilongjiang Province has very suitable natural conditions for potato production and is therefore the main production area for potato in China with an annual production of about 18 million tonnes and growing 2% of China's total potato production. Seed potato production is important in the Heilongjiang province. In 2022, the potato planting area in Heilongjiang was 7.27×10^4 ha, with a yield of 2.78 t/ ha. A large part of the potato production is stored. However, there is no accurate statistics on the storage capacity in the province. In this study we did a survey to get an overview of the potato storage situation in five regions (Daxignanling, Suihua, Yian, Keshan and Harbin) of the Heilongjiang Province and some of the stores are studied further in regards to climatic data and quality measurements of the tubers out of store. From the survey, we found that for the seed potato 40-60 % of the total production is stored, and for the table potato, most of the production is directly sold and only a small part (10–20 %) is stored. The storage period lasts 6–7 months from October to April next year. The seed potato production is stored for longer or shorter period of time as some of the production is exported to Southern part of China for planting in October and November. A large part of the production (approx 50%) is stored in traditional stores without temperature control system, they use natural ventilation with ambient air. Only a little part of the potato production is stored in modern stores with ventilation system and temperature control.

The total storage area for seed potatoes in Daxinganling comprises 5000–6000 m^2, 0.71–1 t/m^2. The total storage area in Suihua is 2000–5000 m^2, 1.5 ton/ m^2. In Yian, the potato storage area is 12000 m^2, 10000 tons and 0.8–1.0 ton/ m^2. In Keshan, the potato storage areas of the company is 10000 m^2, 20000 tons and 1.5–2 ton/ m^2. The potato storage areas of famers in Keshan are 5000-6000 m^2, 0.8–1 ton/ m^2. In Harbin the total storage area is 1.0×10^5 m^2. The majority of the potatoes in the stores are table potatoes and are modern stores.

In the seed potato stores the target temperature is 3–3.5°C from October to November and 1–2°C from December to January. The seed tubers are stored in big plastic bags (500 kg/ bags). It is easy for transport and cost saving.

In the table potato stores the target temperature is 3–5°C. The tubers are also stored in storage room, and stored in plastic bags.

The potato varieties used in the province are Youjin, Kexin No.13, Kexin No.23, favorite, Zhongshu No.5, Longshu No.5, Longshu No.12, Atlantic, Longshu No.4, Wotu No.5, Kenshu No.2, Xingjia No.2, Dongnong 310. All intended for table potatoes of big size. The estimated weight loss during storage is 5–10%. The loss is mainly due to water and soil.

8-04

An improved method for introducing ethylene in stores with potatoes for processing

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Ethylene gas is an effective sprout suppressant of stored potatoes (Prange *et al.*, 1998). It is widely used in Europe and elsewhere on table potatoes, and potatoes for processing. However, in potatoes stored for processing, the use of ethylene is sometimes associated with darkening of fry colour. Previous work has shown that darkening in fry colour takes place early in storage, after the introduction of ethylene, and is then followed by an extended period of recovery (Daniels-Lake *et al.*, 2005). Research therefore focused on the management of the initial introduction of ethylene with both *concentration* gradients and *duration* gradients being considered (Daniels-Lake et al., 2006).

Commercial control systems often use a *concentration* gradient, whereby the level of ethylene in the store is gradually increased over the initial weeks of storage. However, such systems may be limited by the sensitivity of control/measuring equipment. Results will be presented of a novel method for introducing ethylene, resulting in little or no effect on processing quality.

Daniels-Lake, B.J., Prange, R.K., Nowak, J. et al. Sprout development and processing quality changes in potato tubers stored under ethylene: 1. Effects of ethylene concentration. Am. J. Pot Res 82, 389–397 (2005). https://doi.org/10.1007/BF02871969

Daniels-Lake, B.J., Prange, R.K., Kalt, W. et al. Methods to Minimize the Effect of Ethylene Sprout Inhibitor on Potato Fry Colour. Potato Res. 49, 303–326 (2006). https://doi.org/10.1007/s11540-007-9025-6

Prange, R.K., Kalt, W., Daniels-Lake, B.J., Liew, C.L., Page, R.T., Walsh, J.R., Dean, P. and Coffin, R., 1998. Using Ethylene as a Sprout Control Agent in Stored Russet Burbank Potatoes. Journal of the American Society for Horticultural Science, 123(3), pp.463-469.

8-05

Low temperature, reconditioning and CO_2 levels in store during long-term storage of processing potatoes

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Acrylamide has become an important measure in the potato processing industry because it is a possible carcinogenic. In potato, there is a direct relationship between sugar contents in the tubers and the amount of produced acrylamide in the fried products. Potatoes for processing are typically stored at 8–10 ºC to avoid accumulation of reduced sugars by cold induced sweetening. However, with storage temperatures within this range, there is risk of storage losses caused by transpiration, sprouting and diseases. In this study, different storage strategies, including cold temperature storage and cold temperature storage followed by reconditioning, was investigated in different processing potato varieties. During the storage season the air composition in store changes. CO_2 levels can rise due to cold weather conditions outside, when fresh air is not drawn into the store, or during treatment with sprout inhibitors, where the store is closed to intake of fresh air for 48–72 hours. There is little documentation on the importance of air composition in storage for the accumulation of sugar and the formation of acrylamide. In this study, the effect of elevated CO_2 levels during storage on frying quality in different processing varieties was investigated.

The effect on the potato quality of different temperature strategies including a control at 8 ºC, cold storage at 5 ºC and cold storage followed by reconditioning (5 + 15 ºC) was tested in eight different processing varieties (Lady Claire, Kiebitz, Pirol, Lady Britta, Peik, Innovator, Zorba and Gullflaks) in small-scale stores during seven months storage. The same eight varieties were included in small-scale trials investigating the importance of elevated CO_2 levels (15000 ppm) for a period of 3 x 48 hours or 1 x 2 weeks during the storage season compared to a control with natural occurring CO_2 levels (~400 ppm). Temperature and CO_2 levels were also logged in six commercial stores and correlated to quality out of store. Reconditioning and CO_2 trials were conducted during three storage seasons from 2019 to 2022.

Some varieties (Kiebitz and Gullflaks) can be stored at 5 ºC without developing dark fry colour, sugar accumulation and high acrylamide levels. While other varieties benefited from reconditioning after cold storage (Peik, Innovator, Lady Britta). The disadvantage of an increased storage temperature is increased sprouting and greater weight loss. All varieties had significantly longer sprouts after reconditioning compared to cold storage, whereas some varieties (Peik, Zorba and Pirol) sprouted equally much at the control treatment (8 ºC) and after reconditioning (5 + 15 ºC). High CO_2 levels (up to 15000 ppm) in store was not found to be positively correlated with dark frying colour, sugar accumulation and high acrylamide content in neither the small-scale trials nor the measurements done in the commercial stores.

8-06

Ethylene sensitivity and effects on potato storage and quality

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Processing potatoes are stored at temperatures of 6–8 °C because of potential conversion of starch into reducing sugars at lower storage temperatures. These storage temperatures cause a high risk of sprouting. One option to prevent potatoes during storage from sprouting is the application of ethylene with the objective to adjust a steady concentration of ethylene throughout the storage period. At the same time, there is evidence of increased formation of reducing sugars during storage with ethylene. Relating to the development of sprouting or the generation of reducing sugars, different varieties of potatoes respond in different ways to the treatment with ethylene. In the presented study a screening of more than 40 varieties of processing potatoes, used for French fries, crisps and convenience products, was carried out to identify varieties being suitable for storage under ethylene atmosphere.

During 3 years more than 40 varieties of potatoes were grown under controlled field conditions, dessicated, harvested and stored. Storing was done at 8 °C in climate controlled, gastight storage units. After drying and wound healing the tubers, three different treatments for sprout inhibition were realized: A: 1,4 Sight (DMN), B: Ethylen (Biofresh), C: Ethylen (Biofresh) + SmartFresh (1-MCP). Samples were taken from storage at three time points (mid-February, mid-April and mid-June) and the following quality parameters were recorded: storage losses (sprouting, weight-loss, dry and soft rot), starch content, reducing sugar content and color of fried crisps.

Storage of processing potatoes under ethylene atmosphere at 8 °C leads, compared to storage with the sprout inhibitor 1,4 Sight, to higher storage losses due to an increase of sprouting alongside with weight losses, higher values of reducing sugars and a trend towards darker color of crisps. Sensitivity on ethylene-treatment depends on variety, duration of storage and observed quality parameter. An additional treatment of the ethylene variation with SmartFresh (1-MCP) leads to only little impact on sprouting but is able to reduce weight losses (in 2021/22) and decreases contents of reducing sugars.

Storage of processing potatoes at warm temperatures like 8 °C under ethylene atmosphere is possible, but success depends highly on the chosen variety, the duration of storage and the considered quality parameters. A classification of varieties that are suited for storage under ethylene is possible.

8-07

Sustainable solutions to control potato dormancy – a mechanistic approach

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Potato dormancy break during postharvest storage and further sprouting can lead to a reduction in the quality of raw material and food loss. The potato industry has heavily relied on the synthetic chemical chlorpropham (CIPC) as a sprout suppressant; yet its ban by the European Union in 2020 has left a technology gap. Alternative postharvest strategies include low storage temperatures and continuous ethylene supplementation; however, these methods lead to cold- and ethylene-induced sweeting. 1-methylclopropene (1-MCP) application in combination with ethylene supplementation during storage has been explored to mitigate sweetening, although the underlying mechanisms were poorly understood. Additionally, identifying the biological mechanisms of potato endodormancy could be a new sustainable approach to produce cultivars with enhanced dormancy.

Herein, potato dormancy transition was investigated. Plant hormones, such as abscisic acid (ABA) and cytokinins were quantified and RNAseq analysis carried out in apical buds of contrasting genotypes (high *vs*. low dormancy) from a diploid potato mapping population 06H1, stored at 15 °C. Hormone-related genes and several classes of transcription factors were identified as potential dormancy regulators (MYB, WRKY families); while an increase in cytokinins preceded dormancy break.

For the postharvest technology studies, UK-grown processing potatoes were treated with 1-MCP (1 ppm) followed by ethylene (10 ppm) and stored at 8.5 °C. Ethylene delayed sprouting and increased reducing sugars, but when combined with 1-MCP, the increase in reducing sugars was blocked, while the sprouting delay remained unaffected. This indicates that ethylene-induced sweetening can occur independently of sprout suppression. Stored tubers adapted to ethylene supplementation by activating ABA catabolism: upregulating the expression of CYP707A1_a, which encodes ABA 8´-hydroxylase. This results in lower ABA levels, although this effect is negated by 1-MCP. Transcriptome data revealed that ethylene- and cold-induced sweetening share the same underlying mechanism, with similar downregulation of the expression of *Kunitz-type invertase inhibitor*.

The mechanistic understanding of potato dormancy processes is crucial not only to develop targeted sustainable solutions to extend potato storage but to be considered as inputs in potato breeding programmes, which may improve the resilience of the potato supply chain while reducing food loss and waste.

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8-08

Improving Wound-Healing of Potato Tubers Using Natural Elicitors

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Wounding and bruising of potato tubers during harvest and postharvest handling cause severe economic losses to the potato industry. Currently, no practical treatment strategies are available to accelerate the wound-healing (WH) responses of potato tubers. Therefore, finding safe and effective postharvest treatment to improve WH of tubers for minimizing wound and bruising related losses has potato industry-specific relevance. In this study, efficacy of two natural elicitors, such as water-soluble chitosan oligosaccharide (COS 0.125 g L^{-1}) and cranberry pomace residue (Nutri-Cran 0.125 g L^{-1}) was investigated in five agronomically relevant red-skin potato cultivars (Chieftain, Dakota Rose, Dakota Ruby, Red LaSoda, Red Norland) using a mechanically wounded tuber tissue model. Formation of suberin polyphenolics (SPP), which is the first or immediate response of potato tubers to wounding stress, was determined histologically at 0, 3, 6, and 9 days after wounding. The potential role of stress protective metabolic regulation involving pentose phosphate pathway, phenolic metabolites, proline, and antioxidant enzymes were also investigated during WH of tuber tissues. Results indicated that both COS and Nutri-Cran accelerated formation of SPP in wounded tissue surface. However, the positive impact of elicitor treatment on SPP formation was greater with Nutri-Cran in wounded tuber tissues of Chieftain and Red Norland. Elicitor treatments enhanced ferulic acid and chlorogenic acid content, which are part of hydroxycinnamic acid group of compounds and are essential components of SPP domain. Higher activities of total antioxidant and superoxide dismutase were also determined with elicitor treatments at different time points after wounding. Reduced activity of succinate dehydrogenase, an indicator of respiration rate, was observed with Nutri-Cran treatment in tubers of Red Norland and Dakota Ruby after 3 days of wounding. Collectively, these results suggest that Nutri-Cran induces stress protective responses and accelerates formation of SPP at wounded surface, while suppressing respiration during WH of potato tuber tissues. Overall, Nutri-Cran is a promising WH treatment option and can be optimized for commercial use in postharvest storage to mitigate wounding and bruising related potato tuber losses.

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