Proceedings of the 20th Joint Meeting of EAPR section 'Breeding & Varietal Assessment' and EUCARPIA section 'Potatoes', St. Andrews, Scotland, June 2025

Vanessa Prigge[1], Charlotte Prodhomme[2], Thomas M Adams[3], Amanpreet Kaur[3,4], Yuk Woon Cheung[3,5], Vikrant Singh[3], Yuhan Wang[3,5], María Córdoba Sánchez[6], John T Jones[3,7], Xinwei Chen[3], Ingo Hein[3,5,8]
[1] SaKa Pflanzenzucht GmbH & Co. KG, Windeby, Germany
[2] Institut de Génétique, Environnement et Protection des Plantes (IGEPP), INRAE, Institut Agro, Univ Rennes, Le Rheu, France
[3] James Hutton Institute (JHI), Dundee, United Kingdom
[4] International Potato Center (CIP), Peru
[5] University of Dundee, School of Life Sciences, Dundee, United Kingdom
[6] Institute for Sustainable Agriculture (ISA), Córdoba, Spain
[7] University of St. Andrews, School of Biology, St. Andrews, United Kingdom
[8] Corresponding author: Ingo.Hein@hutton.ac.uk

Potato breeders and geneticists convened in the beautiful city of St. Andrews in Scotland as the 20th Joint Meeting of EAPR section 'Breeding & Varietal Assessment' and EUCARPIA section 'Potatoes' was held from 15-18 June 2025 at the University of St. Andrews. The conference was jointly organised by the James Hutton Institute, the University of Dundee and the University of St. Andrews. It was well attended by 105 participants from 17 countries (Fig. 1). The scientific committee consisted of Ingo Hein (James Hutton Institute, UK), Amanpreet Kaur (James Hutton Institute, UK), Charlotte Prodhomme (inov3PT, France), Vanessa Prigge (SaKa Pflanzenzucht GmbH & Co. KG, Germany), Delphine Van Inghelandt (Leibniz Institute of Plant Genetics and Crop Plant Research and Federal Research Center for Cultivated Plants, Germany), Jadwiga Sliwka (Plant Breeding and Acclimatization Institute, Poland), Rodomiro Ortiz (Swedish University of Agricultural Sciences, Sweden), Maria de la O Leyva Perez (NEIKER, Spain), Stan Oome (HZPC Research B.V., The Netherlands), Domenico Carputo (University of Naples, Italy), and Aska Goverse (Wageningen University and Research, The Netherlands).

Held under the theme "**Potato breeding in the era of pan genomes and advanced genetics**", the 3-day conference featured 38 talks including eight keynote lectures as well as 19 posters. In the first session of the conference, we explored ways for **Harnessing Diversity from Genetic Resources** with three talks. In the keynote lecture, Amanpreet Kaur presented how enrichment sequencing of CPC and CIP accessions uncovered novel *R* genes. She also emphasized that these collections represent valuable sources of nutritionally dense germplasm for potato improvement programmes. Session **Breeding for Disease and Insect Resistance** featured 13 talks including two keynotes, covering such diverse biotic stresses as late blight, common scab, PVY, soft rot Pectobacteria, potato cyst and root knot nematodes, as well as insects like Colorado potato beetle, aphids and whiteflies. Dan Milbourne explored ways to closing the gap between breeding disease-resistant potato varieties and building useful management practices for their use in integrated pest management, in the frame of the IPMorama project. He reminded the community that "it's not just about the R gene, it's about what you do with it!”. In the second keynote of this session, Mercedes Torres Torres introduced the audience to the PHENO-TUB project which aims to develop an integrated computer-vision system for plant-to-field health detection and elaborated on the various steps required for transferring research from the (computer) lab to the field.

Session **Breeding Methodology** featured eleven talks including two keynote lectures. Kristian Thorup-Kristensen suggested to the potato breeding and research community that physiological traits, and particularly deep rooting architecture, may be worthwhile exploring when breeding for improved performance under future climate change scenarios. He also presented how their RadiMax platform is being used to study root development and identify genotypes with deeper and more efficient root systems. In contrast, Jeff Endelman focused on novel methods of mating design optimisation and introduced concepts from the animal breeding community to balance short-term genetic gain with maintaining genetic variance for long-term gain, which are practically implemented for polyploids in the R/COMA software tool. Session **Diploid Breeding** featured four talks and was spearheaded by the keynote lecture of Corentin Clot who introduced the concept of Fixation-Restitution Breeding, a novel inter-ploidy potato breeding concept that combines the best of two worlds: rapid stacking and fixation of useful alleles on the diploid level coupled with restitution of the tetraploid level and clonal production in the final variety product.

Session **Leveraging the Pangenome for Breeding** also featured four talks and dived into the recent advances in potato pangenome analysis. The keynote lecture by Lin Cheng highlighted how genomics can assist in designing optimal potato genotypes by identifying and purging deleterious SNPs and structural variations. The final session **Gene Editing and Mutation Breeding** exhibited three talks. In his keynote, Matías González shared the latest news from the GeneBEcon project and related efforts, highlighting recent advances in transgene-free gene editing and the challenges of editing coding sequences in potato. This report publishes abstracts of most of the talks presented at the conference to summarize recent knowledge advances and inspire potato research and breeding. When applicable, the full text paper of a conference contribution is cited for convenience of the interested reader.

SESSION: HARNESSING DIVERSITY FROM GENETIC RESOURCES

Harnessing diversity from potato germplasm collections

Authors: Amanpreet Kaur[1,2], Jie Li[3], Sophie Mantelin[3], Miles Armstrong[1], Gaynor McKenzie[1], Ingo Hein[1,4]

Affiliations: [1]James Hutton Institute, Dundee, [2]International Potato Centre (CIP), [3]College of Plant Protection, China Agricultural University, Beijing, China,[4]University of Dundee, Nethergate, Dundee

Abstract: As climate change threatens global food production, harnessing the untapped genetic diversity of wild crop relatives is critical for sustainable agriculture. Wild potato species, native to Americas and Mexico, harbour a wealth of traits that can improve disease resistance, nutrition, and climate resilience in cultivated varieties. At the James Hutton Institute, we continuously monitor the Commonwealth Potato Collection (CPC), an international genebank of wild potato species, using state-of-the-art, resistance gene enrichment sequencing (RenSeq) in diagnostic mode (dRenSeq) to uncover valuable genetic diversity. In *Solanum bulbocastanum*, we identified novel resistance genes, including Rpi-blb4 (identified in accession 7650 and mapped to Chromosome V) and functional variants of Rpi-blb1 in accessions 7641, 7643, 7644, 7647, and 7648. These variants showed both gain and loss-of-function mutations, offering insights into natural plant immunity and the molecular basis of disease resistance. We also explored *Solanum stenotomum*, a diploid landrace exhibiting high variation in drought tolerance and nutrient bioavailability. Through integrated genotyping and phenotyping, we mapped quantitative trait loci (QTLs) linked to key agronomic traits, demonstrating its value for climate-resilient breeding. These findings illustrate the power of genetic diversity in wild species to inform and accelerate crop improvement. By combining advanced genomics, genetics with global germplasm collections, we are building the genetic foundation for breeding disease-resistant, climate-resilient, and nutritious potatoes.

Pangenome analysis of Solanum section Petota

Authors: Helen Tai[1], Ilayda Bozan[2], Sai Reddy Achakkagari[2], Noelle Anglin[3], Martina Stromvik[2]
Affiliations: [1]Agriculture and Agri-Food Canada, [2]McGill University, Canada, [3]United States Department of Agriculture - Agricultural Research Service

Abstract: Potato is part of the genus Solanum section Petota with over 100 species. A pangenome of Solanum section Petota composed of 296 accessions was constructed using novel and published genomes including diploids and polyploids compared using presence/absence variation (PAV). A phylogenetic tree constructed based on PAVs demonstrated grouping of accessions into clades similar to taxonomy proposed by Spooner et al. based on DNA markers. Core, shell, and cloud genes were analyzed in the pangenome. The core (shared by at least 97% of the accessions) were enriched in genes involved in highly conserved cellular functions such as meiosis, mitosis, and RNA metabolism. The shell (shared by 3 to 97%) included genes involved in response to stress and systemic acquired resistance. The cloud genes (present in less than 3%) showed enrichment in transposable elements (TEs) as well as stress response genes. A cladewise pangenomic approach identified cold stress response among the core genes in clade 1+2 and clade 3, and flowering/tuberization among the core genes in clade 4. The TE content differed between the clades, with clade 1+2 composed of species from North and Central America with reproductive isolation from species in other clades having much lower TE content compared to other clades. In contrast, accessions with a history of in vitro propagation were identified and found to have high levels of TEs. Results indicate a role for TEs in adaptation to new environments, both natural and artificial, for Solanum section Petota. This work has been published as: **Bozan I, Achakkagari SR, Anglin NL, Ellis D, Tai HH, Strömvik MV** (2023) Pangenome analyses reveal impact of transposable elements and ploidy on the evolution of potato species. PNAS **120:** e2211117120 doi: https://doi.org/10.1073/pnas.2211117120

Population genetic parameters and deleterious mutations in tetraploid potato

Authors: Sapphire Coronejo[1], Laura Shannon[1]
Affiliations: [1]University of Minnesota, USA

Abstract: Potatoes have a complex history that has resulted in a complex genome. Over 100 wild relatives, multiple ploidy levels, a series of domestication, range expansion, and improvement bottlenecks, and both sexual and clonal reproductive systems have shaped the potato genome. Using Illumina short read sequence data from a collection of 98 dihaploids derived from US tetraploid cultivars and advanced breeding material, we have found evidence of extensive structural variation and high heterozygosity on an individual and population level. Unexpectedly, we have also observed very low historical recombination rates ($\rho = 4N_{er} = 1.42$ kb^{-1}). In general, populations with high levels of diversity tend to exhibit high values of ρ, but potatoes run counter to this expectation. Observed recombination rates from published tetraploid potato mapping studies are not similarly low. This may indicate that recombination rates have changed over time, or it may indicate a low effective population size. However, low effective population size is not consistent with our observations of diversity ($\theta w=4N_{e\mu}=0.0117$

kb⁻¹) unless potatoes are characterized by an unusually high mutation rate. The derived site frequency spectra for the dihaploids contain a large number of low-frequency variants consistent with a high mutation rate. The spectra also exhibit an abundance of intermediate- and high-frequency derived alleles, indicating a history of allele turnover and retention that may reflect domestication or improvement processes. These frequency patterns provide a context for assessing the distribution of functional variation, including putative deleterious mutations identified through codon-level predictions and comparative genomics. This work has been pre-printed as: Coronejo S, Vaillancourt B, Hamilton JP, Meng X, Mailloux K, Christensen G, Huege J, Shaw KM, Agha HI, Brown-Donovan K, *et al*. (2025) Potato dihaploids uncover diverse alleles to facilitate diploid potato breeding. BioRxiv 668948 doi: https://doi.org/10.1101/2025.08.06.668948

SESSION: BREEDING FOR INTEGRATED PEST MANAGEMENT

Breeding for variety-centric IPM

Authors: Dan Milbourne[1]
Affiliations: [1]Teagasc, Carlow, Ireland

Abstract: Disease and pest resistant potato varieties should form an integral part of integrated pest management approaches but are frequently poorly integrated into existing agronomic systems. This state of play corresponds to a particularly challenging time for potato production in terms of biotic stresses. For instance, the recent appearance in Europe of strains of *P. infestans* such as EU_43_A1 that have evolved resistance to both CAA and OSPBI fungicides is a real threat to production. The situation for PCN is equally challenging; in Scotland, for example, a doubling of PCN infested land area every 7 years threatens seed potato production. As part of the Horizon Europe project IPMorama (Grant no. 101135348), we are proposing a three-component strategy to develop what we call a “variety-centric” integrated pest management (IPM) approach that will make best use of available plant protection products (PPPs) and genetic resistance. This approach is based on: (1) Genome-based breeding tools and strategies that allow the combination of multiple *R*-genes of known pathotype-specificity with the quality and agronomic traits that will drive uptake of new varieties; (2) Disease surveillance networks based on an understanding of the ability of the pest or pathogen to overcome both the specific *R*-genes that are currently deployed (and those in breeding pipelines) and the available PPPs; (3) Specific practicable management approaches that maximally combine the efficacy of the *R*-gene and PPP components, based on easy-to-use decision support systems. Further information can be found at the project website www.ipmorama.eu.

Novel late blight disease resistance gene identification and mapping in tetraploid potato

Authors: Vikrant Singh[1], Amanpreet Kaur[1,2], Thomas Adams[1], Jane Yildiz[1], Brian Harrower[1], Ingo Hein[1,3]
Affiliations: [1]The James Hutton Institute, Dundee, [2]International Potato Centre (CIP), [3]University of Dundee, Nethergate, Dundee

Abstract: Late blight, caused by the oomycete *Phytophthora infestans*, remains the most significant potato disease even 160 years after the Great Famine of 1845. The pathogen causes an estimated annual yield loss of $6.7 billion worldwide. Due to its co-evolution with host plants, *P. infestans* can rapidly overcome resistance genes deployed in cultivated potato varieties, necessitating the continual identification of novel resistance sources within the germplasm. Diagnostic resistance gene enrichment sequencing (dRenSeq), a powerful and cost-effective tool for identifying and validating known resistance genes, detected the presence of *Rpi-R3a* and *Rpi-R3b* in the tetraploid salad potato cultivar 'Athlete'. However, the strong foliage and tuber resistance to late blight observed in 'Athlete' could not be explained by these already defeated genes. Furthermore, the incomplete pedigree information of AR 99-263-5, one of Athlete's parents (Miriam × AR 99-263-5), provides limited insight into its genetic background. To identify the underlying resistance gene, we established a cross between 'Athlete' (resistant parent) and 'Gemson' (susceptible parent). The F1 progeny segregated in a 1:1 ratio ($\chi^2 = 1.44$), indicating the presence of a single dominant resistance gene. RenSeq analysis, combined with SNP and k-mer based approaches, mapped this novel resistance gene to the short arm of Chromosome XI.

Breeding the next generation of late-blight resistant Sarpo potatoes

Authors: Katherine Steele[1], Ingo Hein[2,3], Christine Jones[4], Richard Meridith[4], James Stroud[1], Sarah Vowles[1], Debbie Evans[1], Simon White[†][1,5], David Shaw[5]
Affiliations: [1]Bangor University, Wales, [2]The James Hutton Institute, Dundee, [3]University of Dundee, Nethergate, Dundee, [4]Dyson Farming Limited, [5]Sarvari Research Trust

Abstract: Transformative Reduced Input Potatoes (TRIP) is a multi-partner project exploring strategies that can reduce the ecological footprint of potato cultivation. The UK potato industry currently relies on intensive blight protection programmes, however this reliance could be significantly reduced if future varieties incorporate effective combinations of late blight resistance genes (*Rpi* genes). The aim of the project's Breeding work-package, conducted over three growing seasons, was to test the field performance and late blight resistance of novel clones selected for late blight resistance from crosses between Sarpo varieties with released varieties with different known *Rpi* genes. An additional objective was to evaluate scope for additional trait improvement by additional inter-crosses between selected clones. Field trials conducted in North Wales in 2023 and 2024 were managed with no blight protection and natural infection of late blight was encouraged using spreader rows. Blight incidence was scored weekly following its initial observation in the field and results confirmed excellent field resistance among the novel clones. Two clones were independently tested by Eurofins in 2024 under severe disease pressure, yielding with impressive results. Leaf DNA samples from all trial entries, including a diverse collection of released potential donor parents, were analysed using dRenSeq. These findings revealed novel combinations of *Rpi* alleles among the Sarpo-derived clones. These findings from the first two years provide a valuable foundation for selecting clones to develop the next generation of late blight resistant Sarpo potatoes, potentially incorporating additional resistance to viruses and PCN, as well as key traits such as resilience to abiotic stress and market appeal.

Tetraploid mapping for common scab resistance in potato

Authors: Fatima Latif Azam[1,3,4], Jeffrey B. Endelman[2], Dan Milbourne[1], Denis Griffin[1], Herman J. van Eck[3,4]
Affiliations: [1]Teagasc, Carlow, Ireland, [2]Department of Plant and Agroecosystem Sciences, University of Wisconsin-Madison, Madison, United States, [3]Plant Breeding, Wageningen University & Research, Wageningen, The Netherlands, [4]The Graduate School Experimental Plant Sciences, Wageningen, The Netherlands

Abstract: Common scab, caused by various Streptomyces spp., is the most important skin blemish of potato, with yield losses ranging from 30% to 50% in the most severe cases. Developing resistant varieties is the most effective strategy for managing this disease. Previous studies on the genetics of resistance have identified only minor-effect QTLs. The aim of this study was to identify loci for resistance from two Teagasc varieties that consistently exhibit high levels of resistance to common scab. The varieties Electra and its immediate progenitor, Picasso, were crossed to the susceptible variety Desiree to develop a tetraploid interconnected mapping population of 436 potato clones. Genomic data for the potato clones comprising over 2000 short read haplotypes was generated using the PotatoMASH genotyping tool. Field and glasshouse trials were conducted over two years, resulting in four sets of phenotypic data. QTL mapping was performed using the DiaQTL package with identity-by-descent (IBD) probabilities estimated using the PolyOriginR package. We identified three QTLs using the additive model and seven QTLs using the dominant model. A multi-QTL model built with backward elimination identified five QTLs, explaining 31% of the total phenotypic variance. In addition to the QTL discovery, we also performed genomic prediction utilizing the same datasets, which yielded a Pearson's Correlation Coefficient of 0.37 between the observed phenotypes and genomic estimated breeding values (GEBV). We will further discuss how the identified markers can be utilized to breed for scab resistance more efficiently, as marker-assisted selection (MAS) is unlikely to be effective in this case.

Use of a phased genome assembly in an association study to identify *H1* resistance gene against potato cyst nematodes

Authors: Yuk Woon Cheung[1,2*], Lynn H Brown[1,2*], Thomas M Adams[1], Brian Harrower[1], Amanpreet Kaur[1,3], Gaynor McKenzie[1], Jamie Orr[1], James Price[1], Vikrant Singh[1], Moray Smith[1], Micha Bayer[1] and Ingo Hein[1,2]

Affiliations: [1]The James Hutton Institute, Dundee, United Kingdom, [2]The University of Dundee, Nethergate, Dundee, [3]International Potato Centre (CIP), Lima, Peru

*These authors contributed equally to this study

Abstract: Potatoes (*Solanum tuberosum*) are threatened by a diverse range of unrelated pathogens. Central to breeding for durable resistance is the identification and deployment of disease resistance (*R*) genes, such as *H1*, a key gene conferring resistance to the potato cyst nematode *Globodera rostochiensis*. This research encompasses the identification of *H1* resistance gene candidates and highlights how advancements in phased genome assembly have enabled precise genetic and physical mapping of the underlying resistance loci. Using cutting-edge sequencing technologies such as Oxford Nanopore Technology, we have achieved haplotype-resolved assemblies of dihaploid potato genomes, allowing detailed structural characterization of the *H1* resistance gene cluster with the use of an adapted SMRT-Agrenseq-d workflow. The study integrates high-resolution genome assembly with association genetics approaches, including R-gene enrichment sequencing (RenSeq), to delineate resistance loci at both the genetic and physical levels. The workflow combines ONT Seq (Oxford Nanopore Technology sequencing), AgRenSeq (*k*-mer based association genetics), and dRenSeq (presence/absence diagnostics), together termed ONT-AgRenSeq-d. This pipeline enables the high-resolution mapping of the *H1* locus and its variants, offering a blueprint for discovering additional *R* genes. By leveraging the power of phased genome assemblies, we can not only pinpoint *R* genes such as *H1* but also provide a gateway to unravelling the genomic architecture surrounding them. This provides insight into gene evolution, structural variation, and linkage, ultimately guiding the development of markers for efficient breeding. Our research demonstrates how state-of-the-art genomic tools are reshaping our understanding of plant immunity and accelerating the breeding of disease-resistant potato cultivars. This work has been pre-printed as: Cheung, Y. W., L. H. Brown, T.

M. Adams, B. Harrower, A. Kaur *et al*., 2025 Phased Potato Genome Assembly and Association Genetics Enable Characterisation of the Elusive *H1* Resistance Locus Against Potato Cyst Nematodes. bioRxiv 667887 doi: https://doi.org/10.1101/2025.08.04.667887

NEM-EMERGE: Managing potato cyst nematodes that have overcome current host plant resistances due to genetic selection

Authors: Aska Goverse[1], Charlotte Prodhomme[2,3], Marie-Claire Kerlan[3], Ingo Hein[4,5]
Affiliations: [1]Wageningen University & Research, Netherlands, [2]inov3PT, France, [3]INRAE, UMR Igepp, France, [4]The James Hutton Institute, Dundee, [5]The University of Dundee, Nethergate, Dundee

Abstract: Soil-borne plant-parasitic nematodes are a biosecurity risk for global food production with an estimated annual loss of €110 billion worldwide. Root-knot nematodes (RKN) and potato cyst nematodes (PCN) rank 1 and 2 in the Top 10 of high-impact plant-parasitic nematodes with RKN alone accounting for ~5% of global crop losses. For decades, non-specific, environmentally harmful agrochemicals have been applied to manage PCN. The increasing awareness about their negative impact prompted the phasing out of most nematicides. Consequently, there is an urgent need for novel, durable control strategies that enable adequate responses by stakeholders to prevent crop losses in the EU and beyond. The application of resistant varieties is an essential instrument to control PCN in a sustainable manner. However, recent reports document the emergence of PCN problems in potato cropping across Europe and beyond due to genetic host selection by the application of a limited set of resistance genes over decades. Therefore, the identification and characterization of novel sources of resistance in potato to control emerging virulent populations is key and one of the main objectives of the NEM-EMERGE Horizon EUROPE project. By using a multi-actor and interdisciplinary approach NEM-EMERGE aims to join efforts and provide a spectrum of sustainable, science-based solutions for both the conventional and organic farming sector based on the principles of IPM, including (1) optimized crop rotations schemes including cover crops, (2) tailored host plant resistances, and (3) optimal use of the native antagonistic potential of soils. Further information can be found at the project website https://nem-emerge.eu/.

Breeding for resistance to Columbia Root-Knot Nematode (CRKN) (*Meloidogyne chitwoodi*) of potatoes (*Solanum tuberosum* L.) in the genomics era

Authors: Vidyasagar Sathuvalli[1], Oluwafemi Omilani[1], Brian Knaus[1], Kelly Vining[1]
Affiliations: [1]Oregon State University, United States

Abstract: Breeding for disease resistance to the Columbia Root-Knot Nematode (CRKN) (*Meloidogyne chitwoodi*) remains the most effective and sustainable management strategy. The USDA-ARS, Prosser, USA, developed a resistant genotype, PA99N82-4, from a wild potato (*S. bulbocastanum*) selection, SB22. The gene(s) associated with resistance, as well as the extent of genome introgression from SB22 into PA99N82-4, remain elusive. PA99N82-4 was assembled into a primary assembly with 5k contigs and an N50 of ~16mb, of which 789 contigs were greater than 50kb. This PA99N82-4 assembly was used for a comparative genomics analysis with SB22 and other genomes. The results show comparable levels of genomic and genic synteny between the PA99N82-4 and SB22. The results also suggest a high sequence identity between PA99N82-4 and SB22 in the resistance region. Twenty-nine single-copy orthogroups were identified between PA99N82-4 and SB22 in a multiple sequence alignment including four other genomes, of which three were functionally annotated as resistance genes. The candidate resistance gene had 100% shared sequence identity in the

PA99N82-4 and SB22. While orthologs were found in other genomes, they showed percentage identities only ranging from 64–80%. A multiple sequence alignment of the gene's orthologs in other genomes revealed several SNPs as well as a premature stop codon which corresponds to a leucine-rich repeat (LRR) present in both the SB22 and PA99N82-4 but absent in the susceptible DM (v6.1). A functional validation of the molecular function of this gene remains necessary, but it represents a positive discovery that could be invaluable for advancing Oregon State University potato breeding program's efforts to develop CRKN-resistant cultivars.

PHENO-TUB: Automated, accurate, in-field detection of potato diseases by precision computer vision approaches

Authors: Michael Lee[1], Harshitha Nagarajan[1], Eleanor Southwell[1], Aidan Laing[1], Matteo Bermond[1], Rob Hancock[2], David Nelson[3], Martin Stothard[3], Vidyanath Gururajan[1], Mercedes Torres Torres[1]
Affiliations: [1]B-Hive Innovations, United Kingdom, [2]The James Hutton Institute, United Kingdom, [3]Branston Potatoes

Abstract: High-quality potatoes are the foundation of the UK's annual 4.8M tonne potato production. To maintain this quality, potato crop must be regularly inspected for a range of both biotic and abiotic stressors. Unhealthy seed can result in certification downgrades, reducing value, or even the total rejection of crop. For ware crop, unhealthy potato plants result in reduced marketable yields affecting grower's returns and increasing wastage. Diseases like late blight, known for its quick spread, and blackleg cost £50M each to the potato industry yearly. Currently, growers/surveyors of seed or ware potatoes manually comb fields, visually inspecting plants to understand field status, stressors or risks of stressors. This is specialised, laborious, error-prone and time-consuming work. As such, complete comprehensive surveying is impossible. Computer vision and machine learning approaches have improved to the point where there is an immediate opportunity to adopt a precision approach to identification of plant defects. The PHENO-TUB project aims to develop an integrated computer-vision system for plant-to-field health detection using our state-of-the-art computer vision and hyperspectral imagery. We aim to provide a comprehensive solution to detection of rogue and diseased plants in potato production, focusing on the detection and monitoring of select biotic stressors known to cause the most problems to growers including blackleg, late blight and viral disease, such as potato virus Y.

Metabolite profiling of the potato tuber as a potential tool in resistance breeding

Authors: Paul Himmighofen[1], Christoph Böttcher[1], Stefanie Hartje[2], Jost Muth[3], Karin Gorzolka[1]
Affiliations: [1]Julius Kuehn Institute, Germany, [2]EUROPLANT Innovation GmbH & Co. KG, Germany, [3]Fraunhofer Institute for Molecular Biology and Applied Ecology, Germany

Abstract: Potato tubers contain a huge diversity of specialized metabolites in their peel. Among these, glycoalkaloids are well described as an important factor in breeding, while the majority of metabolites receive little attention. Many metabolites and their bioactivity are unknown; additionally, there is little knowledge about the variation among potato cultivars. In a first step, we performed untargeted analyses using HPLC-QTOF-MS on tuber peel extracts of 45 different cultivars and compared them in quality and quantity of their metabolite profile. Metabolites were putatively identified by MS/MS analyses. We detected approximately 660 relevant mass signals. Each cultivar exhibits a distinct metabolome, which is largely stable over multiple trials. Glycoalkaloids are present in all cultivars at high amounts, while other metabolites are produced by specific cultivars only. This includes hydroxycinnamic acid derivatives, saponins, anthocyanins, and a class of polyamines, which has not yet been described. In a second step, we fractioned peel extracts to test for bioactivity of single components against *Phytophthora infestans* as a potential potato pathogen. We present a comprehensive overview of biologically relevant metabolites in the cultivated potato, which can be useful information for resistance and resilience breeding. Hereby, untargeted metabolite screening can speed up resistance breeding of the potato, reduce the use of chemical agents in plant protection, and extend the value chain of the potato.

Bulked segregant analysis of Colorado potato beetle resistance in *Solanum okadae*

Authors: Hanna McCoy[1], Kyle Gardner[2], Ghaith Zamzam[2], Larry Calhoun[1], Helen Tai[2]
Affiliations: [1]University of New Brunswick, Canada, [2]Agriculture and Agri-Food Canada

Abstract: *Leptinotarsa decemlineata* (Say), the Colorado potato beetle (CPB), is a major insect pest for the potato industry with 30-50% yield losses. There is a lack of resistance in commercial potato varieties, and genetic improvement of resistance is a goal for breeders. Breeding strategies include cross-pollinations with CPB-resistant wild relatives of potato. *Solanum okadae* (PI 458367), a wild potato native to Bolivia and Argentina, was previously reported to deter CPB feeding. Metabolomic analyses of *S. okadae* clone OKA15 have indicated high production of leaf-specific lactone-containing metabolites toxic to insects that are not present in CPB-susceptible *S. tuberosum*. The inexpensive and widely accessible colorimetric Baljet assay to quantify lactone-containing metabolites in leaves was applied for phenotyping CPB resistance. A CPB-susceptible diploid *S. tuberosum* clone W5281.2 expressing low levels of lactones was crossed with CPB-resistant OKA15. An F1 clone (W52OKA) from this cross producing a high level of lactones was backcrossed to W5281.2 to generate a genetic mapping population that was phenotyped using the Baljet assay. A wide-ranging variation of lactone production in the genetic mapping population was found. A bulked segregant analysis (BSA) approach was used for QTL mapping of the lactone-production trait. The leaves from clones in the mapping population with varying levels of lactones were bulked for DNA extraction and sequencing. Pairwise comparison between bulks with varying levels of lactones resulted in different QTL peaks, demonstrating that the trait is controlled by multiple loci on different chromosomes.

Studying insect resistance in wild Solanum species

Authors: Lotte Caarls[1], Miriam Strijker[1], Lize Braat[1], Wendy van 't Westende[1], Jaap Wolters[1], Yury Tikunov[1], Richard Visser[1], Ben Vosman[1]
Affiliations: [1]Wageningen University & Research, Wageningen, Netherlands

Abstract: Insect infestations present major challenges for potato cultivation, not only by directly damaging plants through feeding but also by spreading viral diseases. Key threats include the Colorado potato beetle and the transmission of viruses by the aphid *Myzus persicae* and the whitefly *Bemisia tabaci*. With the phasing out of chemical pesticides, there is an urgent need for alternative solutions, such as developing insect-resistant potato varieties. While cultivated potatoes have limited resistance to insects, wild potato relatives display promising traits. Some wild accessions possess insect-repelling tetraose glycoalkaloids, and others have glandular trichomes, which can trap insects. To identify novel sources of resistance, we have screened more than 300 wild potato accessions for resistance to three major insect pests: Colorado potato beetle, aphids, and whiteflies. Numerous accessions were found to be resistant to Colorado potato beetle, with some also showing resistance to aphids and whiteflies. Metabolite analysis of leaves was performed, and correlation analysis was done to identify potential resistance-conferring metabolites. Ten accessions, where different resistance mechanisms were expected, were chosen for further study. In these plants, type and density of trichomes were recorded, and glycoalkaloids were measured. Several resistant accessions contained glandular trichomes or tetraose glycoalkaloids, which were earlier associated with biotic resistance. Other accessions possess novel, yet unidentified, resistance mechanisms. Segregating populations are now being analyzed for resistance to insects, metabolites, and trichomes. Study of these populations will generate knowledge on the genetics of the resistance and contribution of each mechanism to resistance to the insects. For more information, visit this website: https://research.wur.nl/en/projects/lwv24033-chips-combating-harmfull-insects-in-potato-with-sustaina.

Susceptibility and resistance to soft rot Pectobacteriaceae

Authors: Jack Vossen[1], Elisabeth Yanez[1], Pichaya Cheewapoonphon[1], Jan van der Wolf[1], Brian Lavrijssen[1]
Affiliations: [1]Wageningen University and Research, Wageningen, Netherlands

Abstract: Soft rot diseases are caused by a range of bacterial species, mutually referred to as soft rot Pectobacteriaceae (SRP). Currently, hygiene measures are the only means to deal with SRPs in potato. The complexity of the SRP problem is caused by different Dickeya and Pectobacterium species and subspecies that can cause both latent and symptomatic infections. In addition, the SRP inoculum sources are diverse (seed tubers, flooding, aerosols, rain, and insects), and the different plant organs show different susceptibility levels and symptoms (tuber soft rot, blackleg, slow wilt). Not surprisingly, breeding for resistance against SRPs has not been very successful, so far. In the SuRePec project, funded by the Ministry of Agriculture of the Netherlands and commercial breeders, we pursued a combined approach to reduce susceptibility and to enhance resistance to SRP in potato. To accomplish these two goals, dedicated high-throughput bioassays for the different infection routes and plant organs were deployed and further developed. To reduce susceptibility, we have targeted known susceptibility (S) genes to enhance resistance using RNAi and CRISPR-Cas9 knockouts. Also, we performed a GWAS study to determine why some varieties in the current breeding germplasm are more susceptible than others. To enhance SRP resistance, we characterized the SRP resistance in different organs of a *Solanum chacoense* plant using QTL mapping. Markers for the genes underlying the susceptibility and resistance were developed and will allow selection against or introgression of them, respectively, to select SRP-resistant varieties through classical or genome editing breeding approaches.

SESSION: BREEDING METHODOLOGY

Deep root phenotyping of potatoes, studied by minirhizotrons, deep placement of ^{15}N and ^{2}H labelled water, and d^{13}C as drought stress indicator

Authors: Kristian Thorup-Kristensen[1] and Olga Popovic[1]
Affiliation: [1]University of Copenhagen, Dept. of Plant and Environmental Sciences, Denmark

Abstract: Root traits are important for crop productivity, resilience and nitrogen efficiency, but almost never included in crop breeding as we severely lack methods for root phenotyping. One important trait for water and nitrogen efficiency is rooting depth, as deep rooting give access to otherwise unexploited subsoil layers. Potatoes have a limited root depth development, comparable to spring cereals, but it has a quite different kind of root system, due to its germination from tubers. We have studied potato root development in our field scale root phenotyping facility RadiMax. We found potato roots growing to more than 1.3 meters depth, with a significant difference among genotypes. Using deep placement of stable isotope tracers (^{2}H labelled water and ^{15}N labelled nitrogen placed at approx. 1.2m), we could also measure actual uptake from the deep soil layers. Deep uptake of ^{15}N showed a strong correlation to deep rooting, with ^{15}N recovery ranging from zero to more than 30%. Uptake of ^{2}H water showed similar genotypic variation. We also used the natural ^{13}C enrichment as an indicator of drought stress. We have found good correlations between ^{13}C, deep root growth and deep tracer uptake in other crops, but this relationship was not clear in the potato results, as the potatoes had a higher variability in maturity time. The early maturing potato genotypes developed less deep rooting and tracer uptake, but still also less drought stress, as the earlier maturity helped them escape some of the summer drought. Results from our first study on potato root phenotyping are published in: doi.org/10.1007/s11540-024-09802-4.

Integrating genomic factor analytic models and environmental predictors for potato variety recommendation

Authors: Marcio Resende[1*], Liza Van der Laan[1], Lenin Pereira[2], Tiago Marçal[2], Leo Hoffmann[1], Lincoln Zotarelli[3], Henrique Boriolo[4], Gerrit Hoogenboom[4], NCPT Breeders[5], Kaio Dias[6], Marco Peixoto[1]

Affiliations: [1]Sweet corn and Potato Breeding and Genomics lab, University of Florida, Gainesville, Florida, USA, [2]Departamento de Biologia, Universidade Federal de Lavras, Lavras, Minas Gerais, Brazil, [3]Horticultural Science Department, University of Florida, Gainesville, Florida, USA, [4]Global Food Systems Institute & Agricultural & Biological Engineering, University of Florida, Gainesville, Florida, USA, [5] National Chip Processing Trials Initiative, [6]Departamento de Biologia Geral, Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil

Abstract: Integrating environmental, genetic, and statistical tools offers a powerful approach for optimizing cultivar recommendations under increasing environmental uncertainty. Here, we present a pipeline for optimizing cultivar selection and recommendations for a target population of environments and across future scenarios. Yield data were collected from 43 environments (spanning 2019–2023 and 11 locations). The evaluation was conducted as part of the National Chip Processing Trial, which included over 800 genotypes from different breeding programs. Genotypic data included 15,000 markers. Environmental predictors (EPs) were generated for all environments, derived from soil and climate datasets covering the entire USA. We implemented a factor analytic (FA) model to predict the yield performance of each genotype. A partial least squares (PLS) approach was used, incorporating the EPs and the FA loadings from each environment to predict individual environments. Model performance was assessed using leave-one-environment-out cross-validation, and the FA model was benchmarked against a widely used reaction norms model. In a second step, geographic information tools were combined with genomic data, phenotypic data, and environmental data to generate nationwide cultivar recommendation maps. Spatial interpolation was used to obtain a spatially contiguous interpolation representation of compositional dissimilarity, and a PLS modelling model was used to predict genotype performance in untested locations. Cross-validations showed that the FA model correlations outperformed the reaction norm model's accuracy. Maps were generated to highlight top-performing cultivars, overall performance trends, and the projected impact of environmental changes on cultivar selection. Further results on EP-based recommendations, national trends, global trends, and future projections will be discussed.

Data driven approaches to assess farmer trait-preferences to guide potato breeding programs in East Africa

Authors: I. Barker[1,] T. Mendes[1], M. Gatto[1], D. Borus[1], E. Kihiu[1], A. Meyer[2], G. Kang[3], P. Rukundo[1], A. Nduwumuremyi[4], L. Echessa[5]

Affiliations: *[1]International Potato Center (CIP), [2]RESONANZ Group, Wollerau, Switzerland; Institute of Plant Sciences, [3]Scuola Superiore Sant'Anna, Pisa, Italy; [4]Rwanda Agriculture and Animal Resources Development Board (RAB); [5]County Government of Nakuru, Kenya*

Abstract: Whilst varietal adoption, and hence impact from potato breeding programs, is driven by a number of factors including availability of seed, marketing and promotion and market linkages, farmer preference is clearly also a key factor. Many public breeding programs, including those of the International Potato Center (CIP) and its partners have adopted more "demand-led" processes which includes agreeing trait product profiles (TPPs) for new varieties which match farmer and market needs. The identification and ranking of desired traits that make up the TPP is agreed and reviewed by product design and advancement teams typically including stakeholders with a knowledge of the crop, the local environment and relevant value-chains. Input from social scientists can also be sought to address other relevant issues such as gender and equity. The product advancement teams also have access to data from farmer participatory on-farm trials and ultimately from variety adoption data over time. Recent innovations in collecting such data at lower cost include the *Tricot* methodology and the *VarScout* app. *Tricot* methodology permits collection of data from on-farm trials employing incomplete block design and crowd-sourced data collection. *VarScout* is a digital ecosystem built around a smartphone app which collects varietal-linked data from farmers' fields, principally variety adoption, again using a crowd-sourced approach. Data from both approaches from potato trials and production fields in Rwanda and Kenya will be presented and farmer trait preferences discussed in relation to current potato breeding goals in the region. Supporting evidence for this abstract and more information on *VarScout* and *Tricot* can be found at 10.4160/cip.2025.02.001 and 10.1017/S0014479725100100, respectively.

Iron Roots: Scaling biofortified potatoes to combat anaemia across the global South

Authors: Hannele Lindqvist Kreuze[1], Diego Naziri[1], Moctar Kante[1], Gabriela Burgos[1], Ian Barker[1], Hugo Campos[1]
Affiliation: [1]International Potato Center (CIP)

Abstract: Anaemia affects over 500 million women and 269 million children globally, with the highest burden in low- and middle-income countries. Potatoes—consumed by over 500 million women in the Global South, with per capita consumption exceeding 100 kg in some regions—offer a promising vehicle for iron biofortification. Since 2009, CIP breeders have identified natural genetic variation in iron content and demonstrated high heritability largely independent of environmental conditions. Two tetraploid high-iron potato varieties were released in Peru in 2023 and 2024, supported by dissemination strategies and large-scale seed multiplication. While some yield drag has been observed, these varieties perform competitively under high late-blight pressure and are gaining market traction. Clinical studies in Peru show that iron from these biofortified potatoes is highly bioavailable, delivering 48% more iron than non-biofortified clones. Regular consumption could meet up to 27% of daily iron needs for women with moderate reserves, and up to 50% for those with low reserves. Using the GloMIP tool, CIP identified priority intervention markets based on anaemia prevalence, potato consumption, and production. The South Asian lowlands (India, lowland Nepal, Bangladesh) are top priorities, followed by highland regions (e.g., Meghalaya, highland Nepal, Bhutan), and third-tier targets in Africa (Kenya, Ethiopia, Rwanda). Central Asia also shows strong potential. Future breeding strategies will integrate iron as an "invisible trait" into existing product profiles beyond the Andes. This presentation will share insights from the demand analysis and outline the strategic roadmap for scaling iron-biofortified potatoes globally. Further Information can be found in the following DOI: https://doi.org/10.1093/jn/nxaa267, https://doi.org/10.1016/j.tjnut.2023.04.010, https://doi.org/10.1002/csc2.20170.

Mating optimization with inbreeding constraints in potato

Authors: Jeffrey Endelman[1]
Affiliations: [1]University of Wisconsin-Madison, Madison, WI, USA

Abstract: Plant breeders have long appreciated the need to balance selection for short-term genetic gain with maintaining genetic variance for long-term gain. With optimum contribution selection (OCS), the genetic contributions of the parents are chosen to maximize the genetic merit of the next generation at a target inbreeding rate. OCS assumes random mating and uses general combining ability, i.e., breeding value, for merit. Optimum mate allocation (OMA) extends OCS by optimizing the contribution of each possible mating to the next generation, which enables dominance effects to be included for specific combining ability. A convex formulation of OMA and associated software, named COMA, has been developed. The long-term performance of COMA was investigated via stochastic simulation in both diploid and tetraploid populations. Results from the University of Wisconsin tetraploid breeding program will also be shown, based on genomic prediction of a multi-trait index. More information can be found in the publication: https://doi.org/10.1093/genetics/iyae193

Strategies to improve early generation selection in potato breeding programs

Authors: David De Koeyer[1], Rebecca Standen[1], Robyn Morgan[1], Mohammad Islam[1], Erica Fava[1]
Affiliations: [1]Agriculture and Agri-Food Canada, Fredericton, NB, Canada

Abstract: Genetic improvement of cultivated potato (*Solanum tuberosum* L.) has several challenges, including autotetrasomic inheritance and high levels of heterozygosity. High-throughput, affordable molecular marker-assisted selection allows identification of progeny with desired traits early in the breeding cycle. Genomic prediction can identify better parents and variety candidates much earlier than approaches based solely on phenotypic assessment. Despite these advances, little progress has been made in improving the effectiveness of selection in the early generations of potato breeding programs. Typically, tens of thousands of seedlings are grown in a greenhouse to produce tuber families that are planted the next year in the field. Agriculture and Agri-Food Canada's potato breeding program traditionally grew approximately 50,000 seedlings each year in un-replicated single hills. This represents a large portion of the land used by the program, from which relatively few (1-5%) seedlings advance to the next generation. Since 2019, we have split the families into replicated plots and have been transitioning to growing multiple hills per seedling. More recently, separate plots planted with extra mini-tubers from some families were used to compare tuber uniformity within and between families. These changes provide the framework for comparing parents and families for selection percentage, studying the genetic factors underlying selection in the early generations, and increasing the effectiveness of selection within potato breeding programs. Progress towards these goals will be highlighted in this presentation.

Transferability of genomic prediction models across market segments in potato and the effect of selection

Authors: Kathrin Thelen[1,2], Po-Ya Wu [1,7], Nadia Baig [3,6], Vanessa Prigge[4], Julien Bruckmüller[4], Katja Muders[5], Bernd Truberg[5], Stefanie Hartje[6], Juliane Renner[6], Delphine Van Inghelandt [1,7] Benjamin Stich [1,2]

Affiliations: [1]Julius Kühn-Institute (JKI) – Federal Research Centre for Cultivated Plants, Institute for Breeding Research on Agricultural Crops, Germany, [2] Professorship for Utilization of Plant Genetic Resources for Breeding Purposes, Faculty of Agricultural and Environmental Sciences, University of Rostock, Germany, [3] Institute for Quantitative Genetics and Genomics of Plants, Heinrich Heine University, Germany, [4] SaKa Pflanzenzucht GmbH & Co. KG, Germany, [5] Nordring-Kartoffelzucht- und Vermehrungs-

GmbH, Germany, [6] EUROPLANT Innovation GmbH & Co. KG, Germany, [7] Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany

Abstract: Genomic prediction (GP) can help increase the efficiency of breeding programs, as genotypes can be selected based on their predicted performance. However, to the best of our knowledge, this procedure is not yet routine in commercial breeding programs in tetraploid organisms like potato (*Solanum tuberosum* L.). The objectives of this study were to: i) estimate the prediction accuracy for 26 different potato traits in a panel of about 1,000 genotypes based on 202,008 single nucleotide polymorphisms, ii) evaluate the influence of the size and constitution of the training set on the prediction accuracy, and iii) investigate how the effect of selection in the training set influences the outcome of GP. GP revealed high prediction accuracies using genomic best linear unbiased prediction. Our results indicated that a training set of 280 to 480 clones and 10,000 markers was sufficient. Prediction within a specific market segment led to a higher prediction accuracy compared to adding clones from other market segments to the training set or to predict between different market segments. Lastly, we found a higher prediction accuracy when in a training set of selected clones, i.e., a training set that consists of clones with high trait values, 20% of the clones were replaced by clones that were sampled from the clones that showed the lowest 10% trait values. This observation shows that clones from advanced breeding stages can be used as training set, if some clones specifically from the other side of the distribution range are added to the training set. For further information please see https://doi.org/10.1007/s00122-025-05004-9.

Leveraging phased haplotypes and ultra-low coverage sequencing to track introgressions in potato breeding

Authors: Yuhan Wang[1], Yuk Woon Cheung[1], Thomas Adams[2], Vikrant Singh[2], Moray Smith[1], Amanpreet Kaur[2,3], Ingo Hein[1,2]
Affiliations: [1]University of Dundee, [2]The James Hutton Institute, [3]International Potato Centre (CIP)

Abstract: Phased haplotypes in potato provide a powerful framework to integrate genetic insights with the physical structure of target loci. By precisely mapping genomic intervals associated with disease resistance genes, we demonstrate how these phased regions reveal introgressions from wild species and landraces into cultivated varieties. Our analyses identify recombination breakpoints, enabling us to define minimal introgressed segments in resistant cultivars and estimate average introgression sizes. Remarkably, we show that ultra-low coverage whole-genome sequencing (as low as 0.1×) is sufficient to detect the presence or absence of these introgressions, which can range from several hundred kilobases down to just 20 kb. Given the increasing availability of genomic data, this approach represents a novel class of presence/absence markers that can be used alongside traditional tools to support marker-assisted selection in potato breeding.

Selection limits and yield plateaus in tetraploid potato breeding

Authors: John Bradshaw[1]
Affiliation: [1]Honorary Associate, James Hutton Institute, Dundee, United Kingdom

Abstract: The potatoes being grown today are the products of deliberate hybridizations and selections made by breeders, starting in the 19th century from an unknown genetic base, but one with an increasing contribution from Chilean Tuberosum. Thus, potato breeding at the James Hutton Institute today can be traced back over 18 generations and 180 years to 1845. Hence, about every ten years, there was the opportunity for progress through sexual

reproduction and a new generation of improved cultivars for farmers. In practice, the breeding of successful potato cultivars has been much slower, with many securing the full 30 years of royalty income from plant breeders' rights. Potato breeding in the era of advanced genetics should be much faster, and breeders can contemplate 18 generations in 18 years using genomic selection for quantitative traits such as yield. However, in designing such breeding programs, I think that the theory of selection limits will be relevant. Potato yields in the UK, for example, increased by 50%, from 14.8 t/ha to 22.9 t/ha, over the 76 years from 1887 to 1963, and then nearly doubled to 42.4 t/ha over the 45 years to 2008, but have not increased since then. Simple theoretical considerations indicate the factors that affect selection limits. The amount of additive genetic variation in the base population is all-important, and hence the germplasm used to start or continue a breeding program: no variation, no progress! For a given amount of additive genetic variation, the number of segregating loci determines the selection limit and the number of generations required to reach it. If there is just one locus, the best genotype will exist in the base population, but if there are 64 loci, the selection limit could be 16 standard deviations from the mean of the base population and take more than 20 generations to be reached. Accurate information on the number of segregating loci would therefore be useful to the breeder. In practice, selection would generate disequilibrium both within and between loci and hence reduce the genetic variation available for selection. If the desirable alleles at most loci were at low frequencies, say around 0.05, then with many loci segregating, the desirable allele would be lost at one or more loci, but not at all loci, so that the maximum achievable selection limit would be lower than the theoretical limit. Accurate information on allele frequencies would be useful to the breeder. The presence of non-additive genetic variation for traits such as yield could result in a selection limit with the presence of non-additive genetic variation but no additive variation for further progress through sexual reproduction. Breeders need to know the relative amounts of each type of variation in their populations and how they and breeding values change with allele frequencies. Given the many factors involved in the theory of selection limits, the practical breeder should find the results of computer simulations based on estimates of key parameters from experimental results of help in designing better breeding programs in future.

Assessment of segregation variance estimates via derivation, simulations, and empirical data in autotetraploid potato

Authors: Po-Ya Wu[1,2], Kathrin Thelen[1,3], Stephanie Hartje[4], Katja Muders[5], Vanessa Prigge[6], Benjamin Stich[1,3], Delphine Van Inghelandt[1,2]
Affiliations: [1] Federal Research Centre for Cultivated Plants (JKI), Institute for Breeding Research on Agricultural Crops, 18190 Sanitz, Germany, [2] Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), 06466 Seeland, Germany, [3] Utilization of Plant Genetic Resources for Breeding Purposes, Faculty of Agricultural and Environmental Sciences, University of Rostock, 18059 Rostock, Germany, [4] Europlant Innovation GmbH & Co. KG, 21337 Lüneburg, Germany, [5] NORIKA GmbH, 18190 Sanitz, Germany, [6] SaKa Pflanzenzucht GmbH & Co. KG, 24340 Windeby, Germany

Abstract: To optimize the choice of parents and crosses, the prediction of segregation variance is of high relevance in breeding. Several methods have been developed for this, including correlation with genotypic diversity, progeny simulations, or algebraic derivations in case of a diploid inheritance. To the best of our knowledge, no algebraic derivation using parental genotypic information is available to predict segregation variance for tetraploid inheritance. Our objectives were to (1) develop algebraic derivations based on linkage disequilibrium (LD) between loci to predict the segregation variance for autotetraploid species; (2) compare the segregation variance estimated based on simulated progenies and the algebraic derivations; (3) investigate by simulations how experimental parameters affect the

accuracy of segregation variance prediction; and (4) compare the segregation variance estimated in empirical data and the one based on the algebraic derivations and predicted marker effects. The segregation variance estimated by the developed derivations showed very high correlations with the one observed in large, simulated progenies, but those were lower when phased parental haplotypes were not available or family size decreased. The correlations between segregation variance estimated by the developed derivations and the empirical data were low. This could be attributed to the small family sizes used in the study, which we could show to increase LD between unlinked loci. The proposed algebraic derivations promise to be a precise alternative to simulations to help breeders in optimizing their family choices and sizes considering segregation variance. This work was published as a pre-print at https://www.biorxiv.org/content/10.1101/2025.08.13.670171v1.

Diving into diversity of potato resistance genes

Authors: Paulina Paluchowska[1], Zhimin Yin[1], Erik Lysøe[2], Simeon Lim Rossmann[2,3], Mirella Ludwiczewska[1], Marta Janiszewska[1], Sylwester Sobkowiak[1], May Bente Brurberg[2,3], Jadwiga Śliwka[1]

Affiliations: [1]Plant Breeding and Acclimatization Institute - National Research Institute, Poland, [2]Norwegian Institute of Bioeconomy Research (NIBIO), Ås, Norway, [3]Norwegian University of Life Sciences (NMBU), Ås, Norway

Abstract: Potato virus Y (PVY) and *Phytophthora infestans* are highly destructive pathogens threatening potato cultivation worldwide. Using host resistance is an environment-friendly and cost-effective way to limit their impact. Resistance to PVY and *P. infestans* has been discovered in wild potato species such as *Solanum stoloniferum* and *S. demissum* and was introgressed into some potato cultivars even before the underlying resistance genes (Ry_{sto} gene and *Rpi* genes) were discovered. Using an Amplicon Sequencing (AmpSeq) approach based on PacBio single molecule real-time sequencing method, we investigated the presence and diversity of:

- The Ry_{sto} gene in wild relatives of potato (298 genotypes representing 29 accessions of 26 tuber-bearing *Solanum* species) and six resistant controls (potato cultivars Alicja, Bzura, Hinga, Nimfy, White Lady and breeding line PW363)
- Ten *Rpi* genes in 183 potato cultivars, 98 breeding lines and 54 genotypes of wild potato species.

A total of 55 unique *Rysto-like* sequences were identified, encoding in total 45 unique protein sequences (Paluchowska et al. 2024). We sequenced also 108 variants of 10 *Rpi* genes (from two to 25 amplicon sequence variants per gene). The genes *R1*, *R2-like*, *Rpi-ABPT*, *R3a* and *R3b* are widespread in cultivars, while the *Rpi-vnt1* and *Rpi-ber1* were found mostly in breeding lines. The AmpSeq strategy proved to be reliable and efficient. Data on the distribution and sequence diversity of the resistance genes can facilitate new breeding strategies and lead to the discovery of new gene variants with different resistance spectra.
The research leading to these results has received funding from the Norwegian Financial Mechanism 2014–2021, project DivGene, UMO-2019/34/H/NZ9/00559. This work was published as Paluchowska, P., Lim Rossmann, S., Lysøe, E. et al. Diversity of the Ry_{sto} gene conferring resistance to potato virus Y in wild relatives of potato. BMC Plant Biol 24, 375 (2024). https://doi.org/10.1186/s12870-024-05089-2

SESSION: DIPLOID BREEDING

Fixation-Restitution Breeding: Proof of concept and open questions for an interploidy potato breeding scheme

Authors: Corentin Clot[1], Merit Schulte[1], Christel Engelen[1], Ronald Hutten[1], Herman van Eck[1]
Affiliations: [1]Wageningen University, Wageningen, Netherlands

Abstract: Two main schemes currently compete to shape the future of potato breeding: clonal selection in tetraploids and F1 hybrid breeding in diploids. At the intersection of these approaches, we propose an alternative — Fixation-Restitution Breeding — which combines the efficiency of diploid breeding with the vigour due to progressive heterosis and the agricultural value of tetraploid clones. This strategy relies on two key traits: self-compatibility, which allows for the stacking and fixation of desirable alleles such as disease resistance genes in diploids, and 2n pollen production, which enables the transmission of these alleles to the tetraploid level through 4x × 2x crosses. Over the past five years, we have uncovered the genetic basis of these traits and developed markers for several resistance genes. Using these tools, we bred and selected diploid clones that are self-compatible, carry multiple R-genes, and produce 2n pollen. These improved diploids, our prospective recurrent parents, are now being crossed with elite tetraploids to validate the Fixation-Restitution concept. This transition from genetic research to breeding prompted us to investigate practical questions, such as determining the optimal threshold of 2n pollen production enabling successful crosses at the diploid and tetraploid level. At the same time, broader strategic questions remain regarding the extension of this framework to complex traits, the balance between fixation and inbreeding depression, the need for market-specific recurrent parents, and the strategy to maximize heterosis. In this talk, I will share progress and open questions, aiming to initiate discussion about the future of (interploidy) breeding in potato.

Optimum mate allocation in the UW-Madison diploid potato breeding program

Authors: Maria Caraza-Harter[1], Jeffrey Endelman[1]
Affiliations: [1]University of Wisconsin - Madison, Madison, WI, USA

Abstract: The University of Wisconsin-Madison is applying recurrent selection in a diploid potato breeding program, with the ultimate aim of developing inbred lines for F1 hybrid varieties. Genetic gains under recurrent selection come at the expense of genetic variance, but to ensure sufficient diversity for long-term progress, it is important to control the rate of inbreeding. Our objective was to allocate resources for the 2025 seedling nursery using the software COMA, to maximize genetic gain subject to constraints on inbreeding rate, available seed, and the frequency of PVY resistance. Pedigree-estimated breeding values were used for genetic merit, based on the yield of tubers and true potato seed over four years of greenhouse experiments. Pedigree relationships between our diploid founders and the current generation will be summarized, along with coefficients of inbreeding. Additional traits under selection and recent progress with our field selection program will be discussed.

Capturing the genetics of eastern United States potato germplasm for diploid breeding

Authors: Ek Han Tan[1], Paul Collins[2], Mario Andrade[1], Noah Williams[1], Diana Spencer[1]

Affiliations: [1]University of Maine, United States, [2]Agricultural Research Service, USDA, Orono, ME, USA

Abstract: One of major the undertaking for diploid potato breeding efforts at the University of Maine and the eastern United States is to access the genetics within the conventional varieties and clones developed by breeding programs in this region. Thus far, we have generated several primary dihaploid populations from these clones and are beginning to introgress self-compatibility and male fertility traits using these lines, followed by inbreeding. We also utilize select Solanum phureja-S. stenotomum long-day adapted diploid clones developed by the USDA-ARS that carry desirable traits such as coloured flesh, late blight resistance and resistance to Dickeya dianthicola, a member of the bacterial complex that causes potato blackleg and soft rot disease. In addition, through our collaboration within the Host-Virus Evolutionary Dynamics Institute, we are also focused on understanding the disease dynamics of Potato Virus Y using greenhouse and field methods in Maine. This diploid potato breeding effort with our eastern US network of cooperators and other public diploid breeding programs, allows us to test diploid clones that are representative of the region's conventional potato germplasm and build upon the wide adaptability required in this growing region. This work has been published as: Williams N., Colwell Z., Spencer D., Kornelis G., Mackertich S., Sawitsky B., Balderrama D., Carnes A., Tan E.H., Collins P. (2025) Cytoplasmic Background of Diploid and Tetraploid Breeding Line Families at the USDA-ARS Potato Variety Development for the Eastern U.S., American Journal of Potato Research, https://doi.org/10.1007/s12230-025-10005-x

SESSION: LEVERAGING THE PANGENOME FOR BREEDING

Leveraging a phased pangenome for haplotype design of hybrid potato

Authors: Lin Cheng[1,9], Nan Wang[1,2], Zhigui Bao[1,3], Qian Zhou[4], Andrea Guarracino[5], Yuting Yang[1], Pei Wang[1], Zhiyang Zhang[1], Dié Tang[1,6], Pingxian Zhang[1], Yaoyao Wu[1,7], Yao Zhou[1,8], Yi Zheng[1], Yong Hu[1], Qun Lian[1], Zhaoxu Ma[1], Ludivine Lassois[9], Chunzhi Zhang[1], William J. Lucas[10], Erik Garrison[5], Nils Stein[11,12], Thomas Städler[13], Yongfeng Zhou[1,2] and Sanwen Huang[1,2]

Affiliations: [1]National Key Laboratory of Tropical Crop Breeding, Shenzhen Branch, Guangdong Laboratory of Lingnan Modern Agriculture, Genome Analysis Laboratory of the Ministry of Agriculture and Rural Affairs, Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzhen, Guangdong, China, [2]National Key Laboratory of Tropical Crop Breeding, Chinese Academy of Tropical Agricultural Sciences, Haikou, Hainan, China, [3]Department of Molecular Biology, Max Planck Institute for Biology Tübingen, Germany, [4]School of Agriculture and Biotechnology, Sun Yat-Sen University, China, [5]Department of Genetics, Genomics and Informatics, University of Tennessee Health Science Center, USA, [6]Department of Genetics, Yale University School of Medicine, USA, [7]College of Horticulture, Nanjing Agricultural University, China, [8]Key Laboratory of Plant Molecular Physiology, Institute of Botany, Chinese Academy of Sciences, China, [9]Plant Genetics and Rhizosphere Processes Laboratory, TERRA Teaching and Research Center, University of Liège, Belgium, [10]Department of Plant Biology, College of Biological Sciences, University of California, USA, [11]Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben, Germany, [12]Crop Plant Genetics, Institute of Agricultural and Nutritional Sciences, Martin-Luther-University of Halle-Wittenberg, Germany, [13]Institute of Integrative Biology and Zurich-Basel Plant Science Center, ETH Zurich, Switzerland

Abstract: The tetraploid genome and clonal propagation of the cultivated potato (*Solanum tuberosum* L.) dictate a slow, non-accumulative breeding mode of the most important tuber crop. Transitioning potato breeding to a seed-propagated hybrid system based on diploid inbred lines has the potential to greatly accelerate its improvement. Crucially, the development of inbred lines is impeded by manifold deleterious variants; explaining their nature and finding ways to eliminate them is the current focus of hybrid potato research. However, most published diploid potato genomes are unphased, concealing crucial information on haplotype diversity and heterozygosity. Here we develop a phased potato pangenome graph of 60 haplotypes from cultivated diploids and the ancestral wild species and find evidence for the prevalence of transposable elements in generating structural variants. Compared with the linear reference, the graph pangenome represents a broader diversity (3,076 Mb versus 742 Mb). Notably, we observe enhanced heterozygosity in cultivated diploids compared with wild ones (14.0% versus 9.5%), indicating extensive hybridization during potato domestication. Using conservative criteria, we identify 19,625 putatively deleterious structural variants (dSVs) and reveal a biased accumulation of deleterious single nucleotide polymorphisms (dSNPs) around dSVs in coupling phase. Based on the graph pangenome, we computationally design ideal potato haplotypes with minimal dSNPs and dSVs. These advances provide critical insights into the genomic basis of clonal propagation and will guide breeders to develop a suite of promising inbred lines.

The phased pan-genome of tetraploid European potato

Authors: Hequan Sun*[1,2], Sergio Tusso*[3], Craig Dent[1,6], Manish Goel[3], Raúl Y. Wijfjes[3], Lisa C. Baus[3], Xiao Dong[1], José A. Campoy[1], Ana Kurdadze[3], Birgit Walkemeier[1], Christine Sänger[1], Bruno Huettel[1], Ronald C. B. Hutten[4], Herman J. van Eck[4], Klaus J. Dehmer[5], Korbinian Schneeberger[1,3,6]
Affiliations: [1]Max Planck Institute for Plant Breeding Research, Germany, [2]Xi'an Jiaotong University, China, [3]Ludwig Maximilian University of Munich, Germany, [4]Wageningen University and Research, The Netherlands, [5]Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany, [6] Cluster of Excellence on Plant Sciences (CEPLAS), Germany
*These authors contributed equally to this study

Abstract: Potatoes were introduced to Europe in the 1500s and one species (*Solanum tuberosum* ssp. *tuberosum*) became a staple crop within a few centuries. However, its highly heterozygous, autotetraploid genome has complicated its subsequent improvement. Here we present the pan-genome of European potatoes generated from phased genome assemblies of ten historical potato cultivars, which includes approximately 85% of all haplotypes segregating in Europe. Sequence diversity between the haplotypes was extremely high, owing to numerous introgressions from wild potato species which apparently predate modern breeding efforts. By contrast, haplotype diversity was very low, in agreement with the population bottlenecks caused by domestication, transition to Europe, and late blight epidemics. To illustrate a practical application of the pan-genome, we converted it into a haplotype graph and used it to generate phased, megabase-scale pseudo-genome assemblies of commercial potatoes (including the cultivar Russet Burbank) using cost-efficient short reads only. In summary, we present a nearly complete pan-genome of autotetraploid European potato, and we outline how this resource might be used to accelerate genomics-assisted breeding and research. This work has been published as: Sun H, Tusso S, Dent CI, Goel M, Wijfjes RY, Baus LC, Dong X, Campoy JA, Kurdadze A, Walkemeier B, *et al*. (2025) The phased pan-genome of tetraploid European potato. Nature 624: 389-397 doi: https://doi.org/10.1038/s41586-025-08843-0

The potato pan-NLRome

Authors: Thomas Adams[1], Gaynor McKenzie[1], Micha Bayer[1], Ingo Hein[1,2]
Affiliations: [1]The James Hutton Institute, Dundee, United Kingdom, [2]University of Dundee, Nethergate, Dundee

Abstract: A key constraint on worldwide potato production is crop losses due to a diverse range of plant pathogens. A major method for control of these pathogens is through the breeding of resistant varieties and a major mechanism of disease resistance is mediated by intracellular resistance (*R*) genes. Many of these *R* genes encode for a structurally conserved class of genes, termed nucleotide-binding, leucine-rich repeat (NLR) genes. The full complement of these NLRs in an individual plant is termed an NLRome. Through the use of enrichment sequencing technologies (RenSeq) and the decrease in sequencing costs in recent years, it is now feasible to assess the NLRome of a population, termed a pan-NLRome, as was first done for Arabidopsis thaliana ecotypes. However, for potato, long read technologies, such as PacBio HiFi, are required to accurately represent the NLRome. Through the use of Pacbio HiFi RenSeq reads (termed SMRT-RenSeq) and cutting-edge annotation techniques, including supplementation with the deep learning tool Helixer, we have produced a pan-NLRome of over 100 accessions of diploid Solanum wild species and landraces selected from the Commonwealth Potato Collection (CPC). A *k*-mer based NLRome analysis can reliably distinguish species and reproduces the accepted phylogenetic structure. The total number of predicted NLRs for a species ranges from 188 to 1,571. This pan-NLRome provides critical insight into the diversity and evolutionary dynamics within a key gene family for potato breeding efforts to safeguard potato production into the future.

A deep DNA sequence variation analysis of Pan-genomic disease resistance homologs to identify informative SNPs for universally transferable markers

Authors: Xinwei Chen[1], Micha Bayer[1], Lynn Brown[2], Vanessa Young[3], Ingo Hein[1,2]
Affiliations: [1]The James Hutton Institute, Dundee, [2]The University of Dundee, Dundee, United Kingdom, [3]James Hutton Limited, Dundee

Abstract: Modern molecular technologies enable precise identification of functional allele(s) of resistance genes against various pests and diseases, facilitating informed breeding through molecular marker-based screening. However, marker-assisted selection in potato is hindered by its highly heterozygous and polyploid genome, limiting marker diagnostics and transferability. This study aims to develop a computational pipeline for generating highly robust and universally transferable markers (UTMs) using next-generation sequencing data. We analysed resistance gene enrichment sequencing (dRenSeq) data from 174 genetically diverse potato samples, including both cultivated and wild species. Resistance genes *Rpi-R3a*, *Gpa2*, and *Rx1*, conferring resistance to late blight, potato cyst nematode, and potato virus X, respectively, were specifically examined. At a 0% mismatch threshold, 41, 21, and 20 cultivars were identified as carrying full-length functional gene sequences. Using a relaxed 4% mismatch threshold, SNP variants were systematically assessed for transferability as diagnostic markers. Among 948, 754, and 834 quality SNPs identified for *Rpi-R3a*, *Gpa2*, and *Rx1,* only 1, 4, and 7 met the criteria for UTMs. Conversion of these SNPs into Kompetitive Allele-Specific PCR (KASP) markers successfully reproduced dRenSeq results, allowing unambiguous discrimination between resistant and susceptible cultivars. This study demonstrates a novel approach to functional, big-data-driven UTM development, which can be extended to other resistance and agronomic genes, enhancing molecular breeding in potato and other complex genomes.

SESSION: GENE EDITING AND MUTATION BREEDING

Advancing potato trait improvement through transgene-free gene editing

Authors: Matías González[1], Mariette Andersson[1,2], Per Hofvander[1]
Affiliations: [1]Department of Plant Breeding, Swedish University of Agricultural Sciences, Lomma, Sweden, [2]SolEdits AB, Lund, Sweden

Abstract: Potato (*Solanum tuberosum* L.) is the world's fourth most important food crop and a key component of global food security. In addition to its role in human nutrition, potato is extensively cultivated in northern Europe for starch extraction, serving as a primary raw material for a wide range of food and non-food industrial applications. However, the crop's complex autotetraploid genome, high heterozygosity, and clonal propagation pose significant challenges to conventional breeding, making the development of improved varieties both laborious and time-consuming. Gene editing, particularly via CRISPR/Cas9, offers a transformative solution for potato improvement by enabling targeted mutagenesis without disrupting established genomic backgrounds. An innovative approach for achieving transgene-free gene editing in potato involves the isolation of protoplasts, *i.e.* plant cells lacking cell walls, followed by transfection with preassembled CRISPR/Cas9 ribonucleoproteins (RNPs). Regenerating whole plants from edited protoplasts enables the rapid and efficient introduction of desirable traits while avoiding the integration of foreign DNA. We have established and applied this methodology to generate potatoes with enhanced tuber post-harvest quality and improved starch properties tailored to specific industrial needs. Furthermore, optimisation of this technology to enable precise modifications, like insertions or exchanges of sequences available within the breeders' pool, will further expand the toolbox for potato breeding. Finally, the transgene-free nature of these edits may ease regulatory hurdles and enhance public acceptance, both of which will be crucial for the successful utilization of next-generation potato cultivars. Further information can be found at https://genebecon.eu/ as well as doi: 10.3389/fpls.2019.01649 and doi: 10.3389/fgeed.2025.1661829.

Elucidating genome-wide differences of potato (*Solanum tuberosum* L.) mutants induced using physical and chemical mutagenesis

Authors: Oluwafemi Omilani[1], Solomon Yilma[1], Brian Charlton[1], Sastry Jayanty[2], Kelly Vining[1], Vidyasagar Sathuvalli[1]
Affiliations: [1]Oregon State University, Corvallis, USA, [2]Colorado State University, USA

Abstract: Gamma radiation and ethyl methane sulfonate (EMS) are two popular physical and chemical mutagens. Gamma radiation predominantly leads to structural variations while EMS majorly leads to single-base-substitutions. The relationship between the mutagen, dose and the type of mutation induced was investigated. The preponderance of these mutations across the genome was also analysed. To achieve this, mutations were induced in three potato clones by exposing one-week old internodal cuttings in vivo to seven gamma radiation doses (5, 10, 20, 30, 40, 50 and 60 grays) and twelve EMS doses (0.25%, 0.50%, 0.75% and 1% at 30 minutes, 1 hour and 2 hours). LD_{50} was calculated with a dose-response curve. The genotypic differences were investigated using 'Castle Russet' and the SolCAP Infinium Array. The LD_{50} of the three clones revealed varying levels of sensitivity to the two mutagens. SNP genotyping of 'Castle Russet' mutants suggests that while gamma radiation led to structural variations (SVs), it also induced SNPs at both low and high doses. EMS primarily induced SNPs in mutant genomes, and it only induced SVs at higher doses. The mutation distribution across the 12 chromosomes suggests no chromosome preference. EMS mutations, however, appeared to be more abundant in GC rich regions of the chromosomes while gamma radiation mutations showed no discernible pattern in their chromosome distribution. Hierarchical clustering showed higher similarity within EMS mutants, but higher diversity within gamma radiation mutants. This information can guide a more efficient application of mutation breeding towards the development of improved potato cultivars. Full article information available at: https://ir.library.oregonstate.edu/concern/graduate_thesis_or_dissertations/6969z895q?locale=en

Stem cell technologies for potato variety development

Authors: Bjorn Kloosterman[1], Bipna Rani Shrestha[1], Hugo Hofhuis[1], Jeroen Stuurman[1]
Affiliations: [1]KeyGene N.V., Wageningen, Netherlands

Abstract: High heterogeneity and a tetraploid genome form a continuous challenge for classic potato breeding. Variety development and trait stacking would benefit from techniques that avoid the massive segregation seen in offspring from crosses. We present two novel stem cell technologies to address this challenge.

Graft hybridization, also called 'plant skin transplantation'. By grafting epidermal stem cells of variety A onto variety B, we have successfully made a graft hybrid potato AB with skin traits of A and the core tuber traits of B. Variety AB was distinct, uniform and stable through tuber propagation and was granted plant breeders' rights. Complex skin-related traits, such as pest resistance may now be asexually transferred from the potato germplasm onto modern commercial cultivars.

Protoplast regeneration. We present a technique termed ciPS (contact-induced plant stem cells) that provides a single workflow for regenerating plants from protoplasts, regardless of their genotype. ciPS enables technologies such as transgene-free genome editing to be flexibly applied throughout the potato germplasm, without the need for additional crossings. More details can be found at www.keygene.com/2s1 and www.keygene.com/cips.


Figure 1: Conference participants in front of the University of St. Andrews' historical buildings.

EUCARPIA

eapr

BREEDING AND VARIETAL ASSESSMENT

EAPR EUCARPIA 2025