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ABSTRACT VOLUME

CONTENT

ORAL PRESENTATION

POSTER PRESENTATION

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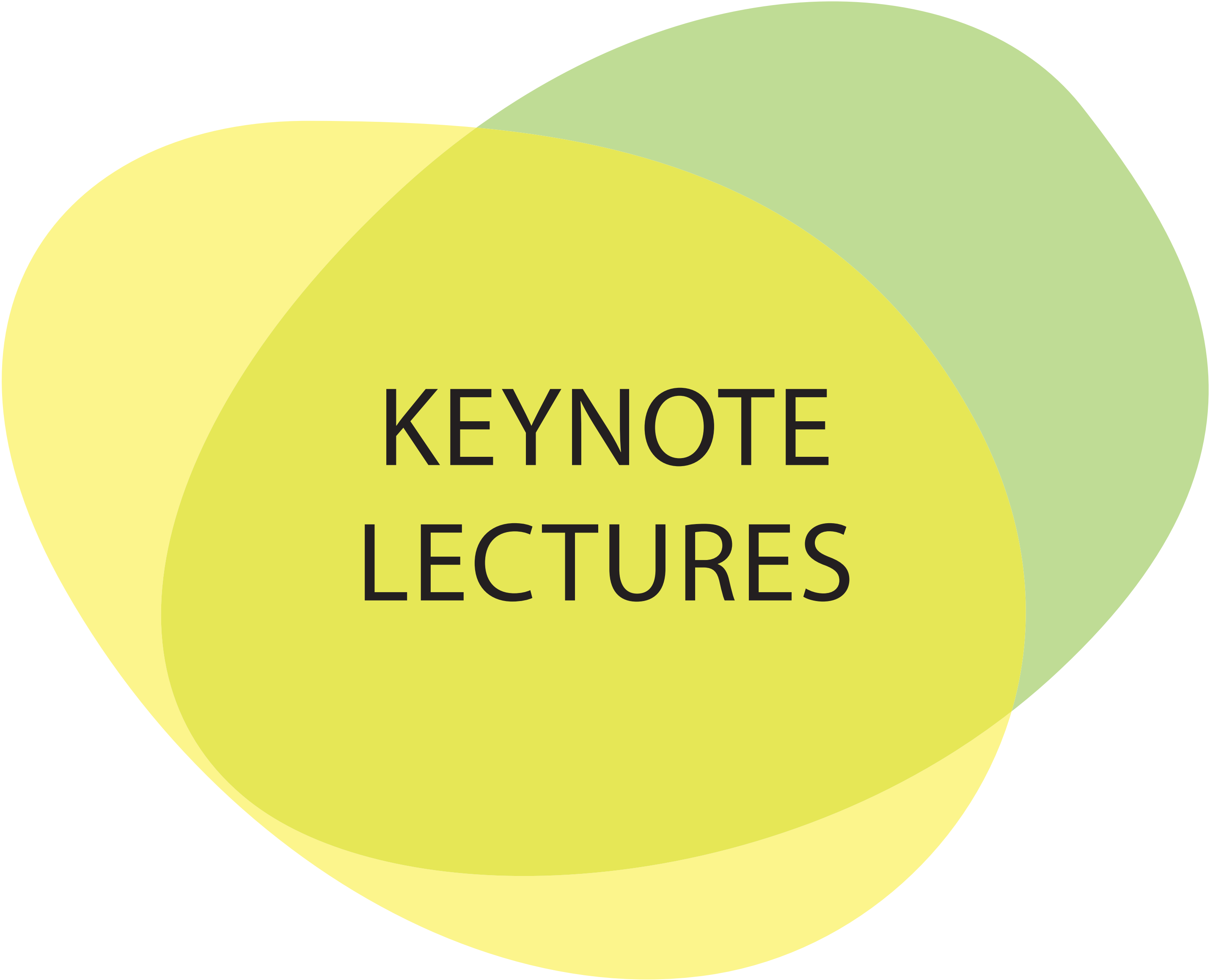

KEYNOTE LECTURES

Potatoes in organic farming – perspectives, challenges and constraints

Christian Bruns

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Potatoes are an important pillar for organic farms. In the European context, there have been significant increases in potato acreage over the last two decades. In 2004, there were about 18,000 ha while in 2020, about 38,000 ha of organically grown potatoes were produced (+111%) in Europe.

However, this occurred at different scales in the countries. In Germany, the cultivated area increased from 6500 ha to 11,350 ha (2020), while in the Netherlands or Switzerland, with similar growth rates, the total area in 2020 was about 2050 and 900 ha, respectively. Basically, however, the potato is an economically very important crop for the farms. The cultivation conditions differ according to the size of the farms and, above all, with regard to marketing. While in the highly professional farms, which also include the seed potato producers, the selection of varieties, fertilization measures, irrigation and plant protection for organic farming and harvesting partly show technologically similar conditions as in conventional farms, in smaller farms, especially with regard to the control of *P. infestans* by the use of copper, a lower effort is made or even wanted. However, the challenges for cultivation are many in each area. Adequate plant nutrition strategies, which especially consider nutrient use efficiency centrally, adapted plant protection strategies for *R. solani* and *P. infestans* as well as adaptation strategies for climate change and drought stress are central elements for a system-based cultivation. In this lecture, examples of modern production methods under organic conditions and the specific problems are discussed. For example, efforts towards growth model-based decision support models for the treatment of *P. infestans*, which can lead to significant reductions in copper input, are explained. Efforts in breeding *P. infestans* tolerant or resistant cultivars and integrating mulch management into potato production will be other topics, along with the presentation of a system for controlling *R. solani* using strip application of suppressive composts.

Developments in automated potato storage management

Adrian Cunnington

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The potato is a major staple food for populations around the world with over 350 million tonnes grown globally in 2020 across 140 potato-producing countries (FAO data).

The need for potato storage varies immensely across the world. This is largely driven by the climatic conditions of the region which dictate when the crop has to be planted and harvested.

Colder and temperate climate zones, including northern latitudes of America and much of Europe, are generally only able to have a single potato growing season. This means that potatoes have to be stored if they are to provide a local source of food throughout the year.

As a natural storage and over-wintering organ for the potato plant, the potato tuber is ideally suited for the purpose. It is a living organism which respires, using oxygen and generating carbon dioxide. The objective of potato storage is always to keep the crop in its best possible condition throughout its time in the store. This means limiting inputs and interventions to those that achieve this aim, whilst minimizing losses and natural wastage during the storage process.

Sustainability

Increasingly, the storage techniques that are used to provide a consistent supply of potatoes to meet an all-year-round demand have to be sustainable. Focus on efficiency is only just coming to the forefront of producers' thinking as cost pressures increase. There is a lot of inefficiency in the system and storage is as culpable as any other element, if only as a result of a lack of attention and investment in the past.

From a strategic perspective, for those who are now without it, the recent loss of the sprout suppressant CIPC in Europe has re-focused the approach to storage. It is now necessary to consider the impact of multiple factors on the propensity of crops to sprout during storage.

The proliferation of the potato's 'genotype x environment' interactions needs to be understood much more deeply now that a single 'blunt instrument' like CIPC is not at our disposal for storage. This genetic base is crucial to give us a good starting point with new varieties. Better natural dormancy and improved low temperature tolerance will reduce the need for chemical solutions and lower the risk from acrylamide.

There is a need to better understand risk – on a variety by variety basis – to improve the capability to accurately forecast potato performance in store so that crops can be *identified in advance* of long term storage as those with the best prospects of delivering the markets' needs at unloading.

Only then, with specifically selected crops with a robust genetic base and strong data available to support decision-making, should it be necessary to intervene with management processes to cope with seasonal challenges of disease and – as a last resort – should chemistry be deployed.

In summary, having a 'one-size-fits-all' tool like CIPC has allowed our industry to forget too much about storage and the holistic challenges of sustainability. The pace of development of storage solutions slowed and it was easier to take the simple - but flawed - approach that relied on a single solution. Now, for some of us, that solution is no longer there and the European industry is having to take the consequences...

Operator skills

Another strategic 'timebomb' looming over our industry – both in the field and the store – is the dearth of skilled operators to look after the crops on their journey through production. Businesses are struggling to access people with the necessary skills and interest to manage large, sophisticated storage installations. Training and succession planning has been neglected by many supply chains who face the challenge of managing many stores, often spread over a wide geographic area. Some technological solutions can help but the fundamental problem remains and there is a need to find ways to incentivise younger people with technical know-how to join our industry and the storage sector in particular.

Storage systems

Despite these big, strategic barriers, there are still positive developments in potato storage management and new solutions coming on stream all the time.

The need for uniform conditions in potato storage buildings cannot be overstated. It is crucial to the proper functioning of a store that there are *not* significant temperature gradients as, at the high humidity prevailing in most storage situations, a difference in temperature will result *in condensation*. Any store where condensation is a regular occurrence will suffer from localised sprouting or even rotting and this can become a difficult problem to have to manage.

The use of fans is fundamental to any potato store. Even in the simplest set-up, it is crucial to have some method of air movement. Air is the primary means by which the store manager can change the crop condition by removing moisture and/or adjusting the temperature.

Management of disease is a key role for the store operator if storage is to be successful and loss of crop avoided. The key bacterial rot affecting storage remains soft rot (*Pectobacterium* spp.); this will develop very rapidly in warm or moist conditions and, if not cooled and thoroughly dried in store, can run out of control very quickly inducing major losses.

The need for continued research and development to tackle all of these changing problems will be discussed.

Using genome-wide markers to assess and advance tetraploid (4x) and diploid (2x) potato breeding

David Douches[1], Alicia Massa[2], Natalie Kaiser[1], Norma Manrique[3], Jeffrey Endelman[4], Joseph Coombs[1], Felix Enciso[1], Maher Alsahlany[1], Gustavo del Los Campos[1]

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SNPs, germplasm, QTL analysis, GWAS

The potato (*Solanum tuberosum* L.) plays an important role in human nutrition as a staple food.
It is considered one of the main sources of carbohydrates, providing the energy needed for development and function. Potato breeding over the past decade has been transformed by the use of genome-wide single nucleotide polymorphism (SNP) markers. The first SNP array queried 8,303 co-dominant SNPs with over 5,000 useful for determining dosage in tetraploid genotypes. The current version of the Illumina Infinium V4 Potato SNP Array has over 30,000 SNPs that provide improved genome coverage and more co-dominant SNPs useful in tetraploid populations. This latest array reduces ascertainment bias drawing from a broader *Solanum* species germplasm pool to select candidate SNPs. The genome-wide SNP arrays have been a foundation marker platform used for multiple breeding related studies including: (i) QTL analyses to map economic traits in diploid and tetraploid populations to provide additional markers for disease resistance that can be used for marker-assisted breeding, (ii) confirming and quantifying ploidy level of breeding selections and clones (diploid, triploid, or tetraploid) in germplasm collections and diploid breeding populations, (iii) examine germplasm relationships of cultivated and wild germplasm, (iv) monitoring the cycles of selection for diversity, heterozygosity and linkage disequilibrium, (v) conducting GWAS to for identify SNPs associated economic traits and genomic selection, and (vi) variety fingerprinting and pedigree identification. As technology advances, there are now more platforms to use genome-wide SNPs and subsets of these SNPs for breeding and genetic purposes.

Potato crop nitrogen status monitoring with spectral sensors: last decade developments and implementation for sustainable N fertilisation management

Jean Pierre Goffart, F. Ben Abdallah, D. Goffart, Y. Curnel, V. Planchon

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For the potato (*Solanum tuberosum L.*) crop, nitrogen (N) fertilization is as a key management factor, as tuber yield and quality are greatly influenced by the highly variable N supply in space and time during the growing season. In such a frame, while combined with split application of mineral N fertilizer, the monitoring of the potato crop N status is a useful and well recognized approach to assess the in-season crop N requirement, to achieve the matching of crop N supply and demand, and to mitigate or even avoid N surplus and N losses to the environment (mainly air and water) from excessive fertilizer N application. From the existing literature, - the critical N concentration of crop biomass [Nc, % of dry matter (DM)], defined as the minimum plant N concentration (%N) requested to achieve maximum crop biomass (W, Mg ha−1) all along the growing season, - the concept of critical nitrogen (N) dilution curve (CNDC) and - the resulting N nutrition index (NNI) defined as the actual %N to Nc ratio, have shown to be robust diagnostic basic elements to assess the crop N status for several plant species. For the potato crop, several CNDC were established for years. To date, eleven different CNDC have been established worldwide and referenced for contrasted potato varieties (G), environment (E) and cropping management conditions (M). However, it still remains to demonstrate whether variations in the CNDC parameters reflect a true variability across G×E×M scenarios, or are rather linked to errors due to sampling and parameter estimation. While recognized as a reference method for potato CNS assessment, the practical application of the %Nc, CNDC and NNI is labour intensive and not easy to apply at field scale on a large number of situations. Therefore, for decades, several attempts were deployed to develop quick, easy but also robust and costless tools for indirect potato CNS assessment. It clearly appeared that from the different methods for potato CNS assessment developed over the years, remotely sensed above crop reflectance measurements from specific spectral sensors and platforms were potentially most promising. On the other hand, other spectral approaches based on the measurements of leaf transmittance and leaf fluorescence were also pointed out as potentially valuable. The main challenge in the use of such tools, able to deliver CNS any-time in the course of the growing season, still remains the accurate assessment of the amount of fertiliser N to be supplemented when observations indicate that a N deficiency is present or imminent. Such an approach is also to be combined with the degree of inter- and intra-field variability mainly linked to heterogeneity of soil fertility (physical, chemical and biological). This keynote lecture aims at: i) review the establishment of CNDCs for the potato crop and its valuable use to assess potato CNS in a more generic approach, ii) review and present last developments and results in the set up and use of remotely-sensed approach for a quick and reliable potato CNS assessment, iii) review the breakthrough in the development of decision support systems for improved fertiliser N application, combining CNS information together with advance in either the set up of algorithms of fertilizer N application or improved potato crop growth simulation models, considering possibilities of management variable zones or variable nitrogen rate concepts for fertilizer N application in situation of within-field heterogeneity (i.e. soil mineral N supply).

The mission of Phytophthora: explore, invade and manipulate

Francine Govers

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The late blight pathogen *Phytophthora infestans* is renowned for causing the Irish potato famine in the 1840s and its impact on world history. Today late blight is still a major problem worldwide and despite the successful release of several resistant potato cultivars, chemical control is still integrated in the disease management strategy of many farmers. *Phytophthora literally* means plant destroyer. Based on its lifestyle, i.e. mycelial growth and dispersal via spores, *P. infestans* was initially classified as a fungus. However, over time remarkable differences with fungi were noted in particular in physiology, cell wall composition and genetics, and molecular identification has confirmed that *P. infestans* and its sister species in the genus *Phytophthora* are not fungi; they belong to the oomycetes, a group of diverse organisms that evolved independently of fungi. Yet, besides remarkable differences, fungi and oomycetes occupy similar ecological niches, and also their weaponry for plant infection is comparable including the exploitation of effectors to suppress host defense. This presentation will highlight several unique features that illuminate the success of *Phytophthora* species as pathogens. During asexual reproduction they produce massive amounts of zoospores, motile propagules that are attracted by plant exudates and explore the environment to find suitable hosts. The zoospores then encyst and the germ tubes emerging from cysts build up pressure in the tip for host invasion. Unlike fungi, that often use brute force for perpendicular penetration, *Phytophthora* slices the host surface at an oblique angle to gain entry. Once inside the host *Phytophthora* deposits numerous effectors that can manipulate the host cell machinery and suppress immunity. Many of these are host specific RXLR effectors, that elicit resistance responses in plants expressing a corresponding resistance (*R*) gene and as such, are instrumental in *R* gene discovery. *Phytophthora* also makes use of alternative signaling pathways and unique cytoskeleton structures, pointing to potential targets for novel oomicides.

Acrylamide mitigation strategies in fried potato products

Vural Gökmen

Hacettepe University, Turkey

Acrylamide, mitigation, fried potato products

Acrylamide formation in foods has been an intensive area of research shortly after its discovery in common heated foods by the Swedish researchers in April 2002. Several researchers have established that the main pathway of acrylamide formation in foods is linked to the Maillard reaction and, in particular, the amino acid asparagine. Thermally processed foods encompass a vast range of different products with many ingredients, processes, recipes and scales of operation. Acrylamide is found in a wide range of heat-treated foods prepared commercially or cooked in the home including bread, crisp bread, bakery wares, breakfast cereals, potato products, chocolate, and coffee. High levels of acrylamide have been detected in fried potato products, such as French fries and potato crisps. The resulting acrylamide concentrations in thermally processed potatoes change with great deviations as influenced by potato composition and thermal processing conditions. Major factors influencing acrylamide formation in fried potatoes are glucose and fructose, and actual frying. The mechanism of acrylamide formation and factors affecting its concentration in thermally processed potato products are summarized in this chapter. Recent research findings for the mitigation of acrylamide by means of potato and process related modifications are discussed in detail.

Genome design of hybrid potato

Sanwen Huang

Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, China

Potato is the most important tuber crop, feeding over 1 billion people worldwide. Cultivated potato is autotetraploid, the genome of which is highly heterozygous. Due to the complexity of tetrasomic inheritance, the genetic gain in potato breeding is limited. Some century-old potato cultivars, such as Russet Burbank (released in 1902) and Bintje (bred in 1904), are still widely grown. Moreover, its clonal propagation bears a considerate carbon footprint. To overcome these drawbacks, we initiated the Upotato Plan, reinventing potato into an inbred line-based diploid crop propagated by seeds. However, self-incompatibility and severe inbreeding depression are two obstacles to hamper the development of inbred lines. We overcome the first obstacle by knockout of the S-*RNase* genes that control self-incompatibility, or application of natural self-compatibility genes. Then, we analyzed the genetic basis of inbreeding depression, and found that the mutation burden in potato is line-specific, suggesting crosses of different inbred lines will mask the effects of deleterious mutations and produce strong heterosis. Based on these, we developed the pipeline of genome design of hybrid potato. Using this strategy, we developed vigorous and fertile inbred lines (up to 99.94% homozygosity), derived from different lineages, and generated the first uniform F1 hybrid “Upotato1” by crossing two inbred lines with different lineages. Due to the genomic complementarity, the F1 hybrid showed strong heterosis in growth vigor and yield. To further accelerate hybrid potato breeding, we constructed the potato pan-genome map by integrating the genomes and variants of 44 diverse potato accessions, providing critical insights for improving inbred lines and precluding potential linkage drag. This study enriches our understanding of the evolution and biology of potato, and transforms potato breeding from a slow, non-accumulative mode into a fast-iterative one, thereby potentiating a broad spectrum of benefits to farmers and consumers.

Genetic approaches to increasing disease resistance in potato

Jonathan DG Jones[5], Jacek Hennig[1], Hannele Lindquist-Kreuze[2], M. Ghislain[2], Marta Grech-Baran[1], Yuxin Jia[3], Kee Hoon Sohn[4], Sanwen Huang[3], Kamil Witek[5], Agnieszka Witek[5], Robert Heal[5]

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Potato yields are reduced by many biotic agents, notably *Phytophthora infestans*, bacterial wilt, potato virus Y, potato leaf roll virus (PLRV) and nematodes. We aim to combine resistance to these diseases, particularly to reduce yield losses in Africa. Genetic variation for Resistance to *P. infestans (Rpi)* genes is found in several *Solanum* species. *Resistance* gene enrichment and long-read sequencing (SMRT-RenSeq) accelerate cloning of NLR-encoding disease resistance genes and we used this approach to clone *Rpi-amr1* and *Rpi-amr3* from *Solanum americanum*. *Rpi-amr1* confers strong resistance against multiple isolates of *P. infestans* even though *Rpi-amr1* alleles from multiple *S. americanum* accessions reveal extensive allelic diversity. We also cloned *Rpi-amr3* and have identified the *P. infestans* effectors recognized by both *Rpi-amr genes*. We used the same genetic approach with the Hennig lab to isolate Ry_{sto} that confers resistance to Potato Virus Y (PVY) and to clone the Rl_{adg} gene for potato leaf roll virus (PLRV) from S. andigena. We continue to map and clone additional *Rpi* genes from *S. americanum*., and recently identified two additional *Rpi-amr* genes using 4 high quality *S. americanum* reference genomes, and 10-deep sequencing of 52 *S. americanum* accessions. We combined *Rpi-amr1* with *Rpi-amr3* and *Rpi-vnt1* in a stack of three *Rpi* genes in transgenic Maris Piper in a field trial in Norwich and this *Rpi* gene stack confers complete field and tuber resistance. We identified lines that yield indistinguishably from Maris Piper and are unaltered in tuber steroidal glycoalkaloids. These lines also carry modules for tuber-specific silencing of polyphenol oxidase and vacuolar invertase genes, improving tuber quality. In a collaboration with CIP and David Douches at MSU to improve African and Bangladeshi potato varieties, we are combining blight resistance with PVY resistance and resistance to bacterial wilt. An update on progress will be reported.

Can marker-assisted selection for drought tolerance in *Solanum tuberosum* replace selection on yield in arid environments?

Karin Köhl

MPI of Molecular Plant Physiology, Germany

drought stress, marker assisted selection, phenotyping

Maintenance of yield stability requires efficient selection for drought tolerance, as climate models predict an increased likelihood of droughts. Yield based selection for drought tolerance requires time-consuming drought trials. Marker-assisted selection (MAS) could accelerate tolerance breeding.

An important crop for drought tolerance improvement is *Solanum tuberosum* ssp. *tuberosum*, which combines high water-use efficiency with low drought tolerance. The significant tolerance variation in tetraploid European cultivars provides a genetic basis for breeding. For this genepool, we developed a tolerance prediction model based on leaf metabolite and transcript levels. We compared the performance of a selection based on this omics marker model to a classic yield-based selection. Furthermore, we tested the predictive value of phenotypic markers gained from laser scanner imaging and thermometry. From a population of 200 lines segregating for drought tolerance, a classic subpopulation was selected for superior tolerance based on tuber starch yield data from 4 stress trials. Metabolite and transcript levels in leaf samples from these trials were used to predict drought tolerance by the random-forest model and select a tolerant MAS subpopulation. To compare their performance, these populations were characterized for yield and drought tolerance in ten multi-environment trials. The micro-meteorological characterization of the test environments indicated a good representation of relevant drought-scenarios in agro-environments. Yield data indicated that lines with drought tolerance above the mid-parent mean and yield potentials similar to released cultivars were identified by both selection procedures. However, the MAS procedure is faster than the selection based on yield trials. Among the parameters gained from automatic phenotyping, pre-dawn leaf angle and canopy temperature were the most promising drought tolerance predictor.

This work was funded by the FNR/BMEL, GFPi and GTZ.

Potato wart disease management and resistance breeding: a genomics approach

Jack Vossen[1], Charlotte Prodhomme[2], Gert van Arkel[1], Jaroslaw Plich[3], Jasper Tammes[4], Johan Rijk[5], Herman van Eck[1], Richard Visser[1], Theo van der Lee[1], Bart van de Vossenberg[6]

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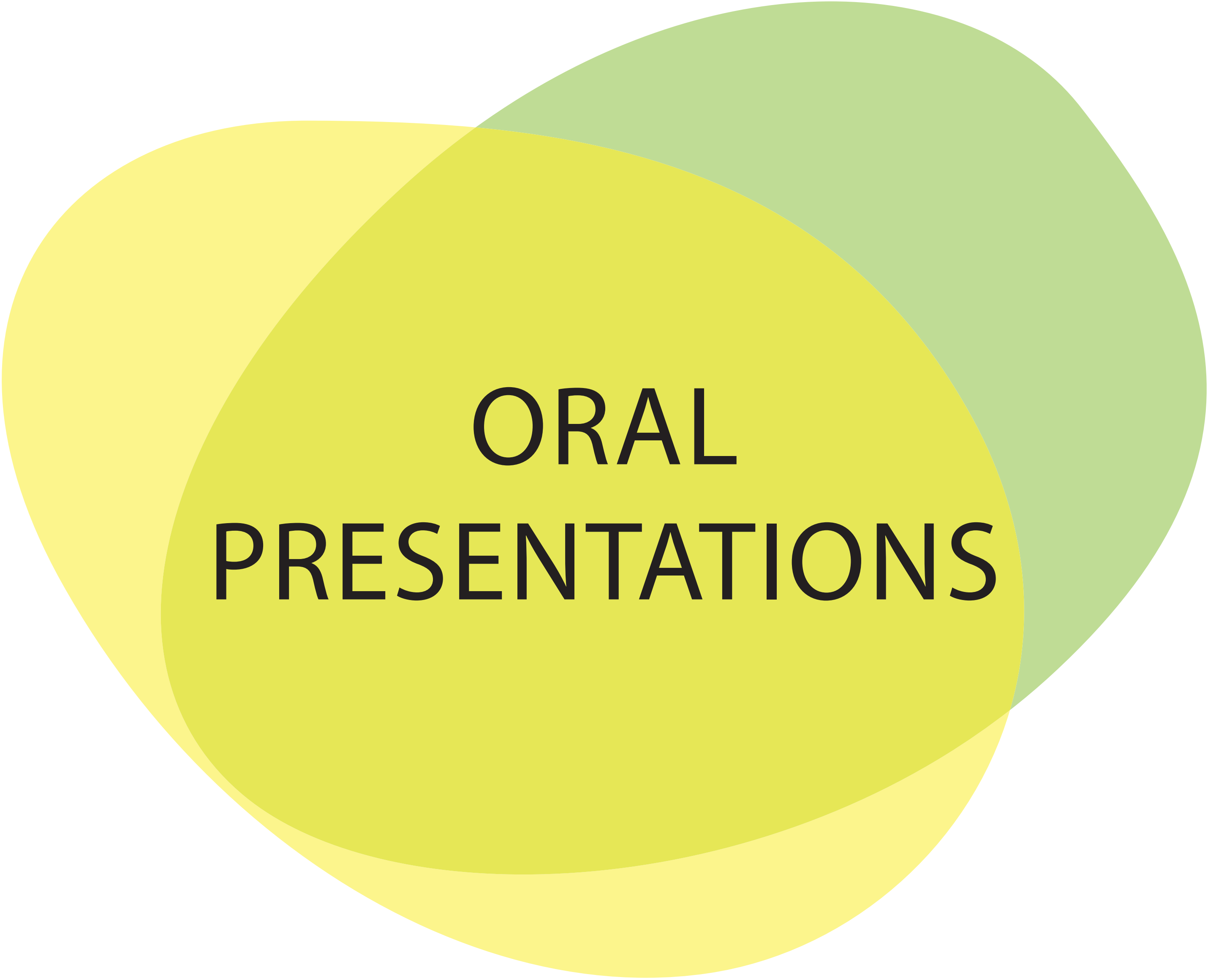
Wart disease, CoSSA, GWAS, Synchytrium endobioticum, disease resistance

Wart disease in potato is caused by the obligate biotrophic chytrid *Synchytrium endobioticum* and is subject to quarantine containment. Quarantine containment largely relies on host disease resistance and the interaction with a differential set of potato varieties is the basis for the pathotype grouping of *S. endobioticum* isolates. Remarkably, the molecular basis of wart disease resistance has long remained elusive. This was mainly caused by the obligate biotrophic nature of the pathogen, which results in variable composition of the inoculum and variations in phenotyping. So it is essential to study both the pathogen and the host to understand how wart disease resistance is brought about. In 2018 we published the sequences of the mitochondrial and nuclear genomes of *S. endobioticum*. The mitochondrial genome was an excellent tool to study the diversity among and within isolates. *S. endobioticum* isolates were shown to be communities of different genotypes. The complexity of these communities appears to increase in the higher pathotypes. Our analysis of wart disease resistant varieties revealed that QTLs often co-localise with clusters of immune receptors, suggesting that effector recognition is causal to *S. endobioticum* resistance. Comparisons of nuclear genome sequences revealed the presence of one Pathotype-1 specific effector protein. This effector triggered a hypersensitive response in plants that contained the *Sen1* resistance gene and was named *AvrSen1*. The *Sen3* gene provided strong resistance to multiple pathotypes and more quantitative resistance to Pathotype-18 (P18). Potato variety Kuba harbours *Sen3* but shows strong resistance to P18. We could identify a QTL on chromosome 8, overlapping an NLR cluster, that provided full resistance to P18 in concert with *Sen3*. We postulate that the quantitative resistance to P18 may be related to the complexity of P18 isolates. Consequently, in order to breed varieties with full resistance to higher pathotypes, stacking of multiple resistance QTLs is needed. Indeed, when studying the wart resistance of the potato variety Andante, we found that four QTLs with individual small effects brought about full resistance to P18. Using haplotype specific markers, we can currently distinguish 5 major- (Sen1, 2, 3, 4, 5) and 7 smaller effect QTLs. Using these markers, we could identify (non)overlapping and unknown resistance sources. Further studies are needed to identify the underlying genes and their matching effector genes. This will be a basis for breeding strategies to cover the diversity in pathogen isolates.



ORAL PRESENTATIONS

2. Resistance breeding

2.01. Quantitative trait loci for tuber resistance to *Dickeya solani* and starch content in diploid potato

Renata Lebecka, Jadwiga Śliwka, Anna Śliwka, Katarzyna Szajko

Plant Breeding and Aclimatization Institute – National Research Institute

potato soft rot resistance, Dickeya solani mapping, diploid hybrids of Solanum spp., starch

Soft rot of potato can cause losses of tubers during storage. The disease is caused by bacteria belonging to many species within two genera: *Pectobacterium* and *Dickeya*. The control relies on using clean seeds, application of hygienic practices, avoiding harvesting in the rain or after rain.

To identify the genetic components of tuber resistance to the highly aggressive strain of *D. solani*, the F1 population of diploid potato consisting of 176 individuals was obtained and assessed for soft rot resistance of wound-inoculated tubers. The resistant parent DG 00-270 is a hybrid of *Solanum tuberosum* with the *S. chacoense, S. phureja, S. yungasense, S. verrucosum* and *S. microdontum*. Quantitative trait locus (QTL) analysis was performed using diversity array technology (DArTseq) genetic map and the results of soft rot resistance evaluation in three- and tuber starch content in two consecutive years. Analysis of variance showed that for both tested traits there was significant influence of genotype, year and genotype by year interaction, however the effect of the interaction was the smallest one. The most prominent QTLs were identified for the proportion of diseased tubers, disease incidence (DI) and for the weight of rot in diseased tubers (disease severity, DS), both on potato chromosome IV. The second significant QTL for DS was mapped to chromosome II. QTLs for starch content were detected on different chromosomes: III, V, VI, VII, VIII, IX, XI i XII. The relationship between tuber resistance to bacteria and starch content in potato tubers was not significant, which makes selection of genotypes highly resistant to soft rot with desirable starch content possible.

2.02. Pre-Breeding for Late-Blight Resistance – A way to an Environmentally Save Potato Production

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2. JBI

plant genetic resources, pre-breeding, quantitative late-blight resistance

Introduction: Novel aggressive races of late blight (*Phytophthora infestans*), together with climate change and restricted options in chemical plant protection, raise challenges to potato growers and breeders. Former efforts to breed resistant potatoes by incorporating major resistance genes from *Solanum demissum* failed due to the enormous adaptability of the pathogen. Breeding for resistance based on a quantitative expression of more than one gene might be a way to meet the challenge.

To this end, plant genetic resources have to be screened and pre-breeding clones selected which gather improved levels of durable resistance and acceptable agronomic and quality traits. Material and Methods: In the frame of a long-termed pre-breeding programme run at JKI, current cultivars and backcross progenies are tested for their reaction to foliage and tuber blight in laboratory tests as well as in field trials under enhanced infection pressure in a replicated block design. Reduced attack by foliage blight in the field often correlates with late maturity; thus maturation time has to be considered. To separate the two characters, Δ-rAUDPC values corrected for maturation time were calculated. Additional characters like maturity, yield, tuber shape, eye depth, skin texture, discoloration, bruising, crisp or table quality were evaluated in a fungicide-treated trial. All characters were assessed over 3 years for each clone. Results: A number of JKI pre-breeding clones belonging to the early or second early maturity group exhibited lower Δ-rAUDPC values than current varieties, demonstrating progress in the breeding for foliage-blight resistance and resolution of the said correlation in these instances. Additionally, improved resistance against tuber-blight was found for some of the pre-breeding clones. Some clones showed useful table or processing quality, respectively, and high levels of tuber yields and starch contents. Still other characters remain to be adapted to meet the levels of current cultivars. Conclusion: The pre-breeding clones tested so far indicate potential as resistance donors and may be useful to genetically enrich potato breeding programmes in order to enable sustainable potato production under reduced fungicide regimes for food as well as non-food purposes.

2.03. How can stem infection tests complement field trials to evaluate late blight resistance?

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Late blight, Resistance breeding, Stem tests, Field trials

Late blight resistance is a key trait for the breeding of new potato varieties and efficient phenotyping methods are therefore required for resistance screening tests and genetic analyses. The aim of this study was to determine how stem infections performed in controlled conditions could complement multiple-year field trials to evaluate potato late blight resistance. We used a panel of 288 tetraploid genotypes mainly composed of European varieties, breeding clones from three breeding programs and some pre-breeding material. The stem tests were performed over four years with two *Phytophthora infestans* isolates: 14P60.06 (6_A1) in 2016 and 2017 and 17P54.16 (13_A2) in 2018 and 2019. Field resistance was assessed in one location over 3 years between 2013 and 2015. A set of 373 markers (SSRs, CAPS, KASP) obtained from literature or designed in house was screened in the panel and their association with the phenotypic data obtained in both types of tests was tested. Phenotypic variability was observed between the genotypes of the panel in the stem tests using both isolates. Although a significant correlation was observed between the AUNPC (area under necrosis progress curve) calculated for both isolates, their phenotypic distributions differed: a bimodal distribution was observed for 14P60.06 whereas the distribution was more quantitative for 17P54.16. The phenotypes obtained from the stem infections for both isolates were significantly correlated to the rAUDPC (area under disease progress curve) evaluated in the multiple-year field trials. Significant associations were identified between several markers and late blight resistance assessed in stem and field tests. Interestingly, for some markers the association test results differed strongly between the two isolates used in stem tests, between stem and field tests and between the different years of field trials. The analysis of these differences helped us to better characterize the effect of the significant markers on resistance. In this study, we confirmed that stem tests can usefully complement late blight field trials performed in natural conditions of contamination. They can help to understand why the effect of late blight resistance loci vary between the years, although other important factors such as meteorological conditions should also be considered. Moreover, stem tests can be used to identify and characterize resistance loci which can also be efficient in the field.

2.04. Rpi-agf1, a non-typical broad-spectrum R gene against *Phytophthora infestans* involved in multivesicular bodies formation

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Late blight is a devastating potato disease caused by the oomycete *Phytophthora infestans*. Wild *Solanum* species have been described to be a source of resistance against this notorious pathogen. In this study we mapped a novel resistance gene, *Rpi-agf1*, present in *Solanum agrimoniifolium* native to Guatemala. This gene provides a broad-spectrum resistance against 26 out of 27 tested *P. infestans* isolates. *Rpi-agf1* is not a classical NB-LRR type of *R* gene; it encodes for lyst-interacting protein 5 (LIP5). LIP5 is a protein conserved in all eukaryotes and is involved in endosomal trafficking via the ESCRT (endosomal sorting complex required for transport) pathway. Particularly, LIP5 is a key regulator of multivesicular bodies (MVBs) biogenesis. MVBs have been described to play a role during both surface and intracellular immune responses. The Rpi-agf1 resistance mechanism is unclear, although we identified helper NRCs as an important downstream signalling component required for the resistance. Additionally, we identified several effectors from distinct *P. infestans* effector families that physically interact with LIP5 via yeast two-hybrid and in planta. Apart from describing a novel resistance gene against *P. infestans*, our results emphasize the importance of multivesicular bodies during pathogen infection.

2.05. Structural and functional analysis of the *Syncytrium endobioticum* effector AvrSen1

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effector, avirulence, hypersensitive response, Synchytrium endobioticum

Synchytrium endobioticum is an obligate biotrophic chytrid fungus responsible for potato wart disease. To promote infection, endobioticum secretes effectors into host cells. So far, only one effector, *AvrSen1*, was reported. *AvrSen1* is recognised in potato plants carrying the *Sen1* wart disease resistance gene and several natural Avrsen1 variants evade detection. However, the biological function of *AvrSen1* and its natural variants remains unknown. Therefore, first we verified the predicted cDNA sequences of AvrSen1 gene and its variants. Next, we analysed the protein structure of AvrSen1 and identified several repeated amino acid sequences. Variants and various AvrSen1 (deletion) truncations were expressed by agro-infiltration in resistant potato to determine the domains required for Sen1-mediated hypersensitive response. Also, the subcellular localization of AvrSen1 was investigated using transient expression in cells of susceptible plants.

2.06 Rysto receptor recognises core structure of Potato Virus Y coat protein

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Rysto, extreme resistance, PVY, resistance breeding, coat protein

Ry$_{sto}$ confers extreme resistance (ER) to PVY and is a valuable trait widely employed in potato resistance breeding programmes. The two known functional alleles of *Ry*$_{sto}$ gene were introduced into the edible potato from a wild relative, Solanum *stoloniferum*. We cloned an allele from the MPI collection (Germany) that encodes TNL-class nucleotide binding, leucine rich repeat receptor, and showed that it was sufficient for PVY perception and ER initiation in transgenic potato plants.
We then cloned the *Ry*$_{-fsto}$ allele from the VIR collection (Russia) to check for variations between those. Unexpectedly, we found the 5 kb assembled regions identical on a nucleotide level in the coding sequence as well as the flanking sequences. There was also no variation among *Ry*$_{sto}$ homologous sequences amplified from several PVY-resistant potato cultivars from the MPI collection. Moreover, a bioinformatic analysis revealed that the whole interval carrying *Ry*$_{sto}$ was introgressed from *S. stoloniferum* and it rarely undergoes recombination in the cultivated potato. To identify a viral component that triggers *Ry*$_{sto}$-mediated ER response, the ORFs encoding PVY proteins were transiently expressed in transgenic plants with the constitutively elevated Rysto levels. Expression of PVY coat protein (CP) resulted in a strong resistance reaction that was not observed for the other proteins tested, demonstrating that the CP is an avirulence factor. To find the minimal fragment recognised by *Ry*$_{sto}$, serial truncations of N and C-termini and deletions within the CP core region were generated. Both CP$_{(1\text{-}218)}$ and CP$_{(77–267)}$ induced cell death when expressed in transgenic *Rysto* plants, while a CP$_{(79–216)}$ variant did not, which implies that the core region of the CP is crucial for the perception. Similarly, the point mutations in the highly conserved residues: S126, R158 and D201 of the CP core compromised Ry$_{sto}$-dependent response. Collectively, these results suggest that *Ry*$_{sto}$ recognises the CP structure. This is supported by our finding that similarly folded CPs from other Potyviruses also induce *Ry*$_{sto}$-mediated response. These findings allow to predict a range of the viral pathogens against which *Rysto* might be applied in new breeding programmes.

2.07. Metabolite analysis and testing of *Solanum* species and accessions for increased pest resistance in *Solanum tuberosum*

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metabolite profiling, LC-MS/MS, resistance, pest management

Pests such as *Leptinotarsa decemlineata* (Colorado Potato Beetle, CPB) or invading *Epitrix sp.* cause high economic losses. Increasingly restrictive regulations for the approval of insecticides, the required reduction in application rates as well as the rapid development of resistance to insecticides increase the need for intrinsic resistance for potato cultivation and the search for new management strategies. Several *Solanum* accessions have different levels of resistance to pests and thus represent valuable resources for resistance breeding. The LEADER project will characterize the accessibility, resistance and tolerance of *Solanum* species and breeding lines in a multidisciplinary approach that includes the analysis of a) the biological performance of different lines of pest species on *Solanum sp.* b) plant surface structures and their role in plant-pathogen interaction c) more than 5000 compounds using untargeted LC-MS metabolite profiling d) genetic markers for pest resistance. Analysis of *Solanum* leaves, stolons, and tubers demonstrates a great metabolic diversity with up to 3000 different detectable compounds in individual samples. Unique metabolic patterns and metabolites were detected in CPB-resistant accessions as well as in breeding and backcrossing lines. This indicates the transferability of metabolic traits. Thus, metabolites could be used in marker-assisted resistance breeding strategies. For some metabolites potentially associated with resistance, initial biotests showed pest-repellent properties after their application to *S. tuberosum*. The findings on the impact of the metabolome on CPB and Epitrix potato feeding will serve the LEADER project, which will combine results from phenotypic, genetic, physical and biochemical studies. With this comprehensive information on resistance mechanisms, LEADER will provide new tools for resistance breeding and bio-based pest management strategies. Funding: Federal Ministry of Food and Agriculture, Federal Office for Agriculture and Food, Germany (FKZ 28A-C8706A19)

3. Organic production & bioagents

3.01. Traits important for organic potato production: yield stability and nitrogen use efficiency

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yield stability, nitrogen use efficiency, organic farming

When organically producing potatoes, the yield stability is essential trait of variety, because it allows obtaining high and stable yield in changing growing environments. The supply of plant-available nitrogen (N) in soil is variable during vegetation season, so high nitrogen use efficiency (NUE) of the potato genotype is important. The aim of the study was to asses yield stability of genotypes and to evaluate genotype NUE in organic and integrated farming. The research was carried out in organic and integrated fields at Priekuli, Latvia in 2020 and 2021. N fertilization was applied in the integrated field at a doses of 60, 120 and 180 kg ha-1. NUE of 19 genotypes was estimated as tuber dry matter yield kg per available N kg in both trial years. To assess yield stability additional trial fields with the same genotypes were arranged in two locations (Stende, Vilani) in organic and integrated farming field in 2021. For evaluation of yield stability, the linear regression coefficient (b) for the slope of the Finlay-Wilkinson regression line was applied. The Kang 's yield stability ranking (KR) was used for evaluation of yield stability (based on Shukla 's stability variance statistics) and for detection of high yield performance. NUE of genotypes observed in organic fields and integrated fields with N supply 60 kg ha^{-1} was higher than in integrated fields with elevated N supply ($p<0.05$) in both trial years. Comparatively, the NUE in 2021 was lower than in 2020 due to unfavorable weather conditions (high air temperature, low precipitation). The assessment of b identified two genotypes with high sensitivity to environmental variability ($b>1$, $p<0.05$), tuber yield level of these genotypes depended on N supply. For two genotypes b proved high stability ($b<1$, $p<0.05$), providing relatively stable yield under less favorable growing conditions, although yield level was low. For other genotypes, b did not differ significantly from 1, characterizing average yield stability and wide adaptability. Genotypes were ranged according yield level and stability using KR. In most cases KR correlated negatively and significantly ($p<0.05$) with genotype NUE detected in organic and integrated fields with different N supply in both trial years. Regression coefficient b of genotypes significantly correlated with NUE only in 2020 ($p<0.01$). The relationship between NUE and yield stability parameters has been detected. This research was carried out with the support of the National FLPP Project - lzp-2019/1-0371.

3.02. Cultivation systems for nitrogen and phosphorus efficiency phenotyping in potato

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Solanum tuberosum, nutrient efficiency, nitrogen, phosphorus, hydroponics

Due to scarcity of resources and a growing ecological awareness, there is a rising demand for organically grown produce. While organic farming focuses on reducing the use of plant protection products and fertiliser application to a sensible minimum, it is aiming to maintain high quality standards and satisfactory yields. However, many agricultural areas are deficient in one or more nutrients essential for plant growth. Given these conditions, the selection of nutrient efficient plant varieties is as crucial as the improvement of fertilising strategies in order to avoid accidental overfertilisation while still maintaining high quality yields. As potatoes have a very limited and shallow root system, they cannot mobilise nutrients from deeper soil layers and are therefore especially prone for nutrient deficiencies. The objective of our project is the phenotyping of a large number of potato genotypes for nitrogen (N) and phosphorus (P) uptake and utilisation efficiency. To find the most favourable method for our purposes, we compared three phenotyping systems for their practicability, comparability as well as repeatability: a climate chamber based glass jar hydroponic system, a greenhouse based hydroponic sand system and a pure greenhouse hydroponics system. For both greenhouse based methods, in vitro plantlets were used as starting material, the third method using in vitro cutlets . All three experiments were conducted over a four week period. The assessment of the systems ' suitability for our purposes was based upon the comparability of the genotypes ' reactions, their biomass yields, and overall practicability. In addition, possibilities for further measurements of e.g. chlorophyll content and root architecture were taken into consideration. The differences in the genotypes ' reactions to nutrient deficiencies, although similar across all three systems, were most pronounced in the greenhouse-based hydroponics system. Here, contrasts in biomass production could be observed earlier and overall biomass production was higher compared to the other two systems. While it was possible to measure chlorophyll contents both in the sand culture as well as the pure hydroponic system, adaptations in root morphology were easier detectable in the latter. In conclusion, the pure hydroponic system was found to be the most feasible method for phenotyping potatoes for N and P efficiency. Using this phenotyping strategy, a total of 180 potato genotypes will be evaluated in subsequent experiments.

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3.03. Adapting value for cultivation and use (VCU) testing protocols to stimulate the release of suitable potato varieties for organic farming

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Organic farming, Variety testing, Desirable traits

Evaluation and identification of varieties suited for organic farming in certain areas is crucial for effective production. In Latvia, besides the conventional "Value for Cultivation and Use" (VCU) tests, variety testing can also be conducted under organic growing conditions (OC) before the including variety in the national Plant Variety catalogue (PVC). Varieties that perform acceptable under OC according to the results of VCU trials, are recommended and specially marked as the suited to OC. Trials include evaluation not only for the suitability of variety to farming system, but also for quality traits relevant for marketing and/or processing of potato. In 2018 and 2019 trials with the aim to assess applications of existing VCU protocols for evaluation of potato varieties under OC in several EU countries were started. Investigations will help developing adjusted protocols for variety testing in different trials under OC across the Europe. In Latvia the same VCU protocol is applied for the evaluation of potato varieties both under conventional and organic farming systems. Ten varieties randomized in full blocks with 4 replications were used in two years' trial. Three out of ten were check varieties of different maturity groups. The varieties were compared with check variety of the corresponding maturity group. Traits evaluated for the determination of suitability of varieties to OC were total and marketable tuber yield, starch content, and both field and tuber resistance to the most important diseases. Data on additional informative traits such as plant developmental phases, starch yield etc. were recorded according to the national legislation. The points according the previously defined point scale were applied for the comparison of the traits. Data on traits referring to yield were expressed as a percentage of the corresponding check variety and then the relevant points were applied. If the sum of points for assessed variety was the same or exceeded check variety, the assessed variety was defined as acceptable for including in Latvia PVC with a mark "Bio". Several of traits are particularly important for OC: (a) - total yield and marketable yield, resistance to pests, (b) consumer's requirements - taste, cooking type, starch content, (c) storage ability -resistance to pathogens etc. Including traits specific for OC - fast canopy development, early maturity, other pest resistance, dormancy would be desirable. LIVESEED This project received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No727230.

3.04. Study on suitability of late blight resistant potato varieties from ecobreed working collection for slovenian market

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organic potato varieties, phenotypization, late blight resistance, market potential

ECOBREED (http://ecobreed.eu/) is EU H2020 project performed by 25 partner's organizations, with the aim of improving the availability of seed and varieties suitable for organic and low- input production. The objectives of the project are: to increase the availability of seeds and varieties for the organic and low-input sector, to identify traits and combinations of traits suited to organic and low-input production environment including high nutrient use efficiency and weed competitiveness/allelopathy, to increase breeding activities for organic and low-input crop production. Activities are focusing on four crop species, selected for their potential contribution to increase competitiveness of the organic sector, and potato is one of them. One of the tasks of potato research within the Work package 3 of ECOBREED project is screening of genetic resources and breeding materials of the potato gathered in working collection of 65 cultivars in four different countries across Europe (Slovenia, UK, Poland and Hungary) and perform a detailed phenotypic analysis on traits suited to organic potato production systems: morphological and phenological traits, tolerance/ resistance to naturally occurring biotic/abiotic stresses according to locality/country (with the main focus on resistance to late blight), yield and yield component parameters, post-harvest traits and market quality of tubers for fresh consumption and processing. The criteria for selecting varieties into working collection were: resistance to late blight, earliness, breeder ‘s preference for suitability for organic production and importance of the varieties in organic production in different countries across Europe. Late blight is the major problem in organic production in Slovenia and use of the varieties with high and durable late blight resistance are the most efficient way to solve it. In order to evaluate the potential and suitability of late blight resistant potato varieties from Ecobreed working collection for organic production and consumption in Slovenia, we compared resistant and some of the most important and widespread organic varieties in Europe using two year data (2019 and 2020) of selected agronomy important traits from organic field experiments in Slovenia.

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3.05. Combining antagonistic bacteria with copper to control late blight disease in potato plants

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Late blight, bacteria, biocontrol, copper, organic

Potato being one of the most consumed crops worldwide, it appears as essential to guarantee its safe and abundant production. Unfortunately, this crop counts many different enemies ranging from insect pests to viruses, including one of the most devastating ones: *Phytophthora infestans*, causal agent of potato late blight. Even if the comprehension of this oomycete's biology is growing day by day, *P. infestans* is still difficult to manage and often requires the use of large amounts of fungicides. Often only copper-based products are available for organic production of potatoes. However, this heavy metal can accumulate in the soil and presents a toxicological danger for non-target organisms at high doses. Many researchers are currently working on the use of living organisms as natural enemies of different pests, aiming at developing environmentally friendly alternatives. However, biocontrol agents (BCA) tend to show lesser reliability when applied under field conditions in comparison to the laboratory assays, which is likely due to the variability of natural conditions and subsequent stress the BCA have to manage. This project thus aims at finding reliable control strategies by combining biocontrol treatments and reduced doses of copper, to ultimately diminish the total amount of copper and fungicides used whilst maintaining sufficient protection against late blight. Therefore, as a first step, more than 200 bacterial strains were screened in vitro against *P. infestans* to select the strains showing the highest antagonistic potential. Then, detached leaf experiments were conducted by applying a mixture of the best bacterial candidates with a reduced concentration of copper as foliar treatments against the oomycete. A selection of the best mixtures was then tested on whole plants grown in the greenhouse. Finally, a field experiment was carried out with the five best bacteria-copper combinations. The assays showed encouraging results especially under greenhouse conditions. Unfortunately, the infection of the field experiment was extremely severe due to the climatic conditions, but, despite the absence of significant results, some promising tendencies could be observed.

4. Bacterial & fungal diseases

4.01. Management of Bacterial wilt by smallholder potato growers: Lessons learned in Ethiopia

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Collective action, Common bad, Disease monitoring, Learning intervention, Ralstonia solanacearum

Introduction

For long, incidence of Bacterial wilt (caused by *Ralstonia solanacearum*) was low in most areas in Ethiopia. Nowadays, it has developed into a serious threat of potato production. The disease probably spread through latently infected seed tubers; locally, it can also spread through water, infested soil on tools, shoes, etc. Moreover, the bacterium is soil-borne and has a wide host range. The disease is difficult to manage if not treated as a 'common bad' in need of collective action, which requires a systematic analysis of social, biophysical and ecological aspects of the pathogen and its dissemination and what these aspects entail for effective disease management in the context of smallholder growers.

Methodology

We assessed the epidemiological aspects of the disease and explored the potential of collective action in disease management through experiential and social learning, disease monitoring by seed cooperatives and designing agronomic practices. The study encompassed a diagnostic analysis, a training for learning among farmers, an analysis of monitoring systems of seed grower cooperatives, a biophysical analysis of the spread of Bacterial wilt and detection and characterization of the pathogen using molecular techniques.

Results and Discussion

All 147 samples evaluated contained only Phylotype II suggesting that there is little genetic variation and the spread is relatively recent. The various actors were hardly aware of their interdependencies in managing the disease and tended to blame each other and the weather, factors that impeded collective action. Many farmers' practices spread the disease instead of controlling it. Narrow crop rotation and reuse of seed are examples of counterproductive practices. Farmers had doubts about the practicality of proposed and effective control strategies. Through the learning intervention, farmers became aware of the interdependencies between seed and ware growers and the need for collective action. Current monitoring systems are still weak, have little impact, and therefore should be improved with strongly enforced control measures. Developing an effective quarantine system to stop free movement of infected seeds should be prioritized. The increase in Bacterial wilt incidence is strongly associated with increasing soil acidification. *R. solanacearum* thrives on acid soils. Applying lime reduces the incidence of Bacterial wilt considerably and therefore can be a strategy for individual farmers to combat the disease, provided they can afford to repeatedly apply large quantities of lime.

4.02. First report of *Alternaria grandis* and *A. arborescens* causing leaf spot of potato in South Africa

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Early blight, brown spot, potato disease

Alternaria species are well known pathogens of various agricultural crops, causing leaf spot, stem cankers and fruit rots. *Alternaria solani* and *A. alternata* are the causal agents of early blight and brown spot of potato, respectively. However, other *Alternaria* species have been implicated in leaf spot diseases of potato, namely *A. arborescens, A. cantlous, A. grandis, A. protenta and A. infectoria.*

South Africa has a large potato industry spread over 16 production areas in the various climatic regions of the country. Symptoms of *Alternaria* leaf spot have been observed in all production regions and previous studies have confirmed that *A. solani* and *A. alternata* are the causal agents of these symptoms. However, most of the identifications from these studies were based on morphological identification of the isolates and many of the *Alternaria* species associated with leaf spot on potato cannot be distinguished based on morphology alone. For example, *A. solani*, *A. grandis* and *A. protenta* are very similar in morphology, while *A. alternata* and *A. arborescens* are similar. The aim of this study was therefore to determine which species are responsible for the symptoms observed on potato leaves in South Africa.

Symptomatic leaf material was collected from 13 potato production regions across South Africa and isolations for *Alternaria* were done. Isolates obtained were characterized based on morphology as well as DNA sequencing and phylogenetic analyses. In addition to *A. solani* and *A. alternata*, *A. grandis* and *A. arborescens* were found to occur commonly on potato plants in all the regions. The isolates were screened for virulence by inoculating onto detached potato leaves. Virulent isolates were chosen to inoculate onto healthy potato plants in the greenhouse. Symptoms similar to those observed in the field were produced by isolates inoculated onto plants in the greenhouse. Subsequent isolation and identification from symptomatic plants were done to fulfil Koch's postulates. This is thus the first report of *A. grandis* and *A. arborescens* causing leaf spot of potato in South Africa. This may have implications for control of these diseases as the diversity of the fungi present in the country is greater than previously thought.

4.03. The presence and distribution of *Verticillium dahliae* and *Colletotrichum coccodes* in relation to Potato Early Dying (PED) in Denmark

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Potato Early Dying (PED), Verticillium Wilt, Colletotrichum coccodes, Disease complex, Potato production

Potato Early Dying (PED) is a serious disease in potato productions all over the world and appears to be an increasing problem in Denmark. The disease is caused by a complex of microorganisms, but research indicates that the main pathogen is *Verticillium dahliae* kleb, causing *Verticillium* wilt. However, it is strongly suspected that interaction with other soil pathogens, such as *Colletotrichum coccodes* (the causal agent of black dot), increases the severity of the disease, resulting in a disease complex. The initial part of this study has focused on investigating the presence and distribution of *V. dahliae* and *C. coccodes* in potato production in Denmark. A study of Danish fields was carried out in the 2021 growing season, to identify and quantify pathogens related to PED symptoms. The hypothesis was that the two fungal species *V. dahliae* and *C. coccodes* are the main causes of PED in Denmark and are present in fields showing premature wilt symptoms and early senescence. Six fields from two different regions of Jutland were identified as suspected PED fields, based on observations of visible PED symptoms and a long potato cropping history with little crop rotation. Likewise, one field from each region, where potatoes had not been grown for at least 15 years, and where crops showed no visible PED symptoms, was selected for reference. From each field, plants with and without PED symptoms, were collected, along with soil samples from PED symptomatic plots. The DNA from each plant- and soil sample was extracted for further molecular identification of the causal agents in the disease complex. The identification and quantity of the two pathogens in each sample, was quantified using quantitative PCR (qPCR). The results are intended to give an indication of the distribution of *V. dahliae* and *C. coccodes* in two regions in Denmark, based on their quantitative presence in soil, stems and roots. This may help to clarify the role of *V. dahliae* and *C. coccodes* in relation to PED, which will contribute to a better understanding of the disease complex and provide a basis for further research in PED interactions and potential influencing factors, for the evaluation of PED management in the future.

4.04. Molecular responses of potato plants to salt stress and *Rhizoctonia solani* Kühn. Combination.

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Eskisehir Osmangazi University

Abiotic stress, Biotic stress, Sucrose metabolism, Gene expression, Solanum tuberosum L.

Soil salinization is one of the critical abiotic stresses that hinders the production and productivity of potatoes and has become a global problem. Abotic stresses alone affects yields and nutritional values of plants, as well as causing the spread of pathogens by negatively affecting the habitats of plant pests and pathogens. For this reason, plants have to evolve to live where they are exposed to different stress factors at the same time. Sucrose catabolism is one of the biggest metabolic breakdown events and sugars have an important role in responding to environmental changes. In this study, it was aimed to determine the changes in sucrose metabolism of potato cultivars that show different responses to salt stress and *R. solani* fungal disease. For this purpose, 19 commercial and widely used potato cultivars were singly screened for salinity tolerance and resistance to *R. solani* by the means of physiological and morphological differences. In the sequel, the experiment was carried out with four cultivars, Russet Burbank (NaCl tolerant, *R. solani* resistant), Desiree (NaCl tolerant, *R. solani* susceptible), Granola (NaCl sensitive, *R. solani* resistant) and Lady Claire (susceptible to both; NaCl and *R. solani*) selected according to the results of screenings. Control, salt stress, *R. solani*, salt stress and *R. solani* combination was applied to these cultivars to determine the differences in sucrose metabolism. In the light of changes in leaf samples taken every fifteen days, the effect of the stress combination was more pronounced, especially after the tuber attachment period. The amount of sucrose, reducing sugar, starch and the activity of sucrolytic enzymes , and changes in the relative gene expression levels, both in leaf and tuber tissues, were consistent with the tolerance levels of the cultivars, demonstrating the importance of sugar metabolism in both biotic and abiotic stress to tolerance.

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4.05. Application of a dielectric-barrier discharge plasma for eradication of plant pathogens, *Dickeya* and *Pectobacterium* spp., from a surface of economically important seeds

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cold atmospheric pressure plasma, dielectric barrier discharge plasma, Pectobacteriaceae, blackleg and soft rot diseases, plant protection

Plant diseases cause significant losses in the agricultural sector every year. Fighting phytopathogens with the use of pesticides is not ideal due to a limited number of microorganisms to be targeted and toxicity of these compounds. There is an ongoing search for novel plant protection methods. One of the alternatives to chemical plant protection may be the use of cold atmospheric pressure plasmas (CAPPs). The antibacterial and plant-growth stimulating phenomena accompanying utilization of CAPPs include: electromagnetic field, reactive oxygen and nitrogen species, UV and heat irradiation. The development of this methodology and optimization of its use may contribute to a significant reduction in the amount of toxic pesticides used, and thus reduce their harmful impact on human health and the natural environment.

The aim of this study was to evaluate antibacterial properties of a direct action of dielectric barrier discharge (DBD) plasma against *Dickeya* and *Pectobacterium* spp. inoculated on glass spheres or mung bean seeds. Besides, the influence of a DBD-type plasma on the germination and early growth of mung bean seeds was investigated.

In terms of eradication of phytopathogens from glass spheres, the noted reductions in CFU ml-1 exceeded 99.93% (3.16 log). Concerning elimination of bacterial cells from mung bean seeds, reductions over 99.91% (3.07 log) were observed. Regarding microscopic visualizations, denaturation and aggregation of bacterial DNA fragments, proteins, and ribosomes occurred. Also rupturing of the cellular membrane was shown. 2 min DBD plasma treatment stimulated by 3-4% seed germination rate and by up to 13.4% subsequent early growth of seedlings. Negative effects of 4 min DBD action were noted shortly after the treatment, however these effects were no longer observable or reduced to 9.7% after the extended seed incubation periods.

It was proven that a direct DBD plasma treatment can be an efficient tool to fight bacterial phytopathogens from the surface of mung bean seeds without impeding plant growth. Thanks to low temperature, CAPPs can be applied without harm on living tissues. Broad application of this technology into agriculture can be foreseen due to its eco-friendliness and antimicrobial potency. As artificial plasmas can be generated with the use of various types of electric discharges, further modifications and optimization of this method would allow for scaling-up this technology. Our future plans include evaluation of the potential of this technology in treatment of seed potato tubers.

5. Seed production; 6. Viral diseases

5_6.01. Variety needs and preferences to establish breeding targets for Sub-Saharan Africa, experience from Kenya and Eritrea

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breeding target, Adaptation, variety preference, preference

Potato is grown by millions of farmers in sub Saharan Africa as both a subsistence and cash crop. In the recent past the area grown has increased greatly and potato is being promoted as a hunger busting crop: because it can be grown in two or more seasons it can fill a gap in food supply between cereal crops. This is increasing reliance on potato. Old varieties originally introduced from Europe are still widely grown but in many countries varieties released jointly by the International Potato Center and National Agricultural Research Institutions (NARs) dominate. However access to healthy seed and improved varieties still remains a major constraint in potato production in most Eastern African countries. In recent years many breeding companies have begun regional production of seed or seed imports of European varieties to the region. In many cases there are demands for the traits exhibited by European varieties particularly for quality and some disease resistance traits but variety adaptation remains a challenge and regional preferences and different agroecologies have different needs. Two PhD candidates conducted focus groups discussions to determine industry and farmer needs in both Eritrea and Kenya for new variety introductions. In semi-arid Eritrea there is a requirement for drought tolerant and early maturing varieties to minimize water use. Access to varieties is severely restricted and both formal and informal seed systems operate from imported seed and also from local production from tissue culture. Access to a greater diversity of varieties is acknowledged as a priority. There is a strong preference from all stakeholders for white skinned varieties with high yield, early maturity, drought tolerance and good disease resistance. Farmers in Kenya have access to many varieties from a range of sources, with seed available from both commercial firms and governmental institutions although the demand for certified seed still far outweighs supply. Due to the cooler highland climate later maturing varieties can bring a yield benefit. Dormancy is an important consideration. Long dormancy varieties often do not break dormancy before the next planting season, while the use of short dormancy varieties which are preferred by farmers can lead to short term over supply in the market. Farmers were able to choose varieties for their own needs based on different traits. Farmers indicated high yield, disease resistance, high market demand, early maturity and long storability as the most important traits in that order.

5_6.02. Monitoring *Verticillium dahliae* infection in local and imported seed tubers using molecular analysis

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Verticillium, microsclerotia, molecular methods, seed tubers

Verticillium dahliae is a soilborne fungal pathogen, surviving for prolonged periods in soil through microsclerotia, causing potato early dying (PED), and *Verticillium* wilt in a wide range of annual and perennial crops. One of the means to reduce the spread of the disease and prevent soil infestation is using pathogen-free potato seed tubers. Monitoring of *V. dahliae* latent infections has been carried out routinely in local seed tubers, but not in lots imported from Europe because of the low prevalence of PED in Europe, however, climate change and global warming might have affected the situation. The objectives of the current study were: a) to investigate the potential transmission of the pathogen via seed tubers imported from Europe; b) to compare sensitivity of RT-PCR analysis in detecting tuber-borne *V. dahliae* to isolation; c) to determine the optimal timing for testing (before or after haulm destruction). In spring 2020, in 29 lots out of total 67 *V. dahliae* was isolated (18 from Netherlands, 4 from Germany, 4 from France and none from Scotland). Twenty isolates that were checked for VCG were all assigned to VCG4B. In spring 2021, 17 out of total 54 lots were *V. dahliae*-infected (7 from Netherlands, 2 from Germany, 7 from France and one from Scotland). Sixteen tested isolates were also assigned to VCG4B. Selected 231 local seed lots (for the fall-winter season) were checked during three years for *V. dahliae* latent infection by microbiological and molecular methods. The incidence of infected seed lots in both methods was 76%, whereas 23% were positive only in RT-PCR, and only 1% of the cases were positive in the microbiological test and negative in the molecular test. The sampling date, before or after haulm destruction, was evaluated in 34 fields during two years. The incidence of infected seed lots assessed using RT-PCR was 69 and 67%, before and after haulm destruction, respectively. With the microbiological test, seed lot infection was 53% and 61% before and after haulm destruction, respectively. In both years, the incidence of infected lots was increased after haulm destruction evaluated in both tests. To conclude, *V. dahliae* is being transmitted via seed lots imported from Europe, the molecular method for detecting latent *V. dahliae*-infection in seed tubers was more sensitive compared to the microbiological method, and the optimal timing for testing the infection was after haulm destruction.

5_6.03. Cultivar-specific alteration of the selected host miRNAs and mRNA targets in potato-PVS resistance interaction

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potato virus S, resistance, susceptible, cultivar dependent, microRNA

°C in a growth chamber; (2) to test the expression pattern of five selected potato miRNAs and their target mRNAs, which are supposed to be involved in plant development, defense responses to virus, incompatible interaction, and hypersensitive response, in tested cultivars following mechanical inoculation with PVS. The experiments were repeated in two years. For each experiment, 10 plants per cultivar were inoculated with PVS, and 5 mock-inoculated plants (inoculation with water) were used as a control. Enzyme-linked immunosorbent assay (ELISA) was used for virus detection. For miRNA study, small pieces of two or three non-inoculated upper leaves were sampled at 42 days post-inoculation (dpi) and were stored at - 80 °C for RNA extraction. The expression levels of miRNAs were quantified by stem-loop RT-qPCR, and that of target mRNAs and viral RNA encoding coat protein (CP) were determined by RT-qPCR. Differences in ELISA results, in infection rate that was calculated based on ELISA test, as well as in gene expression levels between cultivars were analyzed by one-way ANOVA using Statgraphics Plus software. The virus was detected by ELISA at 40 dpi. Cultivars Tajfun and Tonacja exhibited partial resistance to PVS at 22 °C with systemic infection detected in some of the inoculated plants; cv. Bryza was susceptible to PVS with systemic infection detected in all inoculated plants. The infection rate and the viral accumulation levels were significantly lower in Tonacja and Tajfun than that in Bryza, but no statistically significant difference between Tajfun and Tonacja was detected. Expression of the tested miRNAs and mRNA targets exhibited inter- and intra-cultivar variability. Majority of the tested genes were altered only in the partially resistant cvs. Tajfun and Tonacja but not in the susceptible cv. Bryza. Enhanced expression of AGO1-2, DCL1, stu-miR482 and its target Gpa2 was observed in cv. Tonacja and the PVS-infected plants of cv. Tajfun, with the highest induction of Gpa2 in the later (30.2-fold). However, their expression remained unchanged or decreased in the PVS-uninfected plants of cv. Tajfun. Increased expression of stu-miR168a and stu-miR172e was observed in cv. Tonacja and the PVS-uninfected plants of cv. Tajfun, respectively, but not in the PVS-infected plants of cv. Tajfun. This is the first report on cultivar-specific alteration of miRNA in a potato-PVS resistance interaction.

5_6.04. Genetic fingerprints using SSR markers to secure seed potato production in France: method and database improvement

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2. FN3PT
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7. Agroscope
8. INRAE

cultivar identification, SSR, database, electrophoresis, ring test

Single sequence repeat (SSR) markers are essential tools to fingerprint cultivars for their identification. The French seed potato growers' organization (FN3PT) and its regional organizations have set up a method, routinely used in the certification scheme, to check the initial material and the first generations of the multiplication process. Five French labs are using the same procedure. The kit, which was initially composed of 5 markers [1], has been upgraded to 8 markers due to the increase in the number of varieties to be checked. A shared fingerprints database has been built. Ring tests are regularly jointly organized with the Official Certification Body (SOC) to check the ability of the labs.

Our database, named IdeAle, currently contains 4122 profiles representing 2603 genotypes (1300 varieties). It was built with the support of the French Ministry of Agriculture [2]. This is a secured internet platform with user authentication access. Data are updated in real time and can simultaneously be accessed by all users. IdeAle was updated with the addition of 310 profiles from Agroscope Changins (Switzerland). This update strengthened the profiles of 50 varieties for which no redundancy was available until now in the database. In 2019, 5 French labs and our Swiss partner participated to the latest and 9th ring test. Each lab received 8 unknown samples from a list of 10 varieties. All the labs succeeded in identifying all the samples confirming their ability to use the method, the usefulness of the database and the power of the kit.

Since 2019, the French labs are also involved in a new project named IdEvol conducted by FN3PT and supported by the French Ministry of Agriculture to improve the way of resolving the markers. Our current procedure is labor intensive, potentially harmful for the lab technicians and not environmentally friendly (acrylamide electrophoresis followed by silver staining). Therefore, we are working on the markers transfer onto another electrophoresis platform, making sure of its compatibility in order to be able to use the vast amount of informative data obtained with the preexisting system, and on the development of additional markers.

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7. New techniques & hybrid breeding

7.01. Detection of quarantine root-knot nematodes in potato tubers with hyperspectral image analysis

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Hyperspectral image analysis, VNIR (visible and near-infrared), detection, Meloidogyne

The number of outbreaks of the quarantine root-knot nematodes (*Meloidogyne chitwoodi* and *M. fallax*) in Europe has risen in recent years. Above-ground nematode damage is atypical, usually reduced plant growth, but resulting in considerable yield loss if left unmanaged. This highlights the need to detect nematodes in seed potato to prevent introduction, but also in the early stages of field infestation to prevent spread. Field detection should be with high spatial accuracy to allow for effective management. Current detection methods are soil sampling and visual examination of tubers, followed by nematological analysis. However, these approaches are laborious and require expertise. Remote sensing might provide objective and time/cost efficient alternatives.

We examined whether tuber infections can be detected using spectral imaging sensors. The detection of *M. chitwood* and *M. fallax* in tubers was investigated by performing imaging on naturally infected tubers (cvs. Fontane, Hansa, Agria), obtained from fields, and on tubers (cv. Bintje) produced in nematode-infested pot cultures. Different processing methods were compared: (1) whole tubers, (2) peeled tubers and (3) tubers cut in halves. Imaging was performed in lab conditions on infected and non-infected tubers with a Specim FX10 sensor (224 bands; range 400 to 1000 nm; FWHM 5.5 nm), Hyspex VNIR-1600 and SWIR-384 (448 bands; range 400 to 2500 nm; FWHM 3.4 to 5 nm), and a Sony A7r Mark III (35 mm f/2.8). Image pre-processing included background removal and de-noising of hyperspectral imagery. Afterwards, image data was processed with a combination of multivariate and machine learning methods. Preliminary results showed that females and their egg masses could be detected based on spectral signatures and vegetation indices. Peeling (2-4 mm deep) was the most effective processing method to detect the nematodes in the tubers. The imaging was able to detect both *M. chitwoodi* and *M. fallax*. While nematode infection is visible on below-ground plant parts (roots, tubers), the effect on the plant canopy is non-specific and similar to signs of drought stress. However, image analysis of the plant beyond the visible spectrum could reveal nematode infections. Detection of cyst and root-knot nematodes infecting growing potato plants was also studied, in pot experiments as well as in the field. Preliminary results will be presented.

7.02. The intention to incorporate *S. pinnatisectum* in the breeding programme

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Phytophthora infestans, protoplast electrofusion, resistance

A valuable source of resistance to *Phytophthora infestans* is the wild species *S. pinnatisectum* from Mexico; however, it is sexually isolated and not crossable with cultivated potato by conventional means; therefore, the protoplast fusion technique was used. The resulting somatic hybrids were involved in the breeding program. The somatic hybrids and their progeny were evaluated for resistance to *P. infestans*, yield and tuber quality, length of vegetation, ability of flowering etc. Some of them were included in the study of metabolomic response to infection by the pathogen (*P. infestans*). Somatic hybrids are often intermediate between the characteristics of the parents; in their progeny, it is common to associate higher levels of resistance to *P. infestans* with longer growing season. This work was supported by the Czech Republic´s NAZV QK1910045 project and the institutional support of conceptual development of research organization PRI Havlickuv Brod MZE-RO1622.

7.03. PotatoMASH – a low cost, genome-scanning marker system for use in potato breeding

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Breeding, Genotyping, Marker assisted selection, Genomic selection, Multiallelic haplotypes

Potato breeding is a 10-year process that involves combining over 40 characteristics to produce varieties that have improved sustainability, utilisation and consumer characteristics. Genomic and marker assisted selection (GS and MAS) can make breeding faster and more efficient. Strategies for GS to date have tended to employ many thousands of markers. However, the economic burden of deploying such approaches on thousands of plants annually in a breeding programme may restrict the adoption of GS. We are developing PotatoMASH (Potato Multi-Allele Scanning Haplotags), a novel, low cost, genome-scanning marker platform for multiple applications, including GS, MAS and, genome-wide association studies (GWAS). We designed a panel of 339 multiallelic regions placed at 1Mb intervals throughout the euchromatic portion of the genome and a further 94 regions containing SNPs linked to specific traits. These regions will be targeted and assayed using a genotyping by sequencing approach, which uses combinatorial barcoding to allow multiplexing of thousands of samples in a single NGS run. Significantly, capturing multiple SNPs in short read "haplotags" will render each locus multiallelic, increasing the power and resolution of the assay. We discuss progress in the design and validation of the assay.

7.04. Hybrid breeding revolutionizes potato cultivation systems

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Direct field sowing, Hybrid breeding, Hybrid cultivation systems, Stakeholder expectations, Transplanting seedlings

Hybrid breeding of diploid potato is a promising technology enhancing the introduction and stacking of favourable traits, creating an agile breeding process and increasing the turnover of improved varieties. F1 hybrid true potato seed (TPS) allows rapid scaling up and promotes seed health. Hybrid TPS promotes the development of novel potato cultivation systems, with a less prominent role of slow and disease susceptible clonal multiplication, using transplanted seedlings or directly sown TPS instead of seed tubers. The Dutch PotaRei project explored options for a societally responsible introduction of hybrid potato breeding benefiting all stakeholders in the potato value chain. Agronomic studies entailed multi-year field trials with different types of planting material, using experimental hybrids. The feasibility and the yield potential of the novel cultivation systems were studied, as well as the growth and development characteristics of plants from these novel planting materials. Main performance indicators of the different cultivation methods were tuber yield and multiplication rate. Transplanting in the first half of May gave the shortest crop cycle. Earlier or later transplanting did not significantly affect yield but comes with increased risks of harsh environmental conditions. Timing of direct sowing was more critical: highest yields were obtained when sown in May. Increased transplanting or sowing densities resulted in increased yields, but very high densities could reduce yield and always reduced average tuber size. We expect that transplanting seedlings can produce acceptable yields for various outlets in the future. Hybrid seedling tubers can generate acceptable yields of ware. Direct sowing at high densities might make normal seed tuber yields feasible, but further research on rapid seedling establishment is needed. The project's social-technical study showed that expectations of some stakeholders were initially low. Stakeholders expectations gradually increased, first for the sector itself followed by the society at large. The technical feasibility was most doubted by stakeholders, whereas expectations on food security benefits were high. Scenario studies showed that a conducive regulatory and legal environment is essential for this innovation to succeed. We conclude that different novel cultivation systems for hybrid potato are feasible under Dutch conditions. Hybrid potato breeding contributes to the knowledge position of Dutch agriculture, and gives room for innovative stakeholders to contribute to sustainable food security.

7.05. Hybrid breeding in potato: from science to practice

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Solynta

F1 Hybrids, Inbred lines, Genetics, Breeding, Diploid

In 2008, Solynta initiated hybrid breeding in potato by making the first cross between diploid potato and a self-compatible *S. chacoense* line, containing the Sli-locus. The first segregating population was grown in the field in 2010. Most plants showed weak growth, poor flowering and set only few tubers and berries. After crosses, selections and many generations of selfings, we generated highly homozygous inbred lines. Experimental hybrids were made and showed similar yields as some controls in 2017, based on field trials at five locations in NW Europe. Here, we tested diploid hybrids from seedling-tubers against tetraploid cultivars from seed-tubers. However, a cropping system based upon true-seed hybrid will demand a new cropping methods. Therefore in-depth agronomic studies were conducted, showing the attaining yield of experimental hybrid seedlings. The use of molecular markers has made it possible to introgress resistance genes very fast and efficiently in diploid potato backgrounds. We have shown that a hybrids containing two Late Blight resistance genes from wild potato relatives can be created in two years. The hybrids that contained two resistance genes showed higher resistance compared to hybrids with no or one resistance gene, underpinning the need to stack resistances. The ability to map QTLs that segregate in a breeding population is crucial for the success of a breeding program as it can guide breeding decisions on germplasm enhancement, population improvement and choice of hybrid parents. By using innovative methods taking the pedigree and relatedness between individuals into account, QTLs can be efficiently mapped in a diploid potato breeding program. To stimulate research on diploid potato, we are now releasing a good performing inbred as a universal research line. This line, Solyntus, shows vigorous growth combined with high homozygosity. In greenhouse experiments, good tuber yields and numbers were obtained. It produces round tubers with creamy flesh. Jointly, Solynta and WUR-Plant breeding have sequenced this line using 70x Oxford Nanopore reads supplemented with 70x Illumina reads to generate an improved reference genome for cultivated ***Solanum tuberosum***. Additionally, important steps towards commercial applications have been taken by submitting a number of hybrids to the registration process. The Process of commercial release of hybrids is underway in a number of European and African countries. Setting up the supporting supply chain and technical support are next steps to allow farmers the grow hybrid potato.

8. Disease control strategies

8.01. Pre- and postharvest strategies to control potato black dot – an integrated approach

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Keywords: Colletotrichum coccodes, disease management, storage, quality, food loss and waste

Potato black dot is a foliar and tuber blemish disease that costs the potato industry £3M per year in postharvest losses. Black dot is caused by the fungus *Colletotrichum coccodes* and is characterized by silvery lesions on the tuber skin leading to lower quality of potatoes destined for the pre-pack market. The importance of the high-quality tuber appearance has increased considerably because of the growing demand for washed and pre-packed potatoes and the need to reduce food loss and waste throughout the food supply chain. Black dot disease originates in the field and further develops during potato storage. Therefore, both field strategies, such as fungicide application and crop duration, and postharvest treatments can be used as an integrated approach to control and reduce the disease in potato tubers. However, better knowledge and guidance on how best to use fungicide control and when to harvest a crop is required to enable successful management of risk factors affecting potato black dot. In this work, a field trial followed by the postharvest trial was carried out to evaluate the effect of different fungicide application timings (n =5, control, at planting (in-furrow), in-furrow + foliar early, in-furrow + foliar late, in-furrow + foliar early + foliar late) and crop duration (n = 2, tubers harvested after 3 or 4 weeks of desiccation) and their interaction on black dot development in daughter tubers cv. Maris Piper throughout postharvest cold storage. Moreover, the impact of continuous ethylene supplementation during postharvest cold storage was assessed. Preliminary results showed that continuous ethylene supplementation has no negative effect on black dot development during cold storage for any of the stocks tested. Furthermore, a foliar early application of the fungicide would be a useful strategy to keep potato black dot incidence low in tubers harvested after both 3 and 4 weeks of desiccation. Yet, a third foliar application (late) does not have any additional effect. The effect of both pre- and postharvest treatments on potato physiology and black dot development throughout storage will be discussed. The results are part of an integrated approach including the development of models and decision support tools for determining the optimum storage time for different potato consignments based on the incidence and severity of black dot. The outcome would contribute to reduce potato postharvest losses helping to achieve the United Nations Sustainable Development Goal of reducing food loss and waste by 50% by 2030.

8.02. Improving decision support systems for an integrated control of *Alternaria* spp. in potatoes

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1. PCA
2. CARAH,
3. HEPH-Condorcet,
4. Arvalis,
5. Inagro,

Keywords: Potato Early Blight, Alternaria solani, control strategies, disease model, simulation models

Introduction: The potato early blight disease (*A. solani*) is viewed as a growing concern in the North of France and the adjacent regions of Hainaut and Flanders in Belgium. Factors such as more favourable weather circumstances due to climate changes, or fertilisation with stricter nitrogen dosage, could be contributing to this. However, the shift in available late blight fungicides towards more oomycete-specific fungicides, without an effect on early blight, plays an important role. Moreover, specific early blight fungicides are brought to market for the control of the disease. Potato growers pursuing an IPM strategy are faced with the question: how and when should I use these fungicides to achieve an optimal, cost-efficient crop protection? In order to improve decision support systems for the potato growers, a collaborative research project SYTRANSPOM was launched in April 2018 with four partners from these neighbouring Interreg regions.

Materials and methods: At four different locations in the region, field trials were carried out to determine the timing of the first treatment against early blight that proved to be effective and necessary for a good control of the disease. All plots in the trial were left untreated with regard to early blight until the last week of July. From then on, treatments were started for one plot after the other, each with 1 week interval. Once started, a good disease control for the plot was maintained with weekly sprayings. The observed disease levels were used to fit different simulation models that combine both detailed weather data and data on crop maturity.

Results: In all project years (2018 - 2021), a critical date for the first application could be established from the assessments, with a clear distinction between treatments that were applied too early - having no additional effect on disease level -, and treatments that were performed too late, leading to disease levels approaching these of the untreated control. A weather based disease model derived from the FAST model (Madden et al., 1978) proved useful to predict the date for a first application. Age-dependent susceptibility of the potato crop was added to the calculations in the model, as a function of crop senescence. Simulations with an epidemiological model, taking also into account the physiological resistance of the crop, gave a satisfactory correlation with the observed development of the disease. Acknowledgements: The authors want to thank the European Regional Development Fund of the European Union for funding this research project.

8.03. Inoculation of plant growth-promoting microbes at planting limit post-harvest diseases of potato in Swiss field conditions.

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microbial inoculants, silver scurf, common scab, biocontrol, varieties

Plant beneficial microbes are able to improve potato growth. An experiment performed in the US (Hijri et al. 2016) showed that over the course of four years, in 231 different sites, inoculation with the mycorrhizal fungus *Rhizophagus irregularis* allowed an average yield increase of 9.5%. Beside this profitable increase in yield, inoculation with microbes also shows promising effect on infection with potato pathogens. We know for example that symptoms caused by *Rhizoctonia solani*, *Phytophthora infestans* or *Streptomyces* spp. can be reduced by microbial inoculation (Larkin et al. 2005, Hultberg et al. 2010, Sarwar et al. 2019). However, these biostimulant and biocontrol effects are largely dependent on inoculation technique, timing of application of the inoculants, environmental conditions and genetic compatibility with the target crop. We assessed the effect of four microbial strains on cultivars Désirée and Pentland dell, in field experiments. Plants were inoculated with a granular formulation containing one of four strains and twofold or threefold combinations of the strains. We measured a wide set of parameters, including the presence of tuber external defects caused by various pathogens originating from the soil or from the seed tubers. We also monitored the survival of the inoculated strains in potato roots via qPCR. After three years of field trials, we observed that some inoculation strategies tested provided a significant reduction of the silver scurf symptoms (caused by *Helminthosporium solani* and/or *Colletotrichum coccodes*) or common scab symptoms (caused by *Streptomyces* spp) on the surface of the tubers. The dual inoculation of *Rhizophagus irregularis* MUCL41833 and *Pseudomonas brassicacearum* 3Re2-7 provided the best reduction of the silver scurf and common scab symptoms (-14% and -24%, respectively). These two strains inoculated on their own were also able to increase yield of Pentland Dell during the last year of trial (+13% for MUCL41833 and +14% for 3Re2-7). In addition to providing a potential increase in revenue from yield, this inoculation approach could decrease the risk of market-rejection of potato lots due to high infections with skin diseases.

8.04. Small RNAs, Big Impacts

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Host pathogen interactions, RNAi, Disease control, Late blight, Climate change

Phytophthora infestans is an oomycete pathogen that causes late blight disease on potato and tomato. It is to date one of the most persistent pathogens causing massive loss to crop & economies worldwide. Current control strategies include breeding for resistance and extensive fungicide spray.

However, fungicides raise serious environmental concerns and include the risk of *P. infestans* developing resistance. Plant transgene-derived artificial small RNAs can induce gene silencing in certain interacting insects, fungi & oomycetes, a phenomenon called host-induced gene silencing (HIGS). HIGS requires established transformation methods and is also subjected to heavy regulatory and public scrutiny due to the need to generate transgenic plants, thus limiting its use. We explore the RNA interference (RNAi) mechanism for an alternate plant protection strategy against potato late blight by developing a double-stranded RNA (dsRNA) spray targeting specific pathogen genes important for infection, in a method called spray induced gene silencing (SIGS). RNAi is a conserved cellular defense mechanism, wherein dsRNA is processed into small non-coding RNAs (sRNAs) and triggers post-transcriptional silencing of genes via sequence-specific mRNA cleavage/degradation or translational repression; and chromatin modification. In order for SIGS to induce RNAi, it is imperative to know if *P.infestans* can take up dsRNA from the surroundings. In this regard, *P.infestans* sporangia were treated with dsRNA and viewed under the microscope after 24 hours, revealing that the sporangia indeed take up dsRNA. To investigate the effect of targeted dsRNA treatments on the development of *P.infestans* infection, detached leaf assays were performed. Although a significant reduction in infection was observed with most target genes in comparison to control, one particular target produced no significant change, suggesting the efficiency of SIGS relies on the selection of target genes. Studies with dsRNA spray on whole plant assays have shown disease reduction consistent with detached leaf assays. The dsRNA were also detected up to 22 days post spray. Further experiments to understand the effect of dsRNA on the microbiome of potato leaves is currently underway. Thus, we conclude that targeting specific genes in the pathogen using SIGS is a potential sustainable control strategy against potato late blight.

8.05. What is the best treatment strategy to control Potato virus Y (PVY) spread in potato fields?

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treatment strategy, straw mulching, insecticides, mineral oil, aphids

Potato virus Y (PVY) is a virus causing significant losses, which is transmitted from plant to plant by various aphid species. Treatments requiring spraying of chemicals are the most broadly used to control PVY spread in Europe. Mineral oil spraying is the method used most frequently to control PVY spread in continental Europe, while insecticides are also used in some countries to control PVY and/or Potato leafroll virus (PLRV) spread in seed potato crops.

Field trials were carried out in Switzerland over a period of four years to assess the efficacy of three treatments strategies, namely mineral oil treatments, insecticide treatments, the combination of mineral oil and insecticides, and the combination of mineral oil and straw mulching. For the insecticide treatments, three different insecticides were used during the growing season, by alternating molecules from one treatment to the next. PVY-susceptible cultivars were used for these trials. For the first two years, small plots of 25 m2 were used with four replicates, while for the last two years, plots of 1’600 m2 were used with two replicates. Tubers samples were taken before harvest and were analysed by ELISA. In the plots of 1’600 m2, tuber samples were taken in the centre of the plot as well as at the border, and these subsamples were analysed separately. Aphids were captured with yellow water traps to assess the dynamic of the flights during the growing season.

The best protection against PVY spread was obtained with the combination of mineral oil and straw mulching in the 4 years of experiment. Mineral oil was the second best treatment. Treatment strategies using insecticides, with or without mineral oil, revealed to be inefficient in controlling PVY. For the treatments using insecticides alone, higher PVY spread has been observed in some years. No significant differences of PVY infection was detected between the samples taken in the centre or at the border of the plots. Less aphids were captured in the plots covered with straw, mainly during the 4 to 5 weeks after emergence, explaining why a better protection was obtained when straw is added to the PVY-control treatment strategy.

Acknowledgment
The authors thank all the colleagues who participated to the technical management of the trials.

9. Genetics & genetic resources

9.01. Potato diversity at four levels

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Diversity, Admixture, Population Genetics, Gene Bank, Introgression

Potato is complex with several cultivated species and even more wild relatives. Understanding the way in which diversity is partitioned within and between these species and their relationship with one another is crucial for potato breeding especially as breeders increasingly work at the diploid level where introgression is easier. In collaboration with many others our lab has examined potato diversity at four levels. First, as part of the potato pan genome project we looked at heterozygosity in six tetraploid cultivars from the US and Europe as well as allele sharing between those cultivars. Potato is highly heterozygous, with an average of 3 alleles per loci. This seems to be the result of many alleles in the population; looking across two clones over 60% of loci had 6 or more alleles. Introgression is one of the major forces shaping the potato genome with all six clones showing introgressed regions from twenty wild species. Second, as part of our diploid breeding efforts we have re-sequenced 61 primary dihaploids developed from US commercial tetraploids. These sequences exhibit heterozygosity rates of between 0.75 and 1.15%, in line with previous estimates. Notably, this level of diversity is maintained at the population level, with nucleotide diversity () between 0.009 and 0.010 for all three market classes. This suggests that the market classes in the US are panmictic populations with minimal inbreeding or population structure within class. Third, we have analyzed a SNP array genotyping panel from the International Potato Center in Peru representing their entire global cultivated collection. This has allowed us to look at admixture between geographic and taxonomic populations and identify SNPs that have undergone extreme allele frequency changes between populations. Finally, we have examined a GBS genotyped diversity panel including cultivated and wild species from the US potato genebank. Even using measures accounting for ploidy differences we observe almost twice as much heterozygosity in tetraploids (HO=0.273) as in diploids (HO=0.134). However, expected heterozygosity which reflects population level diversity is much closer in diploids (HS=0.291) and tetraploids (HS=0.349), indicating substantial inbreeding in diploid potatoes (GIS=0.541). Examining diversity and relationships on the level of individual clones, the US breeding population, the global cultivated population, and wild and cultivated species together allows us to form a more complete picture of the potato genome and how it was shaped.

9.02. Developing pathways for practical deployment of DNA-based selection strategies in potato breeding

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Genomics, Breeding, Marker assisted selection, Genomic selection,

Marker Assisted and Genomic Selection (MAS & GS) offer great potential to improve the efficiency of potato breeding, but practical, logistical and economic factors can often hinder their deployment. We describe a series of experiments designed to address some of these constraints. A wealth of information exists on molecular markers for loci involved in resistance to biotic stresses of potato but these markers come in many different forms. Ideally a breeding programme would routinely perform annual genotyping on a single unified platform. To address this, we developed an approach to consolidate various types of molecular markers to a single SNP-based platform using whole genome sequencing of carefully constructed pools of DNA using, as examples, markers for the H1 nematode and R2 blight resistance genes. We show the use of this process to drive the cost effective routine deployment of MAS for disease and pest resistance in our breeding programme. Whilst MAS is useful for dominant disease resistance loci, GS is more suited to polygenic traits. To facilitate GS for processing traits, we accumulated fry-colour data on a large population of lines under selection in our breeding programme and combined this with ~50K SNPs identified with reduced representation sequencing to evaluate accuracy of genomic prediction. We were able to predict fry-colour with moderate accuracy (and to identify a major QTL on chromosome 10). We also demonstrated that it was still possible to achieve moderate (but lower) prediction accuracies for fry colour with hundreds of markers. Based on this, we outline potential strategies for simultaneous marker and genomic assisted selection with minimal changes to the current structure of the breeding programme.

9.03. Breeding table potato for Fennoscandia

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Association Genetics, Genomic Prediction, Genetic Gains, Cultivar Development, Microbiome

Potato breeding in Sweden began in 1903 at a semi-public institute and since last decade is a small enterprise at the Swedish University of Agricultural Sciences (SLU). This program plants about 30 –40 bi-parental family offspring for testing every year in Skåne and Norrland and does research on improving the efficiency in the genetic enhancement of potato. For example, we estimated that the annual genetic gains (%) for tuber yield and flesh's starch content for potato breeding in Europe since the 1800s were about 0.3% and below 0.2%, respectively, thus telling that the realised genetic gains of foreign cultivars are small in the Nordic testing sites. Furthermore, multisite testing demonstrated that potato breeding based in Scandinavia offers to the growers of the Nordic Region of Europe cultivars for prevailing farming environments and end-user needs rather than relying, as happens today in the market, on foreign cultivars. The breeding clones appear to be closely related to old Nordic potato cultivars available at NordGen, with a low degree of population structure between these groups, whose heterozygosity, as measured by single nucleotide polymorphisms (SNPs) was very similar (58–60%). There was significant heritable variation among foreign cultivar and breeding clones for host plant resistance to late blight, tuber starch percentage (as measured by specific gravity), reducing sugars in tuber flesh, total tuber weight, which indicates the potential for further improving these traits for Scandinavia through recombination and selection in segregating offspring. Single-site analyses of genome-based prediction accuracy comparing the different structures of marker matrices and methods indicated that the highest were for tuber starch percentage and total tuber weight. Including the G x E interaction in the multi-environment analyses increased prediction accuracy estimates. Data from offspring at later stages of selection cannot be utilised to make selections based on genomic estimated breeding values (GEBV) in early clonal generations. The most promising approach for selection using GEBVs was when making predictions within full-sib families. Bioinformatics research provided means for reducing the SNP number used in GEBV for selection, thereby lowering genotyping costs without losing valuable information. We are investigating deep learning for GEBV, exploring the use of drone imagery for high throughput phenotyping and predicting tuber yield, and researching if cultivar releases over time affect the related microbiota and its extended microbiome phenotype.

9.04. GWAS analysis to identify loci involved in the release of bud dormancy using a panel of diploid potato clones

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GWAS, dormancy period, phenotyping

Dormancy period and sprouting have crucial impacts on quality loss during storage and fast canopy development after planting. Therefore, knowledge on loci regulating dormancy and sprouting represents a high economic importance. After harvesting, potato tubers stay dormant for a certain period of time, even under favorable conditions. Pre- and post-harvest environment, endogenous hormones, and carbohydrate metabolism are known to modulate the release of bud dormancy and subsequent development of sprouts. Unfortunately, the key genetic factors regulating the breakage of dormancy are still unknown. In this project, we developed a time-lapse system to monitor the breakage of dormancy and sprout growth. Ten HD cameras were programmed to take pictures every 12 hours. The dormancy period of a diploid GWAS panel, comprising 139 genotypes, was assessed. Dormancy period varied from 5 to 110 days at 18 degrees in the dark. All individuals were genotyped by PotatoMASH (Potato Multi-Allele Scanning Haplotypes), which is a recently developed genotyping protocol using PCR amplicon resequencing at Teagasc, Ireland. GWASpoly was used to perform GWAS analysis. A locus on chromosome 1 was identified for dormancy period and loci on chromosome 1, 3, 9 are involved in development of sprouts. The expression level of candidate genes in these regions will be quantified by qPCR in the future.

9.05. Screening for phosphorus efficiency in potato genetic resources

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Solanum tuberosum, nutrient efficiency, phosphorus, greenhouse screening,

Potatoes (*Solanum tuberosum* L.) require an optimal amount of phosphorus (P) for their growth, tuber production and starch quality. As the crop has a small and shallow root system, which makes it harder to acquire nutrients from the deeper level of soils, excessive amounts of inorganic P fertiliser are often applied, causing economic and environmental concerns. Our study aims to explore the natural variation among potato genotypes for higher phosphorus uptake efficiency. We screened a set of 179 cultivated and four wild potato accessions of the Gross Luesewitz Potato Collections (GLKS), along with 17 modern starch potato cultivars in response to P stress in a pot experiment. In vitro plantlets were cultivated in sand hydroculture. Two phosphorus treatments (high and low P) were applied to the plants as KH2PO4 in the nutrient solution in amounts of 15 mg l-1 (high P) and 3 mg l-1 (low P), respectively. After four weeks, shoots, roots and tubers, if produced, were harvested and dried (60°C) and the dry matter was determined. P concentration was measured by ICP method (ICP OES Optima 8300, Perkin Elmar). Results from the pot experiment showed a reduction of shoot biomass by an average 67.1 % under low P conditions, while root biomass was only reduced by, on average, 39.8 %. P uptake varied between 0.71 and 5.76 mg pot-1 under high P treatment and between 0.18 and 1.33 mg pot-1 under low P. The extent of reduction in shoot and root dry weight was genotype dependent. However, the majority of the genotypes showed an increase in the root: shoot ratio under low P conditions. Furthermore, roots exhibited an extensive variation in architecture and development. After initial screening, we were able to identify outstanding genotypes such as variety 'Kristall' (GLKS 11578) with a shallow but very dense root system or 'Tiger' (GLKS 10591) with a long and extensive root system, along with varieties GLKS 24106 (wild type), 'Amanda' (GLKS 11242) and 'Fransen' (GLKS 10873) which showed highest shoot biomass under both optimal and reduced P supply. 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 P efficient potatoes. In order to study the genetic diversity among the genotypes, DNA from in vitro plantlets was isolated, sequenced and SNPs were detected. Currently, a genome-wide association study (GWAS) is under progress to identify marker-trait associations for traits related to P efficiency.

9.06. Enhancing productivity and profitability of cereal based system of Indo-Gangetic Plains by planting short duration potato as a sandwich crop

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International Potato Center

Cereal based cropping system, Tuber yield, Short duration, PVS, Stakeholders

Six elite potato clones imported from International Potato Center (CIP) were evaluated to identify locally adapted candidate varieties for cereal based cropping system. Participatory Variety Selection (PVS) was adopted to select varieties of stakeholder's choice. Recommended varieties by Central Potato Research Institute, India were planted for comparison. Field testing was conducted at Potato Technology Center, Karnal, Haryana, India in 2018-19 and 2019-20 winter crop seasons.

The experiment was conducted in Randomized Block Design with three replications. Crop was de-haulmed at 75 days after planting. PVS was conducted at vegetative and harvesting stages to select candidate varieties of stakeholder's choice. Organoleptic test was carried out for sensory evaluation.

Data at vegetative and harvesting stages on growth, tuber yield and tuber characteristics were recorded and analyzed statistically. Variety Kufri Lima ranked 1st in vegetative growth. However, based on yield, taste, and appearance a bright red skin clone CIP304351.109 was most preferred by stakeholders. The clone also secured highest in marketable and total tuber yield among clones and control varieties. Clone was introduced for multilocation testing under different agro-ecologies for final testing and to be released as variety.

10. Late blight

10.01. Interactions between potato defense responses and *Phytophthora infestans* effectors depend on the genotype and condition the effectiveness of induced defense on symptoms development

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potato late blight, Solanum tuberosum, PAMP-triggered immunity, quantitative resistance, plant-microbe interactions

The management of *Phytophthora infestans*, causal agent of potato late blight, involves the use of about 15 fungicide treatments per cropping season. The combination of both induced resistance and quantitative resistance could be an alternative or a complementary strategy to decrease the use of pesticides. However, this method requires a better understanding of the interactions between *Solanum tuberosum* physiological responses and *P. infestans* ecology. Indeed, pathogen recognition by plants leads to the induction of defense responses via the PAMP-triggered immunity, but pathogens can modulate it via the secretion of effectors. In this context, we assumed that in potato, defenses triggered before infection, by a pathogen-associated molecular pattern (PAMP) of *P. infestans*, could alter both disease symptoms and the expression of effector genes depending on the genotype. In order to test this hypothesis, we simultaneously assessed in three potato genotypes, pre-treated or not with a concentrated culture filtrate of *P. infestans* (CCF), the expression of potato defense genes and of *P. infestans* effector genes involved in counter-defense, by qRT-PCR. The effectiveness of the induction was assessed by the measurement of disease symptoms. CCF pre-treatment induced most defense genes in Désirée and Bintje but repressed most defense genes in Rosafolia. On the contrary, effector genes were more expressed in Rosafolia than in Désirée and Bintje after CCF pre-treatment. Interestingly, induced defense responses by CCF significantly reduced lesion areas at 3 dpi only in Désirée. Together, these results show that the differential interplay between host response to elicitation and infection in the expression of defense genes on one side, and of pathogen effector genes on the other side, largely condition the effectiveness of induced defense on symptoms development. It also highlighted that a strain slowed down by a genotype and/or by a pre-treatment could adapt by secreting more effectors to counter induced defenses. These results open research prospects for combining induced resistance and quantitative resistance.

10.02. Targeted mining of potato germplasm collections for novel disease resistance genes

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RenSeq, Structure/Function, Effector diversity, Commonwealth Potato Collection, Novel resistances

Wild germplasm collections contain a wealth of functional disease resistance genes that, so far, remain largely poorly characterised. Using targeted genome enrichment sequencing technologies, RenSeq and dRenSeq, we have developed a pipeline to rapidly identify novel sources of resistance for prioritisation in genetic studies, as well as to identify natural variants of functional disease resistance genes.

DRenSeq analysis of 12 accessions of *Solanum bulbocastanum* has identified three novel resistances that are independent of all currently known disease resistance genes including Rpi-blb1 and Rpi-blb2. We have genetically mapped one novel resistance to potato linkage group 5. In addition, we observed naturally occurring diversity within functional Rpi-blb1-like genes that display enhanced recognition of the cognate *Phytophthora infestans* effectors IPIO1 and IPIO4. Remarkably, the only late blight susceptible accession of *S. bulbocastanum* contains a variant of Rpi-blb1 with four non-synonymous SNPs. A structure function analysis has identified the critical amino acids within Rpi-blb1 and restored full functionality.

Using this approach, we have identified further resistances effective against late blight in *S. jamesii* and *S. doddsii* as well as resistances effective against PCN. The RenSeq-derived reads are currently being utilised in k-mer-based associations studies for other important potato diseases.

10.03. Controlling late blight in susceptible and resistant potato cultivars

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Phytopthora infestans, Decision support systems, Host resistance, Solanum tuberosum, Fungicides

Fungicides are the main means of controlling late blight (*Phytophthora infestans*). For economic and environmental reasons, this excessive use of a fungicide is not sustainable, and reducing the use of fungicide in potatoes is essential. Using decision support systems (DSS) is critical to reducing fungicide usage, but it is also possible to reduce fungicide usage even further by combining the DSS with resistant cultivars. We adapted the BlightManager DSS for timing fungicide applications in susceptible (Folva) and resistant (Nofy) cultivars to control late blight. We conducted field experiments in 2020 with the adapted DSS. In both cultivars, late blight control was effective. However, more fungicide reductions were achieved in the resistant cultivar (60%) than in the susceptible cultivar (25%).

10.04. Update on AsiaBlight's efforts to create a coarse-scale map of the *Phytophthora infestans* population in Asia

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Phytophthora infestans, Potato late blight, AsiaBlight, pathogen population, mapping

Late blight (LB) is a major constraint to potato production in Asia. Co-ordination of studies of the *Phytophthora infestans* population and LB management is lacking. To overcome these problems, AsiaBlight, a pan-Asian late blight scientific network, was initiated in 2014-15 under the auspices of the International Potato Center. AsiaBlight initially focused on establishing a coarse-scale map of *P. infestans* genotypes across the region. FTA cards, which allow pathogen DNA to be collected directly from late blight lesions and render it non-viable, were distributed initially by the Inner Mongolia Potato E & T Center, Hohhot, China and more recently by the CIP–China Center for Asia-Pacific (CCCAP). Challenges highlighted by this project included: obtaining LB samples across a large, politically disparate region loss of contacts and consequently of FTA cards restrictions owing to national biosecurity legislation genotyping: lack of continuity, difficulty in standardising allele scoring The project, nonetheless, achieved voluntary collection of LB samples and their SSR genotyping through participation of contacts across the region, recognition of AsiaBlight, and highlighted the benefits of public-private partnerships. The aggressive genotype 13_A2 (Blue 13), known to be present in China and India was shown to be widespread across continental Asia including in Georgia, Nepal, Bangladesh, Pakistan and Vietnam. In contrast, 13_A2 was not detected in the *P. infestans* populations of sampled islands of Asia; in each case distinct and disparate populations were found. In 2018, CCCAP took on the challenge of developing a self-sustaining AsiaBlight from the initial, largely voluntary, network. An international conference in Beijing in October 2019 was attended by 115 delegates from 13 Asian countries and invited international delegates. For 2021-23, coordinating and scientific committees and 13 regional representatives oversee activities. Opportunities to apply the EuroBlight model, where private companies contribute to the network, are being developed within AsiaBlight. Acknowledgements: This research was undertaken as part of, and funded by, the CGIAR Research Program on Roots, Tubers & Bananas and supported by CGIAR Trust Fund contributors. Bayer Regions APAC 1 and APAC 2 funded FTA cards and the Scottish Government supported genotyping and analysis of FTA card samples. We acknowledge the financial support of the Chinese government CGIAR Fund for CIP's activities in China and thank many colleagues in EuroBlight and AsiaBlight for participating in this work.

10.05. The potato phyllosphere microbiome versus late blight: from infection to disease management

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late blight, microbiome, phyllopshere, copper, biocontrol

From the roots to the shoots, plants are naturally colonized by diverse communities of microorganisms. Some of these microorganisms contribute to plant health by stimulating plant defenses or by directly warding off plant pathogens. In the model plant *Arabidopsis thaliana*, it was demonstrated that the plant itself, upon pathogen attack, can select for protective microorganisms. Late blight control is based on foliar treatments with synthetic or copper-based fungicides. Both infection and disease management are likely to impact the natural potato phyllosphere microbiome, and thus interfere with its natural function. Our interest in the potato microbiome is twofold, (i) understand how late blight management and infection affect the natural microbiome and (ii) find out whether the plant can guide us towards choosing the most promising biocontrol agents. As a first step, we characterized the potato phyllosphere microbiome of two potato cultivars, Agria and Nicola. We monitored the evolution of the bacterial phyllosphere population over time and assessed the effects of repeated treatments with copper and with a bacterial antagonist, as well as the effect of late blight infection. We observed that while treating the plants with a bacterial antagonist had only limited effects on the communities, the copper treatments slightly reduced species richness and lead to a shift in the community structure in both cultivars. Infection with *P. infestans* drastically lowered the diversity and strongly impacted the structure of the bacterial community, favoring bacteria belonging to the genus *Pseudomonas* at the expense of *Sphingomonas* species, commonly found in the phyllosphere. In a second step, we explored the putative ability of potato plants to select for protective bacteria. Two generations of potato plants of susceptible cultivar Bintje and tolerant cultivar Innovator were exposed to *P. infestans*. Microbiome analysis revealed that several strains, belonging to different genera, were enriched in the exposed potato plants. After isolation, the enriched strains were selected for in planta and whole plant assays to identify the most promising candidates for a field trial. Altogether, our data provides a first insight in the changes induced by plant protection products and infection with *P. infestans* in the potato phyllosphere microbiome. Moreover, the combination of microbiome analysis and in planta based selection criteria could potentially allow to identify the strains that are most likely to thrive and express their antagonistic potential on field-grown potato plants.

10.06. Combining the control measures for a significant reduction of treatment frequency index (TFI) for the integrated control of potato late blight

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late blight, integrated pest management, decision support system (DSS), cultivar resistance, fungicide input

Phytosanitary protection of field crops is mainly based on the use of phytopharmaceuticals, but the context is getting tougher, to the point of questioning this path: restrictions on use or bans, Ecophyto II+ plan reaffirming the objective of reducing uses by 50%, implementation of additional precautions regarding the exposure of bees, workers, neighbours. Potato crop in France is highly dependent of fungicide to control late blight. This project proposed to test IPM strategies to reduce significantly TFI while maintaining an acceptable crop protection. Four technics were combined to form consistent protection programs:
-Fungicide treatments were monitored by the DSS (Decision Support System) Mileos, with trigger thresholds based on cultivar resistance and climate conditions
-Cultivar resistance, using the susceptible cultivar Bintje, and the intermediate resistant cultivar Magnum
-Potassium phosphite (does not count for TFI), with 3 treatments at maximum
-Chemical fungicides with doses adjusted to the cultivar and DSS forecast Integrated potato late blight management can be implemented by combining all available control measures
Trials have been set up with the objective of optimizing this combination by testing consistent technical operations from 2018 to 2020. Theses years showed up not to be very favourable for late blight, consequently some trials have been artificially contaminated and misted to ensure the disease development. Protection programs have been compared one another on their efficacy and on their potential to reduce IFT relative to the reference.
Trials highlighted:
The TFI saving brought by using DSS Mileos® is estimated at -30 to 35% of reference TFI.
The TFI saving provided by average varietal resistance is estimated at -30% of the reference TFI and up to -50% for varieties that are not very susceptible.
Biocontrol (potassium phosphite) enabled a TFI saving of 10% of the reference TFI.
The best protection program offered a reduction of TFI by -80%, combining all four strategies with an intermediate resistant cultivar.
The cultivar resistance to late blight can be enhanced by treatment timing fixed by DSS and with doses adjusted to the cultivar resistance. Combine a resistant or intermediate resistant cultivar with a fungicide protection program enables not to rely only on resistance genes, preserving their efficacy. The combination of all integrated protection measures makes possible to reduce very significantly TFI without taking any additional risk on the protection of the fields, especially in years with low disease pressure.

11. Climate change (drought & heat resistance)

11.01. Physiological, biochemical responses and yield components reveal genetic architecture of tolerance to water deficit in diploid potato

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Drought Stress Index-potato, yield component–water deficit; sugar accumulation–water-deficit

Climate change is a serious threat to the basic foods of the family basket worldwide. In this scenery water deficit is the major constraint in some potato-growing areas of the world and its effect is most severe at the tuberization stage, resulting in lower yield. Therefore, the dissection of the genetic architecture of water deficit responses is highly desirable for developing water-deficit tolerant potato cultivars and enhancing the resilience of existing cultivars. Phenotypic variations in response to a water deficit were studied in an association panel, the Working Collection of Potato Breeding Program at the Universidad Nacional de Colombia, constituted by 104 diploid accessions which were evaluated under both well-watered and water deficit treatments at tuber initiation stage. The response to water deficit conditions was assessed with the relative chlorophyll content, maximum quantum efficiency of PSII (Fv/Fm), relative water content, leaf sugar content, tuber number per plant and tuber fresh weight per plant. Drought Stress Index was calculated to assess tolerance of the diploid potato genotypes to water deficit. The soluble sugar contents increased significantly under water deficit conditions in the leaves, with a weak correlation with yield under both water treatments. The Principal Component Analysis results revealed that the physiological, biochemical, and yield-component variables had broad variation, while the yield-component variables more powerfully distinguished between the tolerant and susceptible genotypes than the physiological and biochemical variables. We identified the QTL governing this trait via a genome-wide association study (GWAS). The GWAS was conducted using a matrix of 47 K single nucleotide polymorphisms. We are reporting 38 QTL, seven for well-watered conditions, 22 for water deficit conditions and nine for DTI which explain between 12.6% and 44.1% of the phenotypic variance. A set of six QTL were found to be associated with more than one variable. Marker WDP-9.21 was found associated with tuber fresh weigh under water deficit and gene annotation analysis revealed co-localization with the *Glucan/water dikinase* gene. Of the nine QTL detected from Drought Stress Index on chromosomes 2, 3, 5, 8,10 and 12, three candidate genes with a feasible role in water deficit response were identified. The results of this study contribute to the understanding of the genetic architecture of potato tolerance to water deficit for its subsequent use in plant breeding programs.

11.02. The effect of drought and heat stress on potato root system

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drought, heat, root system, potato variety, proteome

The root system plays a major role in drought tolerance. The breeding of heat and drought tolerant potato cultivars is one of the most feasible and practical approaches to cope with global warming. Potato varieties were tested in several different experiments aimed at determining the size and architecture of the root system under of drought and heat stress. In the research on the potato root system, we also assessed the root/sprout ratio in the initial phase of plant growth. Potato genotypes cultivated in drought and high temperature conditions, in the initial period of development, i.e in the stage of sprout and root formation, produced a greater root mass in relation to the mass of sprouts than the same genotypes cultivated under optimal conditions. The differentiated response of potato genotypes was confirmed, and on its basis, genotypes with higher tolerance to drought stress and high temperature were selected. The differentiation of the root system in different layers of the soil profile was also investigated. Significant differences were observed among cultivars in the size of the root system and its architecture. The biggest differences in the individual layers of soil profile related to the diameter of the root, the root length, and the surface area. Also, a relationship between the size of the root system and yield of tubers was found. The strongest correlations involved the root length and the root surface area with the decrease in tuber yield under the drought, then the dry root mass with the decrease in yield. The decrease of root dry mass was smaller in the more drought-tolerant cultivars. In response to drought, the more drought-tolerant cultivars developed elongated roots, but the roots of the less-tolerant cultivars remained the same length. The decrease in root diameter was also smaller in the more drought-tolerant cultivars. Moreover, comparative proteomic analysis of drought and high temperature response in roots of two potato cultivars were done. LC-MS/MS protein identification showed that in roots of the sensitive cultivar, in response to drought, most changes concern increased abundance of defence- and detoxification-related proteins, while in tolerant plants, significant changes in abundance of energy and carbohydrate metabolism related proteins were observed. In response to high temperatures, in the sensitive cultivar, decreased abundance of proteins involved in cell energetic metabolism was detected, while in the tolerant cultivar, the majority of proteins from this group was abundant.

11.03. Assessing evapotranspiration and the crop coefficient of potato in a semi-arid climate using the Eddy Covariance techniques

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water use efficiency, irrigation, energy balance, South Africa, Penman-Monteith equations

A correct estimation of crop coefficients K_C is essential to assess water requirements of crops from weather variables and thereby optimize irrigation management. K_C depends on crop type and varies with crop growth stage, and to a limited extent, with climate. K_C values are often assumed to be transferable between locations and climates. K_C values have not been determined yet for modern potato cultivars grown under South African, semi- arid climatic conditions. The objectives of this study were (i) to quantify evapotranspiration and water use ef- ficiency (WUE) of potato crops in a semi-arid climate under irrigation, (ii) to estimate K_C values for these crops at different growth stages, and (iii) to assess the usefulness of the Penman-Monteith equation to estimate evapo- transpiration and irrigation requirements. An eddy covariance (ECV) system was used in potato fields planted with the variety Mondial in two production regions of South Africa: Limpopo (crop growing in winter) and North West (spring-summer crop). Additional sensors were added to the system to measure relative humidity, near surface soil temperature, solar radiation, rainfall and irrigation. Capacitance sensors installed at varying soil depths were used to measure the change in soil moisture content of the potato rooted zone. Accuracy of the ECV measurements was evaluated by following the energy balance closure method. Seasonal mean crop evapotranspiration (ET_C) was 3.2 mm d^{-1} for the crop in Limpopo and 5.7 mm d^{-1} in North West. The reference evapotranspiration (ET_O) correlated well with the daily patterns in ET_C for most of the season. ET_O thus serves as a useful indicator of ET_C and can be used for irrigation scheduling of potato. Seasonal mean KC value was 0.99 for the crop in Limpopo and 0.78 in North West. While the KC value in Limpopo likely represented that for a crop free of water-stress, the crop growth in North West was likely somewhat limited by water availability. The winter crop had the highest WUE of 3.55 kg dry potato tuber m^{-3} of water evapotranspired, whilst WUE for the spring- summer crop was 3.03 kg m^{-3}. This difference could be explained by differences in mean vapour pressure deficit between the growing seasons. To optimize WUE of potato growing in semi-arid, water scarce regions such as South Africa, it is advisable to grow crops in the coolest available growing season, outside the frost-prone period.

11.04. Impact of drought and high temperature on the expression of selected housekeeping genes in potato leaves

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Drought and high temperatures significantly affect gene expression in plants. However, even with slightly different genotypes, plants may differ in response to stress. Potato cultivars constitute an excellent model to investigate such differences due to their clonal nature. Therefore, we have selected two potato cultivars sharing one among their ancestors but strongly differing in response to the drought. The pair consisted of cv. Gwiazda, which is drought-tolerant and cv. Oberon - very sensitive to water deficiency. In these cultivars, we have measured the level of expression of ten housekeeping genes and one drought-induced stRAB18. The expression level of the housekeeping genes varied, with elongation factor 1α being the most stable and cullin 3A induced by stress conditions to a level similar to RAB18. Variability in cullin 3A expression may indicate differences in protein ubiquitylation between control and stressed plants. RAB genes in both animals and plants encode a family of GTPases that influence various aspects of membrane transport, with consequent effects on many functions and cellular responses. Here, we have found that drought induced the expression of the RAB18 gene to a greater extent than high temperature. Moreover, the expression level of this gene was generally higher in cv. Oberon, but its peak occurred significantly later than in cv. Gwiazda. This finding fits well with the model where the tolerant cultivar responds faster to the stress than the susceptible one.

Acknowledgment

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11.05. Identification of potato varieties with contrasted susceptibility to drought

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S. tuberosum, variety trial, drought stress, agronomic resistant trait, climate change, phenotyping

Swiss potato industry is facing new challenges due to climate change. Switzerland is regularly affected by drought events during the potato growing season, which affect the harvest on several aspects: e.g. yield reduction, imbalances in starch content, misshaping of tubers, physiological regrowth, and accumulation of reducing sugars in tubers. It is therefore recommended to better characterise the susceptibility to water shortage of the varieties that will be cultivated in Switzerland. Since there are few reference varieties in terms of resistance and/or susceptibility to drought, a screening was carried out through field and greenhouse trials.

A field trial with two irrigation conditions (optimal irrigation and reduced irrigation) and 28 varieties has been implemented in 2020 by Agroscope (Changins, Switzerland). For each variety, two replications of 50 plants were planted and a deficit of 150mm of water was induced throughout the season in the plots with reduced irrigation. A greenhouse trial was set up with 4 replicates, 2 irrigation conditions, and 2 plants per condition, to validate the results of the field trial with the 4 varieties the most resistant and susceptible to water shortage. To simulate a drought period, three cycles of ten days of water shortage were implemented.

Yield loss due to water shortage ranged from 29% for cv. Sound to 51% for cv. Lady Claire in the field trial. The four varieties presenting the lowest yield loss were the following: Sound, Cardyma, Enduro and Agria, while the ones with the highest yield loss were: Jule, Simonetta, Bellanita and Lady Claire. These eight varieties were tested in the greenhouse trial. Two varieties considered as susceptible, cv. Sorentina, and resistant, cv. Kennebec, to drought were also added to the experimental design. In the greenhouse trial, yield reduction from 39% for cv. Cardyma to 68% for cv. Sorentina were observed, in regard to well-watered conditions.

Based on their yield reduction and precocity, four varieties (Agria, Jule, Lady Claire and Kennebec) were selected to monitor morphological and physiological responses to water shortage, in order to find agronomic resistance traits to drought stress. Those results are discussed in regard to yield reduction and quality defects.

Acknowledgment: This work is financed by the Swiss Federal Office of Agriculture.

12. Post harvest & storage technology

12.01.How has the long term storage of potatoes been transformed from relying on CIPC to alternative means of sprout control? Challenges and successes.

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Biox-M, spearmint oil, sprout control, long term potato storage, maleic hydrazide

In Europe, since autumn 2020, the use of chlorpropham is no longer allowed for use in potato storage, since it did not pass the EU renewal criteria. Chlorpropham (CIPC) based products were relatively cheap and easy to use. Therefore, prior to 2020, there was only limited interest to gain experience in commercial practice with the more costly alternative sprout suppressants. This posed huge challenges for the conversion needed to use alternative means of control in storage season 2020 - 2021. Due to adverse harvesting conditions, the storage season turned out to be even more difficult than usual in most of NW Europe. This presentation will deal with the use of maleic hydrazide, spearmint oil, orange oil, 1,4-dimethylnaphthalene and ethylene as replacements for the long term trusted use of chlorpropham for sprout control. Both commercial experiences and results obtained under controlled trial conditions will be shared.

12.02. A European collective and continuous initiative for accompanying CIPC residue monitoring through the Potato Value Chain

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Chlorpropham, Cleaning, Monitoring, Potato Value Chain, Temporary Maximum Residue Level

Introduction: Following the conclusions of the European Food Safety Authority (EFSA) published in June 2017, the Commission Regulation (EU) 2019/989 implemented the non-renewal of Chlorpropham (CIPC) in June 2019 with a prohibition of the active substance at the latest in October 2020. This regulation has had a major impact on the potato sector; not only because of the loss of a key potato sprout suppressant, but also because of the risk of unintended cross-contamination from storages with a history of CIPC use. With its commitment to consumer safety, the Potato Value Chain (PVC*) has pro-actively led European-wide efforts to manage the transition to a CIPC-free way of storing potatoes.

PVC actions and CIPC status evolution: The PVC initiative on CIPC started in 2019 with a first set of European residue data from stores with a CIPC history, already switched to alternative solutions. Provided to EFSA and European Commission (EC), these objective values helped to gain recognition of the need to adopt a temporary Maximum Residue Level (tMRL) and to set it at a level suitable for storage facilities. The adopted tMRL of 0,40 mg/kg sounded as a concretisation of this work. In parallel, the PVC engaged a large consultation on technical ways to clean appropriately the stores and equipment. This action was concluded by a wide multilingual information campaign on cleaning guidelines for all operators with the goal to clean the stores as soon as the 2019 crop had been unloaded. Continuing its action, the PVC prepared a monitoring plan for the storage season 2020-2021 which was carried out already prior to the entry into force ‎of the tMRL. Across Europe, a large number of actors in the value chain were mobilized to take part in the cleaning actions and the data collection. The 2020-2021 monitoring delivered a representative dataset of over 2000 residue samples across seven countries, including the UK. The statistical analysis showed that 61.85% of the values were below Limit of Quantification (LOQ) with a 97.5th percentile at 0,37 mg/kg. However, a small percentage of samples (2.25%) detected residues with values higher than the tMRL. This objective and representative investigation was renewed this campaign to pursue helping the EC in fixing the evolution of the tMRL over the years.

** The PVC is an informal organisation that brings together European organisations ranging from production (Copa-Cogeca) to marketing for the fresh sector (Europatat), to industrial processing for human consumption (ESA, EUPPA) and for starch production (Starch Europe).*

12.03. Using metabolomics to guide sprouting suppression

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Sprouting suppressants, Biochemistry, Metabolomics, Meristems, Storage

With tighter regulations and outright bans on CIPC, the potato storage industry has been left without its most effective sprouting suppressant. One of the challenges in novel suppressant discovery is a lack of understanding of the basic process of sprouting: what is happening at the biochemical level in the bud? A better insight into this process would aid the rationale for development of targeted inhibitors. This project uses an analytical biochemistry approach, metabolomics, to characterise potential metabolic targets for suppression of sprouting. This has allowed us to identify lead enzyme inhibitors for sprouting suppression. Using an in-vitro sprouting assay, dissected buds were sampled at different stages of early sprout development and the chemical composition (metabolome) analysed using mass spectrometry. An analysis of these metabolomes suggests that during sprouting a core metabolic pathway (TCA cycle) is acting in a specific configuration that favours anabolic processes rather than efficient respiration. Using a computational model of metabolism, a transamination pathway connected to the TCA cycle was identified as being of potential importance in the rapid growth of sprouting buds. Chemical inhibition of this pathway led to complete cessation of bud growth in-vitro. This result validates our methods, opening a new pathway to a more rationale based approach to identifying new sprouting suppressants.

12.04. The effect of Genotype by Environment by Management interaction (GxExM) on sprouting and glucose content in potato tubers during storage.

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Potato, Sprouting, Genotype, Environment, Glucose

Sprouting control in potatoes during storage can be improved by better characterization of genotype by environment by management interactions (GxExM). To evaluate the effect of GxExM on sprouting and sugar content in potato tubers during storage, field trials were conducted across two growing seasons (2017 and 2018) at six experimental sites in Switzerland. Sites varied in altitude; Stammheim (CH-8476, elevation of 430 m asl), Goumoëns (CP-1376, elevation of 609 m asl), Changins (CH-1260, elevation of 420 m asl), La Frêtaz (CH-1453, elevation of 1200 m asl), Maran (CH-7050, elevation of 1862 m asl), and Reckenholz (CH-8046, elevation of 440 m asl). Six potato varieties were grown at each site and stored for 4.5 months in two distinct storage chambers; one at 4°C and another at 8°C. Varieties included Lady-Claire, Verdi, Kiebitz, Pirol, Agria, and Markies. After 4.5 months of storage, a sprouting assessment was performed by weighing all the sprouts of five tubers (2018-2019 storage season). Each experimental site, variety, and temperature had four replicates. Sprouting observation data were transformed using "log (x+1)" and analyzed with a three-way ANOVA that included variety, site, and temperature as fixed effects. An F test was used as the test of significance and the effect of significant variables was analyzed using a multiple comparison test (marginal post hoc Tukey's test, emmeans R package) to identify mean differences within factors and interactions. A significant effect was observed for the following factors: variety, site, and temperature as well as the three-way interaction ($p<0.001$, ANOVA). Greater sprouting was observed in tubers stored at 8°C (average of 6.52 g ±0.52 SE) compared to 4°C (average of 0.47 g ±0.06 SE). The greatest sprouting was observed at Reckenholz (6.88 g on average ±1.26 SE), while the lowest sprouting was observed at Maran (0.83 g on average ±0.19 SE). After 4.5 months of storage, glucose content of fresh tubers was analyzed using a glucose titer measurement device (Accu-Check® Active glucometer, Roche). Three tubers were tested for each combination of site, variety, and temperature. Greater glucose content was observed in tubers stored at 4 °C compared to 8 °C, and differences in glucose content among varieties and sites were also observed. The results presented here underline the importance of considering GxExM interactions with the goal of improving potato storage.

12.05. The use of ethylene for the processing market

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Arvalis

Ethylene, Processing, French fries, Frying colouration, Sprout control

Background: Ethylene is a hormone used as a growth regulator of sprouts during the storage period.
It is historically recommended in France only for salad potatoes sold on the fresh market because of some uncertainties concerning the possible colouration after frying for processed products. Ethylene can indeed have an impact on the colour of fried products. It seemed important to better estimate the influence of this molecule on the different varieties used for the processing market. Methodology: Trials were conducted for three years, from 2018 to 2020, to evaluate the possibility of using ethylene as a sprouting inhibitor on industrial varieties with the collaboration of the Restrain company. Different concentrations of ethylene were used in these trials. These concentrations are expressed according to the indication given on the ethylene generator, in percentage of the registered product. Rates varied from 4% to 20% Restrain. The level of sprouting and after frying colouration was observed and compared to a reference treatment during long term storage at 7°C. The colour evaluation was done every month until July on twenty tubers according to USDA scale for French fries. Results and conclusion: The observations made over the trials showed different comportments according to varieties for sprouting control or after frying colouration. A control seems currently suitable for the Markies and Fontane varieties on both parameters. Indeed, the evaluation over three years at different rates of ethylene, allows to confirm the possible use of the product for these two varieties with a limited risk of excessive increase of colouration after frying. Although colouration tends to increase after long term storage due to ethylene treatment compared to a reference treated with mint oil.
A reconditioning can have a very beneficial action in this situation to reduce the colour at the reference level. Reconditioning consists in reheating the tubers between 15 and 20°C for two weeks. Regarding sprouting control, the choice of ethylene concentration can be made according to the variety.
Indeed, it seems possible to reduce the dose of ethylene applied for varieties with a long dormancy period. For a variety with a faster sprouting, it is however wise to keep a high concentration of ethylene.

12.06. Industrial storage of potatoes for frittered products: temperatures, humidity and air-distribution, and formation of Acrylamide

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potato, industrial post-harvest, temperature, weight loss, acrylamide

It is known that acrylamide may be formed during frittering of potatoes if the post-harvest storage temperatures are too low. The amount of acrylamide depends on the content of sugar and asparagine, and where the amount of reducing sugars depends on storage temperatures.

In the project PotetFrit, financed by producers, industry partners and the Norwegian Research Council (NRC), 29 industrial potato storages were studied over three seasons. Potatoes (Lady Clair) from one field were stored at the different storages, with various storage capacities, air distribution systems, storage temperatures and -humidity.

Four 10 kg nets with Lady Clair were dug down in the wooden bins together with the producer's own potato each at the 29 storages. Air- and product temperatures in addition to relative humidity were measured during the storage periods. The storage periods variated from 12 to 36 weeks, before the potatoes were delivered to the three frittering industrial partners. The amount of acrylamide and the weight-loss were measured at delivery.

The results show a distinct correlation between the storage temperature and the formation of acrylamide. For Lady Clair, amount of acrylamide increases dramatically after storage at temperatures below 6°C. Storage temperature will also influence on fouling and respiration. Higher storage temperatures increase the respiration resulting in higher weight loss during storage.

The 29 producers use several different air-distribution systems, but the two most common systems are AgroVent (high air velocity and volume) and Findus (low air velocity and volume). Both systems have positive and negative aspects, which will be discussed.

12.07. Minimizing storage losses by optimalization of the air humidity during different storage phases

Frank van der Linden, Nik Grubben

Storage losses, humidification, relative humidity, pressure bruises, wound healing

One of the main goals of storing potatoes is to preserve product quality during the storage period, and to provide high quality potatoes all year round. The product quality during storage of potatoes should be remained stable for that reason. However, as the storage technology to store agro products become more advanced, storage losses like rot, pressure bruising, and shrink are common quality issues.

To minimize storage losses more attention should be given to the air humidity during the different storage phases (wound healing, drying, cooling and long-term storage). Both the temperature and the air humidity has influence on wound healing, rot, pressure bruising and shrink during storage.
In a conventional potato storage the temperature is monitored and controlled, but in most cases the air humidity is not monitored, and a humidification system is not installed. Therefore, no efficient control of the air humidity can be guaranteed.

Optimization of monitoring and control of the air humidity can contribute to minimize rot, pressure bruising and shrink. The optimization steps are investigated by small- and large-scale experiments. From these experiments, good recommendations can be made for proper sensing and controlling of air humidity during the different storing phases and their effect on product quality.

13. Engineering, DSS & precision agriculture

13.01 In-field assessment of resource use efficiencies for more sustainable potato production on sandy soils

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drainage lysimeter, nutrient leaching, water use efficiency, nutrient use efficiency, yield gap

Resource use efficiencies (RUEs) can serve as indicators of sustainability in crop production. A survey has suggested that RUEs differ substantially between potato growers in South Africa. Assessment of RUEs can help explain variation and optimise practices to improve efficiency. Potato is often grown on sandy soils with low nutrient and water holding capacities, making irrigation and fertiliser management challenging. The aim of this study was to quantify water and nutrient inputs and losses to better understand RUE differences and propose management practices to improve efficiency. Studies were conducted for 15 commercial centre-pivot irrigated potato fields in two regions. Irrigation and rain were measured using flow meters and local weather stations. Water loss through drainage was quantified using drainage lysimeters and leachate was analysed for nutrients. Tuber yields were measured and compared with simulated potential yields. Soil-water balance components, water-use efficiencies (WUE) and nutrient-use efficiencies (NUE) were calculated. Tuber yields for autumn to winter plantings (Mediterranean region) were relatively low (34.7 - 49.8 t ha^{-1}) due to less available solar radiation, while crops grown in summer (both regions) had higher yields (51.2 - 118.2 t ha^{-1}), with small yield gaps. Drainage often followed directly after rainfall events in winter, while in summer drainage mostly occurred when irrigation exceeded crop requirements. Fields with higher clay content or a limiting layer in the soil profile (e.g. clay or hard calcic layer) were less susceptible to drainage. However, these fields had a higher risk of water-logging during periods of high rainfall, which resulted in tuber rotting and lower yields. Water-use efficiencies ranged from 65 to 122 kg ha^{-1} mm^{-1}. In some fields, considerable nutrient losses occurred together with drainage water. WUEs and NUEs varied widely between growers due to differences in water and nutrient levels applied, and yields achieved. Low water holding capacity of sandy soils complicates water and nutrient management, especially in the rainy season, as growers cannot leave room for rain in the soil profile and the risk for drainage is thus high. In summer, water and nutrient losses mostly occurred due to over irrigation. Management strategies should be investigated to limit unproductive input losses, including implementation of irrigation scheduling to match irrigation with crop water demand, evaluation of fertilising practices, and possible use of hydrogels to improve water holding capacity of the sandy soils.

13.02 Early detection of root-knot and potato cyst nematode infections in potatoes using hyperspectral imaging

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Root knot nematodes, Potato cyst nematodes, hyperspectral imaging, Solanum tuberosum, early detection

Root-knot (RKN; *Meloidogyne spp.*) and potato cyst nematodes (PCN; *Globodera spp.*) are considered the most aggressive and economically important groups of plant-parasitic nematodes and are a significant limiting factor for potato production. RKN alone are responsible for approximately 5% of global crop losses, and PCN cause significant damage to potato crops worldwide. Early (i.e. before the appearance of visible symptoms) and spatially accurate detection of RKN and PCN would therefore contribute greatly to effective management of these pests. Detection of these nematodes is currently based on soil sampling, nematode extraction and microscopic or molecular identification. This extensive procedure could be replaced by spatially accurate detection using hyperspectral imaging of plants in the field. We used hyperspectral imaging (recording wavelengths in the 400-2500 nm range, in 448 spectral bands) to detect RKN and PCN infections and their severity in above-ground parts of potato plants, prior to development of visible symptoms. Furthermore, we included drought stress, since visible symptoms, e.g. reduced plant growth, are similar to symptoms of nematode infections. By combining data dimensionality reduction methods and machine learning algorithms, we achieved identification success rates of more than 80%. Identification was successful regardless of infestation severity, nematode species, and presence of drought stress. In addition, because we identified relevant wavelengths for each classification, we were able to determine which groups of secondary metabolites changed their composition, due to infections and water stress. Our results show that accurate early detection of RKN and PCN infections in growing potato plants is possible using remote sensing methods. These methods could contribute to better and timely management of nematode infestations in potato production.

13.03 Crop sensing: Integrating high throughput approaches for quantitative assessment and stress monitoring in potato

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High throughput Phenotyping, UAV, Precision farming, Digital models, Spectral analysis

In order to support the decision-making in precision agriculture, rapid and cost-effective method to monitor crop performance over a large number of plots and field trials is needed. High throughput phenotyping especially in potato has been a major bottleneck especially when targeting morpho-physiological traits in phenotype-genotype association studies and traditional approaches having high-resource requirements and mostly qualitative in nature. To help alleviate many of these challenges, remote sensing techniques have been incorporated in agriculture over the last decade, and now allow the assessment of several key potato traits e.g. canopy growth, tuber shape, stress detection providing the needed quantitative data for QTL identification.

The work focusses on development and refinement of remote sensing based phenotyping methods for evaluating quantitative traits, and linking with precision management techniques for assessing physiological and architectural traits strongly linked to crop performance (particularly creation of 3D potato canopy models and stress assessments). Further, these phenomics based assessment approaches are combined with genomic tools to understand the genetic bases of developmental and quantitatively assessed stress related traits. The knowledge gained will help us facilitate data-driven decision making in potato breeding programmes and refine management techniques for potato production.

13.04 High-throughput phenotyping for crop monitoring in potato (*Solanum tuberosum* L.) using unmanned aerial vehicle

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Potato, HTPP, phenotyping, multispectral imaging, UAV

Precision in plant disease incidence, severity evaluation and its effect on yield and quality is key for improving crop production and plant phenotyping. Thus, it is important to have a timely and accurate assessment of disease incidence and its spread for forecasting and targeted application under field conditions. Traditionally, detection and quantification are mainly based on visual monitoring or using microscopic or molecular methods. These visual assessments lack accuracy and quantitative information while other methods are destructive if needed for temporal monitoring. In consideration of this, this study intends to evaluate the feasibility of low altitude remote sensing technologies as a field phenotyping tool for a potato-breeding program under the field condition over the growing season. The potato canopy image was acquired by an unmanned aerial vehicle (UAV) equipped with a multispectral camera. Canopy height, plant maturity and senescence in an association panel of 290 potato varieties was estimated using UAV-based multispectral imagery and related with the traditional method using hand-held tools and visual assessments. Comparison of the canopy dataset at different temporal points over the growing season showed that the image obtained from a multispectral camera had a high correlation with the traditional approach. The proposed methods were adequate for estimating potato canopy height, canopy area and vegetation indices in a rapid and non-destructive way, representing an alternative method to conventional phenotyping study. Prediction accuracy of estimating crop traits could be achieved using this system and could be used in a breeding program to accelerate the selection of cultivars.

14. Processing (old & new products)

14.01. Prediction of acrylamide formation in French fries with near-infrared spectroscopy (NIRS)

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Near-infrared spectroscopy, contaminants, processing, breeding, deep-fat frying

In Germany a share of 60% of potato consumption are processed potatoes such as fried products like French fries. While final-frying is mainly done in canteens or at home, industrial processing of par-fried French fries includes raw material inspection and quality control, blanching, par-frying and freezing. Acrylamide can be formed in French fries during final-frying depending on the precursor content, reducing sugars (glucose, fructose) and asparagine. Acrylamide formation is accompanied by browning of the French fries' crust. Breeding goals of potato cultivars for frying purposes include high starch and dry matter contents, good suitability for long term storage and low tendency to synthesize reducing sugars. Due to extensive sample number an exact laboratory analysis of acrylamide in French fries or its precursors in tubers is difficult to implement in the breeding process. Yet, good near-infrared spectroscopy (NIRS) predictions of dry matter and starch content have been established for potatoes. Being minor components of tubers and end products, exact predictions for reducing sugars and acrylamide are hardly reachable with NIRS. In the current investigation, applicability of NIRS as a screening tool in identifying potato genotypes with low potential for acrylamide formation in the breeding process was tested. A set of 185 genotypes from different breeding programs was grown in contrasting environments (Germany, Turkey) over two consecutive years. According to the colour of the French fries after frying most suitable samples for model development were selected resulting in a high variation within the target data set. The modified partial least squares (PLS) procedure was performed on the final dataset of 644 samples. After scatter correction and internal cross validation, data were divided into calibration and validation sample sets for calculating an external validation. We confirmed NIRS to be well suited for the prediction of major potato components. As expected, the predictability for minor components was worse. However, mathematical pre-treatments, such as application of first and second derivatives on original spectra were able to improve the model indices for reducing sugars and acrylamide. By applying the calculated NIRS calibration to the validation data set, up to 90 % of samples were correctly categorized as below or above the guideline value for acrylamide in French fries. Modelling of the large and diverse data set indicates the potential of the NIRS technique as a predictive tool in the breeding process for low acrylamide formation.

14.02. Market access and value chain analysis of potato in West Shoa Zone, Ethiopia

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Ambo University

Potato value chain, Potato marketing margin, Potato value addition, Smallholder potato farmers, Ethiopia

The major objective of this study is to assess market access and value chain of potato in West Shoa Zone, Ethiopia. A total of 362 potato farmers, 120 consumers, 40 potato traders, 30 potato processors (hotels/restaurants and chips makers) had been surveyed to generate the primary data used in the study through application of four Survey schedules and two checklists. The results show that farmers produced mean potato yield of 90 quintals per season, out of which 20% was used for home consumption, 80% was sold to market outlets and 15% was used for value addition. About 40.32%, 27.3%, 10.67%, 9.39% and 12.44% were accessed by wholesalers, collectors, retailers, processors and individual consumers' market outlets, respectively. The probit model results indicated that sex of household head, education of household head, family size, landholding size, access to market information, distance to the nearest urban market and potato yield per season played a significant role in the probability of potato sales decision. Gender of the household head positively and significantly influenced marketed supply of the households. In the study area, both male and female household heads were engaged in potato production and marketing. The data show that supply of potato to the market is higher for male-headed households by 23.1 quintals as compared to that of female-headed households, keeping other variables constant. Dissemination of modern input technologies and facilities, with equitable distribution and gender inclusiveness to ensure optimal access is essential in increasing the productivity of potato. The public sector must be involved in trading and marketing process, not only to control the market for tax collection, but also for the welfare of farmers in fair profit distribution. To address the existing gender gap in the potato value chain, providing access to market information, financial services, specialized programs and intensive training efforts, technical training on saving and credit schemes and agronomic practices through extension are steps to improve potato value chain.

15. Physiology

15.01. Sprouting as an expression of physiological ageing of seed tubers of modern potato cultivars

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Potato (*Solanum tuberosum* L.), Physiological age, Sprout growth, Maturity type, Ageing rate Physiological age is a crucial quality characteristic of potato seed tubers. It determines growth vigor, yield and quality of the crop grown from these seed tubers. Sprouting growth and development are expressions of the physiological age of seed tubers and indicators of the performance of the crop to be grown from them. We studied tuber sprouting in four contrasting modern cultivars, namely Agria (slow ager, late maturity), Festien (fast ager, late maturity), Innovator (fast ager, early maturity), and Lady Claire (slow ager, early maturity), and tubers were stored under different temperatures treatments. During the storage period, monthly sprouting tests were carried out. Tubers were de-sprouted and then placed in optimal (18°C, 85% RH, and darkness) conditions for sprouting. Before de-sprouting and after sprouting the number and weight of sprouts were assessed. The measurements were conducted during 3 consecutive storage seasons (2019-2022). In general, higher storage temperature advanced sprouting. Over a certain accumulated temperature, sprouting decreased in tubers of the fast ageing cultivars. Across the range of storage temperatures, the effect of storage temperature was more pronounced in the early-maturing cultivars, while the late-maturing cultivars reacted less strongly. We will further analyze the data and incorporate different types of thermal scales such as storage temperature sum to model sprouting behavior. The model will be designed to provide insights into the genotype-specific development of physiological age in response to storage temperature. Furthermore, it will be incorporated with models of metabolite profiles of tubers during storage and of field performance to improve decision support systems for storage and crop management.

15.02. The transcriptome of potato tuber phellogen reveals cellular functions and genes involved in skin formation and maturation (skin-set)

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Periderm, Phellem, Phellogen transcriptome, Potato skin, Suberin

Potato tubers are covered with a protective corky tissue called the periderm that is formed through cambial activity of phellogen cells. The outer layers of the potato periderm, the suberized tuber skin, serves as a model to study cork development. Phellogen activation results in skin formation; whereas phellogen inactivation is associated with the skin-set process (adherence of layers of skin to the tuber flesh). A transcriptome was prepared from tuber phellogen cells isolated by laser-capture microdissection. It indicated similarity of the phellogen meristematic activity to vascular cambium and cork from trees. Candidate genes for phellogen activity were selected based on their putative function and level of expression in the transcriptome, and their expression in defined developmental stages of the periderm. These analyses allowed the identification of genes with differential and high expression levels during phellogen initiation and the early stages of skin formation, as compared to genes with differential and high expression following cessation of phellogen activity and the induction of skin maturation and skin-set processes. Moreover, this unique differential expression was confirmed in the native periderm of two potato cultivars, Desirée and Rosanna, and in the wound-periderm model system. The characterization of potato phellogen may contribute to the management of costly agricultural problems related to incomplete skin-set and the resulting skinning injuries, and provide us with new knowledge regarding cork development *in planta*.

15.03. Involvement of glycoalkaloids and flavonoids in potato (*Solanum* sp.) phytotoxic interactions

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differentially expressed genes, flavonol synthase, glycoalkaloids, phytotoxic potential

Allelopathy is an important ecological phenomenon, a type of plant communication with the environment that shapes plant and microorganism communities in natural ecosystems and agroecosystems. Allelopathic interactions between potato (*Solanum tuberosum* L.) and other plants can be observed. Glycoalkaloids (steroidal alkaloids) are *Solanum* bioactive compounds involved in allelopathic interactions. Glycoalkaloids, especially those accumulated in leaves, are involved in host-plant resistance and in plant–plant and plant-microorganism interactions. To achieve a better understanding of the phytotoxic response between plants, it is essential to deeply examine the trait distribution in a segregating population. In the present paper, we used transcriptomic and metabolomic approaches to recognize the phytotoxic potential (PP) of potato plants originating from a diploid segregating F1 population with particular emphasis on glycoalkaloids in potato groups characterized by high glycoalkaloid contents. A population-level approach allowed for the influence of the genetic background on the expression of the quantitative trait to be minimized. We used a potato leaf extract of F1 individuals to obtain PP against the test plant, mustard (*Sinapis alba L.*). The RNA-seq analysis of differentially expressed genes, total glycoalkaloids content (TGA) and LC-MS glycoalkaloid profiles were studied. Potato F1 individuals were assigned to six bulks that characterized various PP and TGA content. Analysis of glycoalkaloids profiles in each group, six glycoalkaloids were recognized: solasonine, solamargine, α-solanine, α-chaconine, leptinine I, and leptine II. Glycoalkaloid composition played an important role in shaping of PP in the bulk samples characterized by a high TGA content and various PP, high - A', low - B' and hormesis-F'. The RNA-seq analysis revealed *a flavonol synthase/flavanone 3-hydroxylase-like* gene responsible for flavonoid synthesis as one of the most expressed in comparison A' vs. B' and A' vs. F' (Log2FC=8.30 and 6.40, respectively). The population-level evaluation of phytotoxic potential confirmed a significant negative correlation between total glycoalkaloid content and phytotoxic potential (r=-0.211) but only after correction for total flavonoid content. We demonstrated that the involvement of both the quantity and composition of glycoalkaloids and flavonoids play a role in the expression of phytotoxic potential and revealed the involvement of flavonol synthase/flavanone 3-hydroxylase-like in this phenomenon.

15.04. Screening of potato genotypes for nitrogen stress tolerance under in vitro conditions

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in vitro, low input farming, organic farming, NUE

Testing of potato genotypes for nitrogen stress tolerance in vitro has advantages over conducting field trials, however, little is known about the extent to which the results obtained in vitro would be compatible with those obtained under field conditions. As a part of a larger study, a set of 19 genotypes was screened for nitrogen (N) stress tolerance. In vitro experiments were performed in three time-shifted series in 2022. MS medium used as a control contained 60 mmol L-1 of N (N60), medium providing stress conditions contained 7.5 mmol L-1 of N (N7.5). Traits included in the screening were N related traits (N use efficiency (NUE), N uptake efficiency (NUptE) and N utilization efficiency (NUtE)) and phenotypic traits such as plant height, fresh (FW) and dry (DW) weight of plant, FW and DW of shoots, FW and DW of roots. N stress tolerance coefficients (NstC) were obtained for each genotype and trait by dividing the value of the trait in N7.5 by the value of the trait in N60. Genotypes were ranged according to their N stress tolerance using membership function value of stress tolerance (MFVS) averaged over MFVS of each trait. This approach identified one genotype that was highly tolerant to N stress, two genotypes were tolerant, one genotype was sensitive and one was highly sensitive to N stress. Remaining 14 genotypes were moderate tolerant. Two of the most sensitive genotypes had the highest NUE values at N60, these genotypes still had high to average NUE at N7.5 when compared to other genotypes investigated. Multiply stepwise regression analysis revealed that NstC of just two traits alone (NUE and FW) could explain 93% of average MFVS value variation. Adding only NstC FW shoots to the model resulted in a significant regression model explaining 95% of MFVS variation. When only NstC of phenotypic traits were left in a regression model, FW and DW of plant and DW shoots together explained 97% of MFVS variation. Adding data on roots performance resulted in regression model that did not differ significantly from the previous model. NstC of all traits significantly ($p<0.01$) and moderately to strongly positively correlated with average MFVS values of the genotypes, except NUptE and NUtE. This indicates that the latter traits can be excluded from the further screening of N stress tolerance in vitro. The next step will be to compare the data obtained in vitro with the N stress tolerance data for the same genotypes grown under field conditions.

The study was conducted with the support of the National FLPP Project lzp-2019/1-0371

15.05. Transcriptomic and proteomic data provide new insights into cold-treated potato tubers with T- and D- type cytoplasm

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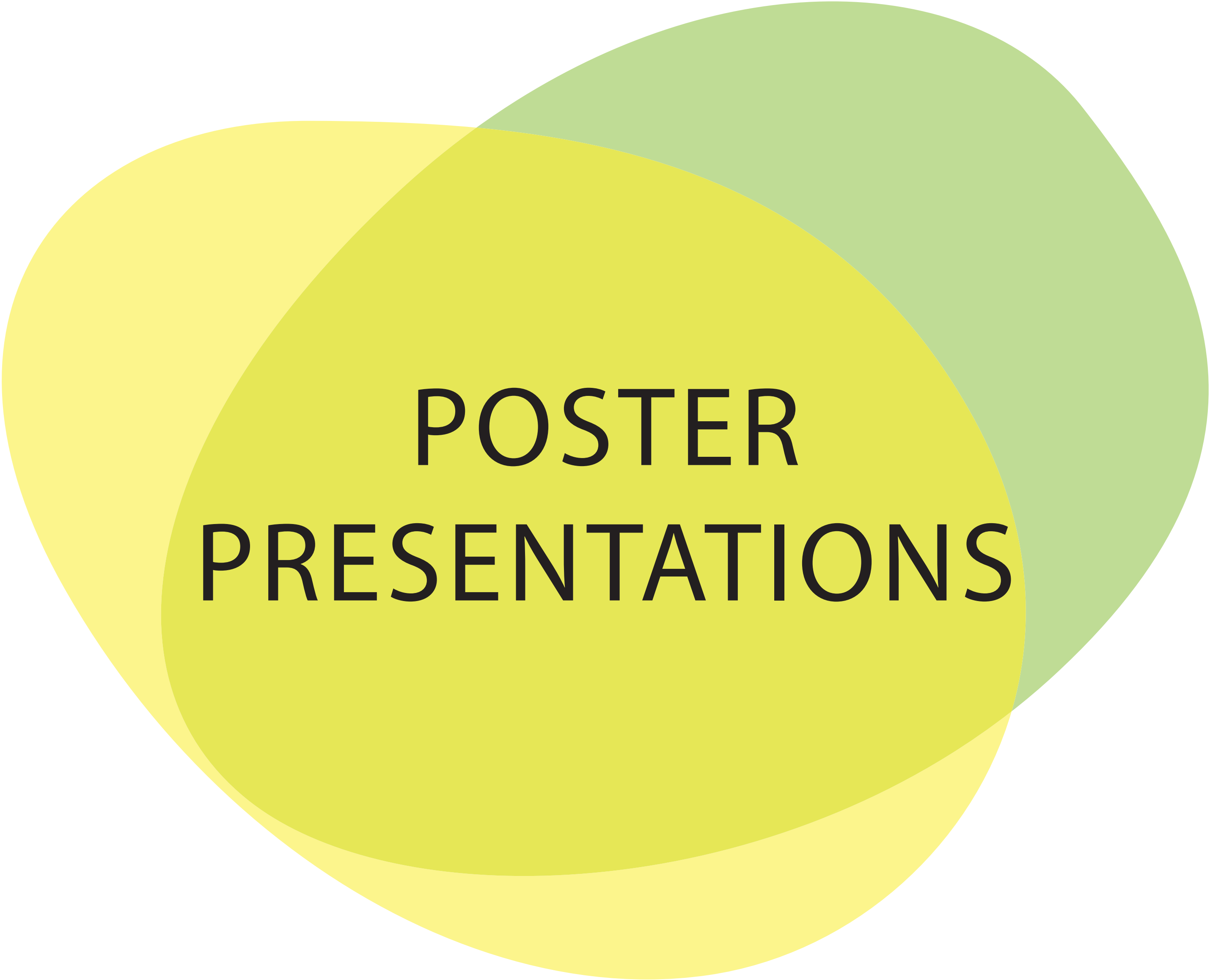
cold-sweetening, cytoplasm types, gene expression, potato tubers, protein expression

In potato (*Solanum tuberosum* L.) tubers, during cold storage starch is broken down into the reducing sugars glucose and fructose. This phenomenon is referred to as cold-induced sweetening. High reducing sugar content is not desirable for thermal treatment because it causes a dark coloration in final potato products, such as fries and chips. We report for the first-time differences in gene expression in potato tubers with T- and D-type cytoplasm in response to cold treatment. We recognized differentially expressed proteins (DEPs) associated with amyloplasts and mitochondria isolated from tubers characterized by light and dark chip colour after cold storage. Two potato diploid progenies derived from reciprocal crosses of parental clones that differed in cytoplasm type were used. Based on RNA-seq data, after comparison of between the bulks from for the T and D progenies 48 and 15 differentially expressed genes (DEGs) DEGs were selected. In population T, the *putative calcium-transporting* ATPase 13, *plasma membrane-type* (LOC107058116) gene was upregulated in potato tubers characterized by light chip colour with 10.75 Log2 fold change. This is a magnesium-dependent enzyme that catalyses the hydrolysis of ATP coupled with the translocation of calcium from the cytosol out of the cell or into organelles. A central role of the intracellular calcium ion concentration generated by the inhibition of ATPase activity in sugar accumulation in low temperature stressed plant tissues cannot be excluded. A significantly higher number of DEPs predicted as mitochondrial was identified in the mitochondria-enriched fractions isolated from tubers with D-type cytoplasm than with T-type cytoplasm. Among 37 DEPs recorded for mitochondria in the D-type cytoplasm, as many as 14 enzymes are involved in tricarboxylic acid cycle metabolism. This suggests that the respiratory pathway may play an essential role in the response of D-type potato tubers to cold stress. The results have been published in Planta journal. The research was supported by The National Science Centre in Poland, Grant UMO-2018/29/B/NZ9/00542.



POSTER PRESENTATIONS

2. Resistance Breeding

2.P01. Reproducibility of phenotyping for soft rot resistance in a petiole maceration assay

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Reproducibilty, Phenotyping, Petiole test, Potato

Many efforts have been done to introgress resistance against soft rot bacteria in potato but success has been limited. One of the main obstacles has been the low reproducibility of plant disease assays to reliably identify resistant plants that can be associated to genetic markers. In this study, we used a petiole test to characterize the resistance to maceration by *Pectobacterium parmentieri*[VR1] using a segregating population derived from a *Solanum chacoense* accession showing resistance to petiole maceration. The study was conducted using two non-overlapping genotype sets from the offspring. Each genotype set was evaluated twice in assays independently performed and the agreement between results was assessed. Disease scores were integrated in one AUDPC value (area under the disease progress curve) for each of the genotypes in each assay. To assess the agreement between result assays, AUDPC values were adjusted to remove additional interference exerted by differences of the disease pressure in the independent assays and a Lin's concordance coefficient correlation was calculated. To determine phenotype reproducibility, the same susceptible individual was used as common reference inside each of the assays to be compared to allocate genotypes into a susceptibility scale. Result agreement between assays determined by a Lin's concordance coefficient correlation fluctuated between 20 and 49%. However, the phenotype reproducibility based on the percentage of genotypes with a consistent phenotype was higher (54-78%) especially for the very susceptible and the resistant categories

2.P02. ScabEomics: Developing effector-based breeding for resistance to *Spongospora subterranea* (powdery scab) in potato.

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Potato, Powdery scab, Effectoromics

Powdery scab caused by *Spongospora subterranea sp. subterranea* (Sss) can cause significant yield losses in potato. Lesions on potato skin affect marketability and provide entry points for other pathogens. Moreover, Sss can spread Potato MopTop Virus (PMTV). Efforts to breed for Sss-resistant varieties are impaired by troublesome phenotyping methods. Plants possessing a specific resistance (R) gene are resistant towards a pathogen that produces the corresponding avirulence (Avr) gene product, also known as effector. Highly expressed effectors that do not trigger hypersensitive response (HR) in susceptible plants, are considered candidate AVRs. Effectors triggering HR are most prominent among the diverse part of the secretome (Van de Vossenberg et al 2019). Therefore, candidate AVRs can be identified using comparative genomics, and transcriptomics of the secretome. In order to identify such AVRs in the Sss genome, we re-sequenced over 20 different isolates from 15 different countries in 5 continents. We mined for Sss effectors in the secretome. We selected candidate genes based on their diversity across different isolates and expression analysis with available RNAseq data. These AVRs will be used to screen a germplasm collection for hypersensitive responses to identify novel R gene sources and to develop molecular markers for marker assisted selection.

Cited references: van de Vossenberg, B. T., Prodhomme, C., van Arkel, G., van Gent-Pelzer, M. P., Bergervoet, M., Brankovics, B., ... & Vossen, J. H. (2019). The *Synchytrium endobioticum* AvrSen1 triggers a hypersensitive response in Sen1 potatoes while natural variants evade detection. Molecular Plant-Microbe Interactions, 32(11), 1536-1546.

2.P03. Phenotypic stability of late blight resistance in potato advanced genotypes

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resistance, potato, late blight, stability

One aim of the PoTStaR project, funded by Agence Française pour la *biodiversité*; as part of the national action plan ECOPHYTO II, is to identify sources of stable resistance to late blight. For this purpose, a collection of 122 advanced genotypes, selected from 1992 to 2011 for their late blight resistance from INRAE research programmes, was re-evaluated for this resistance in field trials in 2017 and 2018. These advanced genotypes are classified in 5 categories, according to their origin and/or type of resistance: genotypes without any R gene (RNS), genotypes originating from South-American varieties (Ecopapa), genotypes harbouring R genes (GR), genotypes obtained from a cross with CIP Pop A genotypes (PopA_CIP_1), genotypes obtained from a cross with PopA_CIP_1 genotypes (PopA_CIP_2). Each genotype was therefore evaluated 4 times: in a 2-years field trial during the period 1992-2011, in 2017 and in 2018. The percentage of foliage destruction was weekly scored on each genotype and rAUDPC, delta_t and delta_a parameters were calculated. Isolates of *Phytophthora infestans* were sampled from these trials since 2000 and genotyped according to the Euroblight method. The phenotypic data were analysed considering they represent an Augmented design trial (Petersen, 1985): the field trial carried out each year represents one block which includes the advanced genotypes to be assessed and 3 control genotypes (Bintje, *Désirée* and Arka) which were present in the experiments each year. The analyses were performed using the variable rAUDPC and corrected values were calculated. The resistance stability was visually evaluated for each advanced genotype using XY graphs. The resistance is considered stable if the corrected rAUDPC values are similar between both periods of evaluation and if their variability between the 4 trials is small. Around 60 advanced genotypes show a stable late blight resistance, three quarters of them belong to PopA_CIP_2 or PopA_CIP_1 categories. Two types of unstable resistance were observed: a decrease of the level of resistance resulting from R genes being overcome, a high variability of corrected rAUDPC values due to quantitative resistance factors being influenced by environmental conditions (climate and late blight strains).

2.P04. A novel allele of 57R marker found during assessment of H1-linked markers in screening for resistance to *G. rostochiensis* in Estonian potato breeding programme

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Globodera rostochiensis, potato breeding, disease resistance, H1 gene

Potato cyst nematode (PCN) *G. rostochiensis* is a quarantine pest in many countries around the world. Breeding for resistant potato cultivars is beneficial both economically and environmentally. In this study, we aimed to introduce marker-assisted selection into Estonian breeding programme. First, we analysed phenotyping data from 11 years of pot tests of 4601 tubers of 2918 potato breeding clones. The majority of clones were grouped either as resistant or susceptible, while 76 clones (2.6 %) could not be classified. To better understand such clones, genetic markers are needed. We assessed the ability of two *H1*-linked G. *rostochiensis* resistance markers, TG689 and 57R, to identify resistance genotype, on 212 breeding clones with known resistance phenotypes. Both markers were PCR-amplified. Matches and mismatches between phenotype and genotype were calculated. There was no significant difference between the two markers. Further, only 57R was used, for its more stable amplification. To test the reliability of genetic marker analysis, 258 breeding clones from 50 crosses with no pre-selection were analysed with 57R, followed by phenotypic testing. The concordance between 57R results and phenotypic resistance was 99.1%, while for susceptibility it was 60.0 %. Interestingly, we found that Estonian cultivar 'Anti' has a 887 bp PCR product of 57R, that corresponds neither to resistant (450 bp) nor to susceptible (1500 bp) allele. This cultivar also exhibits partial resistance to PCN. Sequencing of the PCR product from 'Anti' and its alignment against susceptible reference sequences revealed 2 major deletions, 14bp and 419 bp. According to the sequence annotation, 57R marker is located in a genomic region coding a protein of unknown function. While susceptible allele of 57R encompasses the second and third exons, the third exon is absent due to a deletion in the novel allele, similarly to the resistant allele. It cannot be excluded that the deletion of an entire exon could alter protein structure and affect the resistance to PCN in 'Anti'. Another plausible explanation is that the 57R marker is be linked to a hypomorphic allele of *H1* gene or another R-gene, that results in a different phenotype. To conclude, we showed that 57R is a reliable marker in detecting resistant breeding clones, but not effective in identifying susceptible ones. We also found a novel allele of 57R marker, that could be potentially used to identify partially resistant clones. More research is needed to elaborate the possible linkage between the new allele of 57R and resistance to PCN.

3. Organic production & bioagents

3.P01. Farmer participatory trials and breeding in Poland – the results of the project Ecobreed

Beata Tatarowska, Jarosław Plich

organic production, Ecobreed, potato cultivars, Phytophthora infestans

IHAR-PIB in Młochów is a participant of European project ECOBREED: Increasing the competitiveness of the organic breeding and farming sectors (acronym ECOBREED), funded by Horizon 2020 programme. The project is coordinated by the Agricultural Institute of Slovenia and carried out in collaboration with 24 partner organizations representing 15 countries. ECOBREED will improve the availability of seed and cultivars suitable for organic and low- input production. Activities will focus on four crop species, selected for their potential contribution to increase competitiveness of the organic sector, i.e. common wheat, potato, soybean and common buckwheat. Since potato cultivars suitable for organic farming should have a slightly different set of 'mandatory characteristics' than conventional ones, breeding of such cultivars differ from conventional breeding. It is believed, that selection of cultivars destined to organic farming could be strongly improved by active participation of farmers (Participatory Breeding). Vision on organic plant breeding is based on the cyclic interaction between plant and environment, and between farmer (and the rest of the production chain) and breeder. Cultivars will be optimally adapted to organic growing conditions when they have been selected, maintained and multiplicated in these conditions. Therefore, in the Ecobreed project conduction of a series of field trials in contrasting soil and climate zones were planned. In the frame of this network of field trials local organic farmers will be involved into breeding process and their activities will includes among others evaluation of cultivars and selection of breeding materials that are particularly suited to their requirements and preferences (Farmer Participatory Trials). In the case of potatoes, each participant committed to cooperate with at least four farmers who run their farms under the organic system. IHAR-PIB started cooperation with four such farms. Two of them are located in Podkarpackie voivodeship (Połomia and Tuligłowy) and are located in the Mazowieckie voivodeship (Jadwisin and Grabów). Thanks to this, farmers can actively engage in the breeding process, having the opportunity to choose cultivars adapted to their specific environment and growing conditions.

3.P02. ECOSOL: Ecofriendly solutions for the control of late and early blight in potato

Hans Hausladen, Nicole Metz

TUM

EB

Late blight (LB) caused by the oomycete pathogen *Phytophthora infestans* and early blight (EB) caused by the fungal pathogen *Alternaria solani* are the main diseases affecting potato production. Both diseases are currently managed through multiple applications of fungicides. Given the potentially negative impact of pesticides on the environment, problems of reduced efficacy due to increased pathogen resistance and the de-listing of many fungicides under the EU Pesticide Directive (2009/128/EC), there is an urgent need for a more sustainable long-term integrated pest management strategy. Here we explore the key components of such an IPM strategy for LB and EB that require development and testing to enable their successful implementation in the field. With a current emphasis on sustainable agricultural production, biological control of plant pathogens is increasingly attractive. ECOSOL will integrate biological control into IPM programs to manage late and early blight. To reach this goal, the efficacy and behavior of biological control agents (BCAs) will be tested in planta. The most promising pesticide alternatives will be tested under field conditions in a range of participating countries to ensure transferability. ECOSOL will adapt decision support systems to tailor them for the integration of biocontrol agents and for both early blight and late blight management decision making. IPM strategies will be developed which include the most effective BCAs with optimal timing of application, host resistance and reduced fungicide inputs. These strategies will be tested across a wide range of locations to ensure practical applicability.Our working group at Technical University Munich is mainly responsible for screening different biological candidates for their ability to control *A. solani*. Therefore, our first step was to test 25 candidates with a leaf disc assay in 24-well plates. The best 15 candidates were then applied in greenhouse trials with whole plants and several different potato cultivars. With the best six biological control agents in the whole plant assay, we conducted further greenhouse trials to get deeper knowledge about timing and dosage of applications and with the four most promising ones, we also studied possible mode of actions. The results of this screening process and future steps will be shown here.

3.P03. Evaluation of potato genotypes produced in the organic farming system in different regions of Latvia.

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Institute of Agricultural Resources and economics

potato variety, tuber yield, organic farming

Potatoes are one of the most consumed vegetable crops in Latvia, and the fourth most consumed crops in the world after rice, wheat and corn and act as a food provider. The demand for organic products, including potato, increased significantly in last years. The area under organic farming in the EU has increased by almost 66% over the last ten years, from 8.3 million hectares in 2009 to 13.8 million hectares in 2019. One of the challenges of the EU Green Deal is to increase the production and amount of organic products, which is very important for society as a whole. Different potato varieties and potato genotypes and their suitability for production in the organic farming have been studied with aim to improve genetic diversity and provide sufficient yields. Research and creating of new potato varieties in Latvia has been carried out at the AREI, Priekuli, for 91 years. Developed potato varieties are suitable for both production systems: integrated and organic. The demand for varieties with high-stress tolerance, high nutrition use efficiency, yield stability is important in different regions and due to climate changes. The aim of the study was to evaluate the yield and quality of potato genotypes at three locations in Latvia. Trials were established in organic fields at three regions of Latvia - Vidzeme, Kurzeme and Latgale. Twenty genotypes were included in trial at each region in 2021. According to the data analysis (ANOVA), the yield of varieties differed significantly between the regions ($p < 0.05$). The impact of genotype on tuber yield was 16.74%, impact of location - 62.12%, interaction of both factors -10.54%. Significantly higher potato yield was obtained in the Kurzeme region (Stende). There were no significant differences ($p > 0.05$) between potato yield in Vidzeme (Priekuli) and Latgale (Vilani). The highest (in all locations) tuber yield was obtained for the early potato genotype 'S 03067-33' (21.4 t ha-1). The starch content was significantly influenced by genotypes ($p < 0.05$) while the location appeared with no significant impact ($p > 0.05$) Acknowledgement This research was carried out with the support of the National FLPP Project lzp-2019/1-0371. Key words: potato variety, tuber yield, organic farming.

3.P04. Effect of *Trichoderma atroviride* in organic seed potato production (*Solanum tuberosum* L.)

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potato, Trichoderma atroviride, greenness index, yield

Fungi from the genus *Trichoderma* have the ability to positively influence the growth of plants, by releasing otherwise unavailable nutrients and increasing their uptake by plants, for example. The use of these fungi is allowed in organic plant production. The aim of the presented studies was to evaluate the effects of applying *Trichoderma* fungi on leaf greenness index (SPAD) and the yield of potato plants. The experiments were conducted in central Poland, at the Plant Breeding and Acclimatization Institute - National Research Institute, Jadwisin Research Center in 2019- 2021. Two in vitro bred potato cultivars, Gwiazda and Gardena, were used for the study. Potato transplants were planted individually into a horticultural medium, designed for organic cultivation. After planting, the plants were watered with a suspension of *T. atroviride* spores, strains TRS14 and TRS20, and with a mixture of both these strains in 0.85% NaCl solution, at a rate of 5ml per plant. The spore density in the suspension was 106 cfu/ml. The results were compared with control plants, watered with the same volume of sodium chloride solution. Leaf greenness index was measured during the vegetation period. For the potato cultivar Gwiazda, higher SPAD values were found in leaves of plants treated with *Trichoderma fungi*. However, these values were not significantly different from the control. On the other hand, in the case of the Gardena cultivar, the highest SPAD values were recorded in plants treated with TRS14. The difference in relative chlorophyll content in the leaves of these plants was significant compared to the control combination α=0.05). As the leaf greenness index remains in close correlation with the supplementation of plants with nitrogen, its higher value after application, in the soil, of the TRS14 strain may suggest a higher availability of nitrogen to plants. However, the tuber yield obtained from these plants was not significantly different compared to the control.

3.P05. Evaluation of quality traits for potato varieties – VCU organic farming test optional part

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potato, breeding, organic farming, quality traits, liveseed

Evaluation of potato varieties suitability to organic farming as 'Value for Cultivation and Use' (VCU) test has to be done in organic farming conditions. Several of traits are important for evaluation as they describe yield performing, resistance to biotic and abiotic stress. Other traits are attractive for consumers, so those would be optional for variety assessment. The aim of study was to evaluate quality traits of tested varieties in organic growing conditions The VCU test trial was carried out at the AREI, Priekuļi, during 2018 and 2019. Ten varieties randomized in full blocks with four replications were used in field trial. "Brasla", "Prelma", "Imanta", "Rigonda", "Jogla", "Monta" and "S 04065-2" were bred in Priekuļi, "Kuras" was bred in the Nezerlands, but "Laura"and " Vineta" were bred in Germany. For quality traits one combined sample from four replications was used. The starch content in tubers was determined indirectly via specific gravity as percentage of fresh weight. The boiled tuber taste was assessed by expert panel in scale 1 - 9 (1 = unsavoury, 9 = delicious). The discoloration of tuber flesh after peeling and after boiling was detected one hour after peeling or boiling in scale 1 - 9 (1 = strong discoloration, 9 = no discoloration). The Expert panel defined mealiness based on scale 1 - 9 (1 = very firm, 9 = very mealy). The starch content in 2018 was higher than in 2019, there was significant environmental and variety impact ($p>0.05$) to these results. The environmental conditions between two years varied dramatically. High temperatures and high intensity of sun light in 2018 promoted starch synthesis in potato tubers (15.6 - 23.47 %). In 2019 the weather was warm. On the first decade of July precipitation level was really high (67 mm, 328 % more than long - term data showed). That reduced starch content of potato varieties (11.61 - 20.38%). Between two years there were not any significant differences ($p<0.05$) between taste assessments, but there were significant differences ($p>0.05$) between genotypes. There was significant environmental and variety impact ($p>0.05$) to discoloration of tuber flesh after peeling (2018 - 5.7, 2019 - 7.3), but there was not significant difference ($p<0.05$) between discoloration of tuber flesh after boiling. Some of the varieties showed different levels of mealiness through the years.In 2018 'Prelma' was assessed as 3 (not so mealy), but in 2019 as 6 (medium). Other varieties did not have significant differences ($p<0.05$) between two years, but there was significant impact of variety.

3.P06. Evaluation of potato genotype canopy development parametrs and nitrogen use efficiency in organic farming

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canopy cover, nitrogen use efficiency, maturity type

Canopy cover (CC) is a good measure of intercepted solar radiation in potato, which is also reflected in dry matter production. The availability of nitrogen in soil significantly affects the development of CC. The maximum of plant CC (CCmax) can be used for the prediction of potato yield and nitrogen use efficiency (NUE). Trials were carried out in the organic field at the Institute of Agricultural Resources and Economics (Priekuli, Latvia) in 2020 and 2021. The plant's available nitrogen in the soil was 7.07 g m-2 in 2020 and 8.26 g m-2 in 2021. The set of 20 potato genotypes was divided into three groups according to their maturity type (early, medium early and medium late, late). Four replications were applied. CC was monitored by taking pictures of each plot twice a week with camera and by quantifying CC using Canopeo app. The canopy growth parameters - the percentage of maximum CC (CCmax) and the time period under maximum CC (CCmax period) expressed in Beta thermal days (Btd) - were obtained by using the beta sigmoid growth function to model canopy growth. The CCmax values in 2020 exceeded the values obtained in 2021 and were in the range from 41.1 to 82.1% in 2020, and from 22.5 to 70.7% in 2021. Therefore, the value of CCmax was significantly affected by the growing year and genotype ($p<0.05$), but differences between maturity type groups were not significant ($p>0.05$). NUE of genotypes was higher in 2020 than in 2021 and ranged from 0.037 to 0.150 kg g-1and from 0.003 to 0.061 kg g-1 in 2020 and 2021, respectively. NUE was significantly influenced by the growing year, maturity type and genotype ($p<0.05$). In addition, CCmax period was in the range from 3.1 to 20.6 Btd in 2020, but from 0.7 to 30.5 Btd in 2021. The CCmax period was significantly affected by genotype ($p<0.05$) and maturity type ($p<0.05$), but the effect of growing year was not significant ($p>0.05$). A significant correlation was found between CCmax and NUE $r=0.75$ ($p<0.05$). The correlation between CCmax period and NUE was $r=0.26$ ($p<0.05$). Acknowledgments Research was carried out with the support of the National FLPP Project lzp-2019/1-0371

3.P07. The effect of continuous cropping of potato on its weed infestation and yielding.

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crop rotation, continuous cropping, weed infestation, yield, yield structure

Strict field experiment was carried out on medium heavy soil derived from silt loam, classified as good wheat soil complex. The experiment was established in an Agricultural Experimental and Production enterprise of Warmia and Mazury University, localized in Bałcyny near Ostróda. The experiment with continuous potato cropping was initiated in 1973. However only data from the period of 2016-2018, i.e. data from 44, 45 and 46 year of potato continuous cropping, were a base of this experiment. The results were compared to those obtained in a 6-course rotation: potato - oats - flax - winter rye - field bean - winter triticale. To compensate the lack of rotation in continuous cropping plots: two potato cultivar Catania and Red Sonia were chosen and herbicide was applied. The aim of this study was to assess the effect of weed infestation on potato yielding. The weed biomass in continuous cropping was 20 and 16-times higher, in Catania and Red Sonia cultivars, respectively. The most frequently observed weeds were Echinochloa crus-galli, Agropyren repens and Equestium arvense. Tuber yield in crop rotation were 48.9 and 38.3 t per ha, and 24.6 and 21.6 t per ha in continuous cropping for Catania and Red Sonia cultivars, respectively. Due to continuous cropping yielding of potato was lower, higher proportion of smaller tubers and share of marketing yield were lower. The second aim was saying that application of herbicide might minimize the adverse effect of resigning from crop rotation. The application of herbicide had no effect on potato yield in crop rotation and had positive effect on tuber yield in continuous cropping only in some years.

4. Bacterial & fungal diseases

4.P01. Detection and identification of different strains of *Ralstonia solanacearum* using selected molecular primers in PCR and Real-Time PCR tests

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Ralstonia solanacearum, molecular diagnostic, potato, phylotypes

Ralstonia solanacearum (Rs) (Smith) Yabuuchi et al. the causal agent of potato brown rot is one of the most important quarantine potato pathogens. Due to the pathogenicity ot the bacteria pose a serious phytosanitary threat to the EPPO region. Of the four phylotypes of the *Ralstonia* species listed in EPPO diagnostic protocol No. PM 7/21, each consisting of many different phylogenetic and pathogenic variants, one of the most virulent genotypes is phylotype IIB 1 (formerly known as race 3 biovar 2). This phylotype is particularly dangerous because it has a relatively low growth temperature (approx. 27°C) and often causes latent (asymptomatic) infections. It also adapts to colder climatic conditions. Therefore, it is very important to develop a sensitive and specific method for the detection of these bacteria, in particular for the potato starting material. The aim of the research was to develop conditions allowing for specific and sensitive molecular diagnostics of the *Ralstonia* species tested. As a result of the conducted research, the conditions were developed and the PCR and Real-Time PCR primers were selected, enabling the achievement of the high sensitivity and specificity threshold for the DNA of the tested *R. solanacearum strains.*

4.P02. Virulence comparison of Ukrainian and Western European pathotypes of *Synchytrium endobioticum*

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S. endobioticum, pathotypes, virulence

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 (Nevșehir) was detected in The Netherlands.
In Ukraine the most relevant pathotypes are 11(Mizhhirya), 13(Rakhiv), 18(Yasinia) and 22(Bystrets).

In this project about scientific- technical cooperation between Ukrainian scientific-research plant quarantine of Institute of Plant quarantine station of Institute of Plant Protection NAAS of Ukraine and Plant Breeding and Acclimatization Institute (Poland), we tried to compare the virulence of these two groups of pathotypes on a much larger collection of potato differential varieties. The results showed that pathotypes from Ukraine are significantly different from Western European ones. However, one of them drew special attention, namely 11(Mizhhirya). The virulence profile of this pathotype is very similar to 38 (Nevșehir). This was found by comparing virulence with data from the literature. Perhaps it is the same pathotype or they have a common origin. Especially since pathotype 38 is also found in Turkey and Georgia.

4.P03. *Alternaria alternata* populations from potato, tomato and citrus in South Africa

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Agricultural Research Council – South Africa

Brown spot, virulence, cross-infection

Alternaria alternata has a host range of more than 100 plant species, including many agricultural crops. Diseases caused by the pathogen include brown spot on potatoes and tangerines, leaf spot on rough lemon, black rot on several citrus fruits and black mould on tomato, amongst others. The objectives of the study were to isolate *Alternaria alternata* occurring on potato, tomato and citrus in three of the provinces in the northern part of South Africa, namely, Gauteng, Limpopo and Mpumalanga. Isolates obtained were used in a cross-infection, in order to determine the ability of isolates obtained from one host to infect other hosts.

Symptomatic plant material of citrus, tomato and potato were collected from 15 different farms in Gauteng, Mpumalanga and Limpopo Provinces. A total of 242 isolates were obtained and screened for virulence using a detached leaf assay, infecting the same crop it was obtained from. The most virulent isolates selected were characterised based on morphology and phylogenetic analyses of the Alt a 1 gene region. The three most virulent isolates from each crop were used in the cross-infection study in the greenhouse.

Results from the greenhouse trial showed that all the *A. alternata* isolates evaluated were able to cause disease symptoms on the tested crops during cross infection. The findings of the study will serve to guide future disease control strategy development, since the ability of a single population to infect multiple hosts will have a significant impact on the success of the control measures.

4.P04. Structural diversity of O-antigens in *Pectobacterium parmentieri* lipopolysaccharides

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soft rot Pectobacteriaceae, O-antigen chemical structure, LPS, biodiversity, virulence

Pectobacterium parmentieri is an economically important phytopathogen responsible for potato blackleg and soft rot, and for which current control strategies are limited. The main virulence factors of *P. parmentieri* involve production of plant cell wall degrading enzymes (PCWDEs) and siderophores, bacterial motility and lipopolysaccharide (LPS). LPS plays a major role for bacterial growth and survival. Moreover, LPS is directly implicated in plant-pathogen interactions and considered as pathogen-associated molecular patterns (PAMPs). Structurally LPS is composed of three distinct domains, namely, lipid A, core oligosaccharide, and O-specific polysaccharide (OPS). We hypothesized that the great genomic diversity in *P. parmentieri* may be correlated with the diversity of OPS in this species. The structures of OPS isolated from LPS of five *P. parmentieri* strains: SCC3193, IFB5432, IFB5408, IFB5427 and IFB5441 were investigated. The purified polysaccharides were analysed by utilizing NMR spectroscopy and chemical methods. Sugar and methylation analyses of native polysaccharides, absolute configuration assignment of constituent monosaccharides and NMR spectroscopy data revealed that these five investigated *P. parmentieri* strains exhibit three diverse OPS molecules. Interestingly, two *P. parmentieri* strains SCC3193 and IFB5432 isolated in different countries possess the same structure of OPS with a very rare residue of pseudaminic acid. *P. parmentieri* strains IFB5427 and IFB5408 exhibit a different OPS molecule than SCC3193 and IFB5432. A third structurally diverse OPS was noted in *P. parmentieri* IFB5441 strain. There were no significant structural similarities between the polysaccharides isolated from described *P. parmentieri* strains and the OPS of closely related species *P. atrosepticum*, *P. carotovorum* and *P. brasiliense*. We investigated the genetic and molecular basis of differential OPS phenotypes in *P. parmentieri* and examined whether OPS diversity is associated with strain virulence. The obtained results constitute a basis for examining the importance of LPS in the infection process caused by *Pectobacterium* species. Further work may allow us to unveil the role of LPS in the virulence of the studied phytopathogen.

4.P05. Investigating possible biotic causes of poor potato emergence by DNA metabarcoding – a case study

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Metabarcoding, Damping off disease, Arctic agriculture, Plant-parasitic nematodes

Delayed emergence of potato plants and reduced yield and quality were observed in large areas of several potato fields in Engeløya, 150 km north of the Arctic circle in Norway, in 2018-2019. Since no obvious cause was found, soil samples were collected in zones showing normal and delayed growth, and in the transition zones between these, in three fields in 2020 and 2021. DNA metabarcoding was performed with Illumina MiSeq, using primers targeting bacteria, fungi, oomycetes, and nematodes. Soil samples were also analyzed for plant-parasitic nematodes, including cysts, to compare DNA metabarcoding with traditional methods. Furthermore, nematodes were extracted from potato tubers showing symptoms of *Streptomyces* (common scab), as *Pratylenchus* spp. have been shown to cause similar symptoms on tubers. The extracted nematodes were counted and identified morphologically. The most prevalent plant-parasitic nematode in the soil samples was the root lesion nematode *Pratylenchus crenatus*. Amplicon sequence variants (ASVs) designated *Pratylenchus* were also the most abundant among plant-parasitic nematodes in the metabarcoding analysis. However, no *Pratylenchus* spp. were detected in potato tuber samples showing common scab symptoms. ASVs designated *Paratrichodorus* were more common in areas with delayed growth than in areas with good growth, however, this genus was not detected in the nematode extractions. Potato cyst nematodes (*Globodera rostochiensis* and *G. pallida*), which are obvious nematode candidates of poor growth, were not detected. In one field, *Rhizoctonia* was present in the parts of the field with poor growth. In this same field *P. crenatus* was also detected, but the number of nematodes ranged from 87-116 individuals per 250 mL soil, which is likely below the expected damage threshold for this species. *Rhizoctonia* and free-living nematodes have been found to join in disease complexes. The oomycete *Globisporangium irregulare* was more prevalent in the poor-growing parts across all fields. *G. irregulare* has a broad host range and is known to cause damping off disease in many plants, however, it is not described as a potato pathogen. ASVs designated *Aphanomyces* were common in all three fields. Plant-pathogenic *Aphanomyces* species are known to cause root rot in legumes, and a few other species, but not in potato. The main cause(s) of the delayed emergence in the potato fields has not been revealed, but several interesting correlations were found. To determine the cause, further studies are needed, including isolation of potential pathogens and infection trials.

4.P06. Species prevalence and fungicide resistance of *Alternaria* populations responsible of early blight in France

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Alternaria, Section Porri, qPCR, fungicide, disease management

Early blight and brown spot caused by *Alternaria* species can cause important economic losses to potato crop. Both diseases are often difficult to discriminate as symptoms are closely related and can also be confused with abiotic stresses. In this disease complex, *A. alternata* is often considered as a weak pathogen, but there is not a consensus in the scientific community, and *A. solani* is considered as the most aggressive pathogen. Nevertheless, recent studies have shown that the situation is much more complicated with the reporting of several species closely related to *A. solani* (large-spored species of the section Porri) and to *A. alternata* (small-spored species of the section *Alternaria*). This study is part of the SYTRANSPOM Interreg project which associates four European partners (CARAH, PCA, INAGRO, ARVALIS) in order to improve our knowledge of the pathogens responsible for early blight and brown spot diseases. We developed real-time PCR methods specific to pathogens of each section (*Alternaria* section *Porri* and *Alternaria* section *Alternaria*) in order to quantify predominant section throughout the growing season during 3 years. We isolated and identified at species level more than 100 strains from different fields by sequencing several genes. We also assessed the frequency of mutations in cytochrome b and succinate deshydrogenase genes responsible for resistance to different fungicides. The results showed a seasonal shift in the composition of *Alternaria* populations with *Alternaria* section *Porri* becoming more predominant at the end of the growing seasons in France. We also identified the species *A. alternata*, *A. arborescens* and probably *A. gaisen* for section *Alternaria* as well as the species *A. solani*, *A. grandis* and *A. protenta* for section *Porri* which demonstrates, for the first time in France, that several species are responsible of early blight and brown spot diseases. Finally, results showed an evolution of the frequency of isolates resistant to different fungicides. This study provided a better understanding of the potato *Alternaria* populations in France and may lead to more robust integrated pest management.

4.P07. Preliminary results regarding black scurf influence on potato yield using different agricultural practices

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Potato, black scurf (Rhizoctonia solani), fungicides, control, yield

Black scurf and stem canker on potato caused by *Rhizoctonia solani* Kühn is a seed and soil born disease of potato with high level of survival. Managing it is a difficult task. Field experiments (using crop rotation and monoculture) were conducted with various fungicides along with treated and untreated checks at NIRDPSB Brasov, Romania, in 2018. Two different varieties, Brasovia and Cezarina, were planted in 19, respectively 25 April. Cultivation and maintenace was in line with current good agricultural practice. Field experiments conducted to evaluate the efficacy of various fungicides showed that Sercadis (300 g/l fluxapiroxad) , Serenade (1015.1 g/l Bacillus subtilis strain QST 713), Prestige Extra 370 FS (pencicuron 250 g/l + imidacloprid 120 g/l), Amistar (250 g/l azoxistrobin) and Ortiva (200 g/l azoxistrobin + 125 g/l difenoconazol) provide control of the disease. Difference among treatments for emergence were observed in the second location (in monoculture), the percentage of emerge plants varied between 73.1% (Serenade) and 23.9% (Ortiva). Also row closure differences, highest (46 thousand hills/ha Brasovia variety and Serenade 8 l/ha) and lowest (11 thousand hills/ha Cezarina variety and Ortiva 1 l/ha), another way to estimate the health of crop early in season, were observed between the two fields and the different treatments applied. The tubers were harvested 9 September, graded and placed into storage at 4-10°C. Total yield with different black scurf degree of attack was between 12.48 t/ha to the untreated (control) variant and 20.32 t/ha to Prestige variant on monoculture field and between 12.00 t/ha to the untreated (control) variant and12.38 t/ha to Serenade 8.0 l/ha variant . On 25 October, 100 tubers from the 35-55 mm and >55 mm size category were selected and assessed for presence of sclerotia. The total yield and % of tubers with attack was between 35.64 to untreated (control) variant and 25.86 to Amistar variant in the field with rotation and between 18.33 and 15.58 to sercadis variant in monoculture field. The level of tubers disease was analyzed using a four step scale: trace (0-1% percentage coverage), light(>1-5%), moderate (>5-10%) and severe (>10). High prevalence of black scurf of potato is due to the favorable climatic condition for the inoculum, monocropping and poor cultural practices. Low soil temperature and high moisture level was the major factors favoring the development of disease in the monoculture. The results confirm that black scurf reduces progeny tuber quality and marketable yields.

4.P08. Characterization of *Pectobacterium brasiliense* in Israel

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Pectinolytic bacteria, primarily *Dickeya solani* (Ds), *Pectobacterium carotovorum* subsp. *carotovorum* (Pcc), *P. brasiliense* (Pbr) and *P. parmentieri*, are the causal agents of pre-emergence seed rot, blackleg and wilt, and tuber soft rot. Disease symptoms and development vary with climate; disease expression in the field may particularly be favored under warm-climate conditions, which prevail in Israel. Latent infections with Ds and Pbr in seed lots imported from Europe to Israel for the spring season, affect yield in both spring and winter seasons, causing economic losses. The latent infection in seed tubers and plants was assessed by RTPCR analysis.

Pbr strains obtained from imported seed tubers, potato plants and progeny tubers grown in Israel were characterized by Pulse Field Gel Electrophoresis (PFGE) and by sequencing the *gapA* gene. A major group of 49 strains out of 68, produced the same pattern with either *Avr*II or I-*Ceu*I, while the other strains, including Ds showed different patterns.

Pathogenicity of the tested Pbr strains evaluated by tuber maceration test revealed a considerable variation in the maceration ability related to the source of the plant material.

Pathogenicity of Pbr strains from carrot, celery, fennel, onion, broccoli, pepper and wash water of potato tubers before marketing, was compared with Pbr strains from potato. The maceration caused by the onion and wash water strains was significantly the highest, compared with the strains originated from potato tubers and potato plants.

During 4 years (2017-2019 and 2020), selected 61 certified imported seed lots were detected for Pbr latent infection and planted in experimental plots. Seed lot infection was correlated with disease expression in the field in 77% of the cases, 18% were false positive, while only 5% of the cases were false negative. Monitoring latent infection of pectinolytic bacteria enables rational management of blackleg in the field, especially to reduce the risk for local seeds produced for the fall/winter season.

4.P09. Determination of reactions of some potato cultivars to *Rhizoctonia solani* Kühn

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Disease severity, Solanum tuberosum L., Screening, Stem canker

Rhizoctonia solani Kühn. is worldwide known, destructive soil-borne pathogen and can be mainly disseminated to different regions in the world through contaminated potato tubers. This disease can arise on potato plants at some time during planting to harvest and potato plants are most seriously damaged at early stages soon after planting. In order to determine the severity of stem canker, nineteen potato cultivars (Agata, Agria, Banba, Bettina, Challenger, Désirée, Granola, Hermes, Innovator, Lady Claire, Lady Olympia, Lady Rosetta, Marfona, Melody, Musica, Orchestra, Russet Burbank, Sultan Ecem, Van Gogh) were screened against *R. solani* AG-3. Pre-sprouted tubers were grown at 25-18 (±2) °C (day/ night) and 70% relative humidity, under controlled greenhouse conditions. Disease severity was calculated using Townsend-Heuberger formula. Thirty days after the inoculation the highest disease severity was found in Banba variety, followed by Lady Claire, Désirée and Innovator cultivars. Besides, Russet Burbank, Granola and Sultan Ecem cultivars were identified as highly tolerant cultivars due to their low disease severity index value, yet no immune cultivars were found.

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4.P10. Potato purple top outbreaks and multiple stakeholders’ reactions in the Andean Highlands of Ecuador

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Emergent diseases, Disease-human interactions, phytoplasma, zebra chip, psyllids

Introduction

Management of emergent plant pests and pathogens outbreaks not only relies on technical solutions. It also depends on the interaction between the “new” plant disease epidemics and human responses. This research aimed to understand this interaction using the case of potato purple top and the potato psyllid (*Bactericera cockerelli*) in Ecuador.

Methodology

Official documents, journal articles, and governmental surveillance data were used to document the case. The participation of the authors in multiple activities with different stakeholders enabled data collection.

Results and Discussion

A report of potato pests and diseases indicated that purple top was scarcely present in Ecuador in 1986. However, it went unnoticed until 2012 – 2013 when it was found in Carchi (border province with Colombia). Infected fields showed plants with aerial tubers, erected leaves, and witches’ broom. These symptoms were confused with the ones caused by *Rhizoctonia solani*, but epidemiological patterns in infected fields revealed the existence of an unknown causal agent. Two hypotheses have been suggested for the appearance of purple top: (1) illegal trade from Colombia (due to the appearance in Carchi), and (2) changing weather conditions. In 2015 – 2016, purple top showed up in three provinces: Carchi (incidences ranging from 15 to 75% per infected field), Pichincha and Cañar. During this time, *Candidatus Phytoplasma aurantifolia 16SrII* was found in plants showing purple top symptoms. The third outbreak began in 2018 – 2019. It was accompanied by the appearance of the potato psyllid and *C. phytoplasma* in the aster yellow cluster, subgroup 16SrI-F. The high incidence of the problem in farmers’ fields stimulated attempts to create public-private alliances. Unfortunately, political instability led to undermining of institutional networks and lack of governmental funding. Uncertainties around the epidemic limited clear communication with other actors. In response to the disease, farmers increased the number of sprayings, modified seed exchange networks, and changed crops after being affected by purple top, losing up to 3 potato varieties. Some farmers even began to plant potatoes in the “paramos” to escape purple top and the psyllid, affecting carbon sequestration rates and potentially contaminating water sources. Managing purple top becomes more challenging due to the recent identification of *C. liberibacter solanacearum*. This case offers valuable insights to improve how to deal with emergent plant pathogens and pests from technical and social perspectives.

4.P11. Differentiation between *Pectobacterium* and *Dickeya* species based on their infrared spectral and volatile signatures

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Blackleg, Early detection, Spectroscopy, GCMS

Accurate and rapid detection of *Pectobacterium* and *Dickeya* spp., the causal agents of potato blackleg and soft rot, is important for reducing damage. Infrared spectroscopy was used to measure the mid-infrared spectra of three species of *Pectobacterium* and two species of *Dickeya*, a total of 24 strains. The measurements were analyzed by machine learning methods in order to differentiate among them at the genus, species and strain levels. Results show that it is possible to differentiate among different bacterial pathogens at the genus level with ~100% success rate, at the species level with ~99% and at the strain level with < 95%. Volatile organic compounds (VOC's) profiling was used as a sensitive method to detect tuber infection with these pectinolytic bacteria, and to discriminate between *Pectobacterium* and *Dickeya* spp. Sampling of inoculated discs was performed using Solid Phase Micro Extraction (SPME), coupled to a Gas Chromatography Mass Spectrometry (GC-MS). Strains demonstrated a unique volatile profile, differentiated at the genus, species and strain levels. P*ectobacterium* strains were characterized by high percentage of alcohols, e.g. 2-methyl butanol, alongside a complete absence of nitrogen compounds, while *Dickeya* strains specifically induced the biosynthesis of sulfur compounds, e.g. propyl thiophane. Additionally, several molecules were identified as general inoculation biomarkers, e.g. 2-pentyl furan. Early detection of pectinolytic bacteria using VOC's allows to determine the presence of infected tubers by sampling the atmosphere, rather than testing single tubers, thus providing the grower a rational tool in management of seed and ware potato tubers in storage.

5_6.P01. Bacterial and fungal potato seedborne diseases in seed lots imported to Israel, survey 2011-2020

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Common scab, Powdery scab, Silver scurf, Black dot, Black scurf

Potato cultivation in Israel in the spring season is based on seed tubers imported from Europe, while local seeds (early-harvested at spring) are used for the fall-winter season. Each year ~ 30,000 tons of seed tubers are imported from The Netherlands, France, Germany and Scotland. Infected seed tubers are the major source of disease development during the growing season and also a source for soil infestation. Although only certified seed lots are imported, previous surveys indicated that most imported lots were affected by latent or active infections caused by bacterial and fungal pathogens. Visual assessment was carried out in a sample of 200 tubers per lot (taken by the Plant Protection and Inspection Services inspectors), in a scale of low (index ≥ 0.45), medium (index 0.45 – 1.2) and high (index ≤ 1.2) infection levels. The index was calculated as follows: [(# of tubers in low infection level X 2 + # tubers in medium level X 5 + # tubers in high level X 7)/total number of tubers]. Common scab, caused by Streptomyces scabies, was present in 68% of the lots at a low level, 15% at a medium level, and 4% at a high level. Powdery scab, caused by *Spongospora subterranea*, was observed on 8.3, 1.1 and 0.3% of the lots at a low, medium and high levels, respectively. Silver scurf, caused by *Helminthosporium solani*, was observed on 44, 23, and 18% of the lots at a low, medium and high levels, respectively. Black dot, caused by *Colletotrichum coccodes*, was observed on 46, 13, and 9% of the lots at a low, medium and high levels, respectively. Black scurf caused by *Rhizoctonia solani* was observed on 49% of the imported lots, at a low level and only 2.2 and 0.1% of the lots were infected at medium and high levels, respectively. Fusarium dry rot, caused by *Fusarium* spp. was detected in 12.5% of the lots. Latent infections with *Dickeya solani* (Ds) and *Pectobacterium carotovorum* subsp. *brasiliense* (Pcb) in the imported seeds were determined by PCR/qPCR with species-specific primers. The incidence of seed lots latently infected with Ds in 2017 was 30%, 55% in 2018, and only 7% in 2019. The incidence Pcb-infected lots was 48, 62, 95, and 86% in 2016, 2017, 2018, and 2019, respectively. The dynamics of bacterial populations of Ds and Pcb have changed over recent years, in accordance with their prevalence in Europe, Ds decreased whereas Pcb increased. Monitoring diseases on seed lots enable the grower to have a better decision on the use of each lot.

5_6.P02. Potato production in a second crop as an alternative solution for quality seed production in South East Europe

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Second crop, Viruses and ecological degeneration, Varieties, Time of planting, Seed quality

Among the many factors contributing to low productivity in South East Europe viruses and ecological degeneration of potato seed tubers are a critical factor. Potato seeds are imported in to Republic of Moldova from traditionally production zones, such as coast of Baltic sea. However, the climate change more and more affected this and others zones. For example, climate condition during the vegetation period in 2018 dramatically affected potato production in general and seed potato production in specially. As a results price of seed potato is growing up and the needed quantity per varieties some times are not sufficient or available. Global warming, lead to changes in the time of planting, the use of new adopted cultivars, and a shift of the location of potato production In such condition local seed potato production in a second crop is one of the most economical way to get high quality seeds. In the result of the research where established that because of this method the pressure of viruses diseases are lower and tubers are not affected by ecological degeneration. Harvested tubers due to better physiological condition stored better, show less weight loss and are not sprouting. The gained results show that under the climate condition of Republic of Moldova seed potato in a second crop can be done with early harvest fresh tubers and with last year old tubers. The highest yield with less cost, in both methods can be obtained only if the varieties choice is done in concordance with zone and method of cultivation. For fresh harvest tubers method are recommended extra early and early variety (Riviera, Minerva, Agata, Ranomi, Artemis). In case of last year tubers method, a large number of varieties can be used, including second early varieties. Quality of the seed produced in the second crop are higher than quality of the seed produced by traditional method in the first crop. Number of plants affected by heavy viruses form are three times lower, have not been detected tubers which lose sprouting capacity, compared with seed tubers produced in the first crop where this number can reach 12%. Seed potato production in Republic of Moldova, Ukraine, Russian Federation are gaining in popularity due to les viruses accumulation and ecological degeneration. Seed potatoes tubers produced in the second crop are at the same quality level as imported seed, more quality than local traditionally produced seeds. Tubers are not affected by ecological degeneration less affected by viruses infection, not sprouted during the storage.

5_6.P03. Experience in aeroponic technology for potato seed propagation in Czech Republic

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aeroponics, minitubers, potatoes, solutions, aeroponic unit

Aeroponics is a method of growing plants in an aerial or foggy environment without the use of soil or aggregated nutrient medium (Farran and Mingo-Castel, 2006). Aeroponics would appear to have a number of potential attributes to make potato production more efficient (Christie, Nichols, 2004). For potatoes it is used especially for the breeding and potato seed multiplication. This paper presents two years experience in the use of aeroponic technology for the production of seed potato minitubers in Potato Research Institute Havlickuv Brod, Czech Republic. We used plant tissue cultures of three potato varieties – Adela (early), Zuza (medium early) and Ornella (medium late). Plant density was 25 plants.m2. The nutrient solution specifically designed for aeroponics (1) and solution by Otazú (2010, 2) were used. In 2019 and 2020 years in the aeroponic unit minitubers weighing more than 1 g (sizes 10 – 30 mm) were harvested until the aging of the crops (104 - 130 DAP) at weekly intervals. In 2019 plants fed a solution for aeroponics formed more tubers per plant (Adéla 5,3 pcs, Zuza 7,2 pcs, Ornella 4,2 pcs) compared to plants nourished with Otazú solution (Adéla 2,4 pcs, Zuza 3,8 pcs, Ornella 2,5 pcs). However, this difference was not statistically significant. In 2020 the number of tubers per plant ranged from 14,4 pcs for the Ornella in solution 2 to 19,5 pcs for the Ornella in solution 1. For the Adéla, the number of tubers per plant in solution 2 was 14, 7 pcs. In a special solution 19,2 pcs. Zuza had numbers of tubers 17,7 pcs (Solution 1) and 18,5 pcs (Solution 2). A statistically significant effect of the nutrient solution was demonstrated for the Ornella and the Adela variety in both nutrient solutions. Statistical significance was further found for solution 1 for the Adéla to the Ornella and for solution 2 for the Ornella to the Zuza and Adéla. When comparing the effect of nutrient solution composition on the number of tubers between years (2019 and 2020), a statistically significant effect of both nutrient solutions in 2020 compared to 2019 was demonstrated. In 2020 a significant increase in tuber growth was achieved in all evaluated potato varieties.

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5_6.P04. Detection of Rysto homologues in wild potato species

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Potato virus Y, resistance gene, Solanum species

One of the most important viral potato pathogens is Potato virus Y (PVY). This virus is transmitted through aphids, mechanically by machinery or tools. Plants infection, by PVY leads to necrosis, drooping and yellowing leaves, dwarfism and premature plant death. It is estimated that yield losses caused by PVY could be more than 80%. Wild potato species are the source of resistance genes against many diseases that attack potatoes, including the PVY (Slater et al. 2020). Gene Rysto derived from *S. stoloniferum* was mapped on chromosome XII, it confers extremely high level of protection against all known strains of PVY and it is widespread in European potato cultivars (Flis et al 2005). The aim of this study is to detect homologues of the Rysto resistance gene originating from *Solanum stoloniferum* in wild potato species and to analyze their nucleotide sequence polymorphism. The plant material used in the study comes from the IHAR-PIB collection (Smyda-Dajmund et al. 2020). We tested 29 accessions of 26 wild potato species, 10 clones per accession. At first, using three PCR markers designed on the basis of the Rysto gene sequence (Grech-Baran et al. 2020), we detected homologues DNA fragments in 101 of the 298 DNA samples. The markers were located in the 5'UTR region, TIR domain and LRR domain. Subsequently, we amplified the full length gene (approximately 5000 bp) from 80 samples. Homologues of the Rysto gene were present in 10 out of 26 tested species, including *S. stoloniferum.* In the next step, an attempt will be made to sequence the obtained PCR products and analyze their polymorphism. Selected clones will be also tested for PVY resistance by mechanical inoculation in greenhouse conditions. Knowledge on PVY resistance and resistance gene contents in analyzed accessions will enable their exploitation in potato breeding programs.

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5_6.P05. Monitoring *Verticillium dahliae* infection in local and imported seed tubers using molecular analysis

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Verticillium, microsclerotia, molecular methods, seed tubers

Verticillium dahliae is a soilborne fungal pathogen, surviving for prolonged periods in soil through microsclerotia, causing potato early dying (PED), and *Verticillium wilt* in a wide range of annual and perennial crops. One of the means to reduce the spread of the disease and prevent soil infestation is using pathogen-free potato seed tubers. Monitoring of *V. dahliae* latent infections has been carried out routinely in local seed tubers, but not in lots imported from Europe because of the low prevalence of PED in Europe, however, climate change and global warming might have affected the situation. The objectives of the current study were: a) to investigate the potential transmission of the pathogen via seed tubers imported from Europe; b) to compare sensitivity of RT-PCR analysis in detecting tuber-borne *V. dahliae* to isolation; c) to determine the optimal timing for testing (before or after haulm destruction). In spring 2020, in 29 lots out of total 67 *V. dahliae* was isolated (18 from Netherlands, 4 from Germany, 4 from France and none from Scotland). Twenty isolates that were checked for VCG were all assigned to VCG4B. In spring 2021, 17 out of total 54 lots were *V. dahliae*-infected (7 from Netherlands, 2 from Germany, 7 from France and one from Scotland). Sixteen tested isolates were also assigned to VCG4B. Selected 231 local seed lots (for the fall-winter season) were checked during three years for *V. dahliae* latent infection by microbiological and molecular methods. The incidence of infected seed lots in both methods was 76%, whereas 23% were positive only in RT-PCR, and only 1% of the cases were positive in the microbiological test and negative in the molecular test. The sampling date, before or after haulm destruction, was evaluated in 34 fields during two years. The incidence of infected seed lots assessed using RT-PCR was 69 and 67%, before and after haulm destruction, respectively. With the microbiological test, seed lot infection was 53% and 61% before and after haulm destruction, respectively. In both years, the incidence of infected lots was increased after haulm destruction evaluated in both tests. To conclude, *V. dahliae* is being transmitted via seed lots imported from Europe, the molecular method for detecting latent *V. dahliae*-infection in seed tubers was more sensitive compared to the microbiological method, and the optimal timing for testing the infection was after haulm destruction.

5_6.P06 Total content of polyphenols, antioxidant properties and behavior at PVY inoculation of several Romanian potato genotypes

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Potato Virus Y, polyphenols, antioxidant potential

Potato Virus Y is one of the most dangerous pathogens with a major impact on seed potato production, being wide spread in many cultivated areas. The purpose of this study is to estimate the total polyphenol content, the antioxidant potential of 10 Romanian genotypes (breeding lines: BV 1791/1, BV 1871/4; varieties: 'Christian', 'Roclas', 'Sevastia', 'Marvis', 'Castrum', 'Brasovia', 'Cosiana'; genotype 'Blue Purple of Galanesti'). Another aime of this research was to evaluate the behavior of plants obtained from starting biological material with different antioxidant potential at the mechanical inoculation with potato virus Y (necrotic) and establish the correlations between the level of infection rate and the antioxidant properties. The virus infection level of the material was determined by DAS ELISA (Enzyme Linked Immunosorbent Assay). The total polyphenols content was evaluated using Folin Ciocâlteu method and expressed in mg Gallic Acid equivalents per 100 g Dry Weight. A spectrophotometric method was used for estimated the % of free radicals DPPH inhibition of the samples. In all the experiments, the plants from tubers that initially had higher total polyphenol content values and higher percentage of DPPH inhibition were more resistant to PVY inoculation. The total polyphenol content and the antioxidant potential of potato tubers had higher values in potato tubers with intensely pigmented tissue (the variety 'Sevastia' and the genotype 'Blue Purple of Galanesti').

7. New techniques & hybrid breeding

7.P01. Automatic phenotyping of early foliage and root development under controlled greenhouse conditions of potato (*Solanum tuberosum* L.)

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Automatic phenotyping, Foliage and root development, Controlled greenhouse conditions, Nitrogen use efficiency, Potato breeding

Potatoes show a slight early root development compared to other important crops like maize and wheat, simultaneously the highest nitrogen demand is at the early growth phase around planting. Especially under organic farming conditions the nitrogen management plays a key role to maintain quality and quantity of potato yields. Therefore, robust potato cultivars with a fast foliage and root development are strongly needed. An enhanced early root development may improve the nitrogen use efficiency and reduces climate effective N_2O emissions. Earlier studies revealed that root images of transparent plant jar sides are consistent with the whole plant root system. In this study, four established potato cultivars and four breeding stems were examined in a jar trial under optimal and reduced nitrogen conditions. The two nitrogen input levels were comparable to 159 and 53 kg/ha/yr in the field. The foliage and root development were assessed via RGB cameras of the LemnaTec phenotyping platform three times a week. Beside automatic phenotyping, chlorophyll contents and leaf length were determined manually. The results revealed that a better root development can maintain the nitrogen uptake efficiency. Genotypes with an earlier root growth maximum can exhibit higher tuber yields on average.

8. Disease control strategies

8.P01. Widespread QoI and upcoming SDHI fungicide resistance in Bavarian *Alternaria solani* and *Alternaria alternata* field isolates

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G143A, F129L, QoI, SDHI, mutation

Reduced sensitivity of *A. solani* and *A. alternata* field isolates towards fungicides of the Quinone outside inhibitors (QoI) class (strobilurins) has been observed in Europe for a decade. QoI-insensitive *A. alternata* isolates characteristically carry a G143A amino acid exchange caused by a single nucleotide polymorphism (SNP) in the cytochrome b gene. *A. solani* has evolved a similar F129L mutation that reduces sensitivity towards QoIs. In this study, 55 *A. alternata* and 47 *A. solani* isolates were collected in 2016 from major potato growing areas in Bavaria (southeastern Germany), to update the current status of QoI mutation spread. 85.1 % of *A. solani* and 74.5 % of *A. alternata* field isolates showed the F129L and the G143A mutation, respectively. German *A. solani* populations are composed of two genotypes. F129L mutations were previously exclusively observed in genotype II. We found 74.5 % of *A. solani* isolates to belong to genotype II with a 100 % of them carrying the F129L mutation. However, we also found the F129L mutation in genotype I with a frequency of 41.7 %. To get a hint on the mode of spread, we analyzed the composition of the underlying SNPs causing the F129L mutation. Albeit there was some diversity in the SNPs and also an indication for the region Lower Bavaria as hotspot for *A. solani* F129L mutation evolution, the dominance of the TTA SNP in genotype II (88.6 % of isolates) and of the CTC SNP in genotype I (80 % of isolates) in the examined regions rather pointed to a physical spread than to multiple independent evolutions. Reduced sensitivity of *A. alternata* and *A. solani* field populations towards succinate dehydrogenase inhibitors (SDHI) fungicides (boscalid), which are the other major compound for *Alternaria* control, are recognized as an emerging problem in Europe. We randomly selected 23 of our *A. alternata* and 19 of our *A. solani* field isolates and screened them for the presence of SDHI mutations in the subunits SDHB, SDHC and SDHD of the succinate dehydrogenase enzyme complex (SDH). 43.5 % of *A. alternata* and 42.1 % of *A. solani* isolates were found to carry a mutation in one of the examined SDH subunits. Mutations in the SDHB subunits were with a frequency of 26.1 % of isolates predominant in *A. alternata*. It was in 83.3 % caused by the H277Y mutation. The H278Y mutation of subunit SDHC was with 36.8 % of isolates most common in *A. solani*. Remarkably, all identified SDH-mutant *A. solani* and *A. alternata* field isolates simultaneously carried a QoI fungicide resistance mutation.

8.P02. *Verticillium* wilt disease resistance protein Ve2 precursor and its orthologs in *Solanum*

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Verticillium wilt, disease, resistance protein Ve2, orthologs, Solanum

Verticillium wilt, caused by the soil-borne fungal species *Verticillium dahliae* and *Verticillium albo-atrum* is a serious disease of many plant species, including trees, shrubs, ground covers, vines, fruits and vegetables. The pathogen spreads in the plant through the vascular system which may become blocked, causing the typical wilting symptom.

Therefore selection of *Verticillium* resistant varieties of plants, including *Solanum tuberosum* is needed. Groups of proteins with anti-verticillium wilt properties have been identified. It is hypothesized that protein Ve2 can provide and increase resistance of *Solanum* species to *Verticillium*. Therefore, the search for Ve2 precursor proteins is of interest and the aim of this research was to detect orthologs of the Ve2 precursor proteins in *Solanum*.

Amino acid sequences were obtained from GenomeNet Database Resources and alignment was made using the BLASTP program across the protein database. Ve2 sequences were identified. Evolutionary history was inferred using the Maximum Likelihood method based on the JTT matrix-based model and the phylogenetic tree with the highest log likelihood (-3625.7770) was constructed. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. All positions containing gaps and missing data were eliminated. There were a total of 144 positions in the final dataset. Evolutionary analyses were conducted in MEGA6.

It was found that the Ve2 protein found in *S. tuberosum, S. lycopersicum* and *S. torvum* creates a clade in the phylogenetic tree, while the protein Ve2 precursor of *S. pennellii* with hypothetical protein EJD97 of S. chilense and protein SlVe2 precursor of *S. lycopersicum* creating a separate clade in the phylogenetic tree.

This information shows the available orthologs of *Solanum* proteins and gives interesting insights into the evolution of *Solanum* proteins which can be very useful for *Solanum* breeding. As *Verticillium* wilt disease is quite difficult to manage and results in yield losses, control strategies based on host resistance are seen as long-term, durable solutions. However, this is difficult to achieve given the complex genetic nature of the host and the challenges associated with resistance evaluation. The orthologs of *Verticillium* wilt disease resistance protein Ve2 precursor described here, which are able to provide and increase disease resistance in *Solanum* species may help to solve this persistent problem worldwide.

8.P03. Sytranspom: development of collaborative and innovative alert and decision systems promoting integrated protection against fungal potato diseases.

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Potato crop, Fungal pathogen, Molecular tools, Decision support system (DSS), Integrated pest management (IPM)

Fungal pathogens cause many damages in potato crops in Belgium and France. The main leaf fungal pathogens are *P. infestans* and *A. solani*, responsible of late blight and early blight respectively.
To improve decision support systems for the potato crop, the collaborative research project SYTRANSPOM started in April 2018 with the multidisciplinary expertise of four partners. SYTRANSPOM is structured around 4 main research axes: i) development of a cross-border collaborative platform to centralize knowledge and register new data, ii) development of laboratory qualitative and quantitative molecular methods to characterize fungal pathogens, iii) implementation of experimental field trials to obtain early diagnosis of infections, monitoring the development of diseases and improving integrated disease management, and iv) development of complete decision support systems. From 2018 to 2021, agronomic trials were done with a triple objective (i) to monitor the late blight epidemic and develop new analytical tools (ii) to improve the results of the FAST simulation model and (iii) to validate the efficiency of different fungicides. Visual observations were done (weekly assessments of the percentage of foliage destruction by the disease), as well as random sampling of symptomatic and not symptomatic leaflets to complement observations by molecular analysis. Some parameters were also analysed after harvest (yield, sizes etc.) and spore monitoring in air was achieved with spore trap placed nearby trials during cultivation. The trials set up in these four years allowed to validate the following points: i) The treatments carried out before mid-August did not provide any efficacy for mid-late or late varieties. This confirms that early blight is a disease often correlated with the onset of senescence, ii) all modes of action have shown comparable efficacies in the three regions, iii) due to the late onset of the disease, it is not possible to see a significant effect on yield and quality of the tubers. These results confirm that *Alternaria* is a secondary pathogen on potato in France and that treatments before August are very often useless. The symptoms predicted by the two models (P-Days coupled to FAST modified) showed a good correlation with field observations and with the spore monitoring in air by spore trap. The authors thank the ERDF of the EU for funding this research project SYTRANSPOM (Interreg France-Wallonie-Vlaanderen).

8.P04. Aphids and aphid-borne potato viruses (PVA and PVY) in Norway

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seed potato, PVA, PVY, aphid vectors, transmission

The aphid-transmitted potato viruses A and Y cause significant economic losses in the potato production in Norway, which is based exclusively on domestic produced seed potatoes. A project that aimed to reduce the prevalence of the aphid transmitted PVY and PVA in seed potatoes was carried out in 2016-2018. In order to reveal which aphid species that immigrate into the potato fields, and to what extent they transmit PVA and PVY, the geographical and phenological variation in the occurrence of aphid species and virus transmission in 11 experimental potato fields were studied in four potato varieties at five sites in South, East and Mid-Norway. No insecticides were used in these experiments. In addition, three spraying regimes for aphid control with the aim to prevent virus infection were tested in six experimental fields: Two treatments with flonicamid (Teppeki, ISKBC), weekly treatments with mineral oil (Fibro, Belchim) and a combination of the two treatments. All the experimental fields were placed in commercial potato fields with low levels of PVY and PVA and had some PVY and PVA infested plantlets in the plots. Aphids were caught weekly in yellow water traps throughout the growing seasons. Tubers were tested for virus infection before planting, potato leaves in the beginning of the growing season and immediately before harvest, and sprouted leaves from harvested tubers.

A total number of 73 aphid species was caught in the water traps at the five locations. The total amount of aphids and number of species were highest in Southern Norway (50 species) and lowest in Mid-Norway (10-19 species). Species known as vectors for PVY and PVA was amongst the most numerous at all locations. The level of PVY and PVA in the plants varied with potato variety, location and year. "Lady Claire" was always less infected by virus (0-21% infected plants) than "Mandel" (17-93%) and "Asterix" (1% in one experiment, and 18-85% in 10 experiments). Else, there was no clear relationship between virus infection level and location and year. The relationship with aphid occurrence are currently under analyzis. None of the spraying regimes had significant effect on the virus infection level in the variety 'Innovator', except in one experiment where all three treatments resulted in slightly reduced viral infection compared to the untreated control. The virus infection level was low in all the experiments, with only 2-12% infected plants in the untreated control and 0-8% infected plants in the treated fields. There were no significant difference between the different treatments.

8.P05. Cold atmospheric pressure plasmas (CAPs) for eradication of soft rot Pectobacteriaceae

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Soft rot, Cold atmospheric pressure plasmas, Pectobacteriaceae, Dielectric Barrier Discharge, Bacterial eradication

Soft rot *Pectobacteriaceae* are responsible for high economic losses in cultivation of crops, vegetables and ornamentals. Our research group studies the applicability of indirect and direct actions of cold atmospheric pressure plasmas (CAP) for eradication and limitation of the spread of soft rot *Pectobacteriaceae*. In terms of the indirect cold plasma approach, we synthetized the so-called post-plasma solutions of antibacterial and plant growth promoting properties by treatment of mineral salts solutions with direct current atmospheric pressure glow discharge (Patents 236665, 236377). The application of post-plasma solutions diminished soft rot disease. The observed antibacterial properties of these liquids were associated with the generated deeply penetrating, reactive oxygen and nitrogen species (RONS). Direct implementation of CAP showed, a 2 min dielectric barrier discharge (DBD) plasma exposure turned out to eradicate over 3.07 logs of *Pectobacteriaceae* cells from the surface of economically important seeds (Patent application P.438360). The antimicrobial properties of DBD were linked with denaturation and aggregation of bacterial DNA and proteins in addition to rupturing of the cellular membrane leading to outflow of the cytoplasm contents as visualized with confocal laser scanning and transmission electron microscopy. Also a 3-4% stimulation of seed germination and early seedlings growth (by 13.4%) was noted in the DBD-subjected plant seeds. The CAP-as innovative and eco-friendly technology show possibilities to limit the spread and economic impact of soft rot *Pectobacteriaceae*. Funding information: National Science Centre 2019/33/B/NZ9/00940

8.P06. Efficacy of biological and chemical products in control of Agriotes wireworms in potatoes

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Agriotes, wireworm, field trial, chemical control, biopesticide

Wireworms are serious pests damaging a wide range of agricultural crops. One of the most affected crops is potato, where more than half of the tubers can be damaged in case of heavy pest infestation. Due to the restriction of chemical insecticides, there is an increasing need in looking for new effective control measures for wireworms. The efficacy of various chemical and biological plant protection products in the reduction of potato tuber damages caused by wireworms was assessed in field trials carried out in Eerika experimental field (Tartu, Estonia) in 2020 and 2021. The following plant protection products were used: entomopathogenic nematodes containing Entonem (*Steinernema feltiae*), Larvanem (*Heterorhabditis bacteriophora*) and Capsanem (*Steinernema carpocapsae*), Attracap containing entomopathogenic fungi (*Metarhizium brunneum*), chemical insecticide Columbo 0.8 MS (a.i. cypermethrin 8 g kg-1), Force Evo (a.i. tefluthrin 5 g kg-1) and fertilizer Perlka containing cyanamide known as a repellent to wireworms. Used products reduced wireworm damages in potato tubers from 36.2 to 47.7% in 2020. Controversially, none of the used treatments reduced wireworm damages in 2021, when the weather conditions during the field experiment were extremely hot and dry. The results did not show principal differences in the efficacy between the biological and chemical products. Controversial results from different years showed that yearly climatic factors can heavily influence the control efficacy of wireworms.

8.P07. SYNAPTIC Project: creating a synergy between farmers, gardeners, and other stakeholders to eradicate late blight primary inoculum and adopt IPM control strategies

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Phytophthora infestans, potato late blight, primary inoculum, prophylaxis, integrated pest management

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 seeks 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 strain 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. In the end, efforts will be taken to inform stakeholders of the project's results with demonstrations, articles and conferences. Initial results have revealed that the 36_A2 strain is predominant. 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. A cultivar showcase will be 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 alone, showing good protection with a combination of IPM levers.

This action is being spearheaded by the Ministries for an Ecological Transition, for Agriculture and Food, for Solidarity and Health, and for Higher Education, Research and Innovation, with the financial support of the French Office for Biodiversity, with the fees for diffuse pollution coming from the Ecophyto II+ plan.

8.P08. Influence of glycoalcaloids in leaf extract of different *Solanum* plants on the growth of *Dickeya solani* and *Pectobacterium brasiliense*

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glycoalcaloids, potato soft rot, Dickeya solani, Pectobacterium brasiliense, Solanum spp.

Soft rot of potato tubers is caused by bacteria that belong to many species of two genera: *Dickeya* and *Pectobacterium* Plants of *Solanaceae* produce glycoalkaloids, secondary metabolites that contribute to plant pest and pathogen resistance. Glycoalkaloids (GLA) were obtained from leaves of nine potato genotypes: four cultivars, three wild species and two interspecific *Solanum* spp hybrids. S. *garsiae* was characterized by the highest content and the most complex composition of GLA (α-chaconine, he leaves, limited to α-solanine and α-chaconine, was observed in the cultivars Tajfun and Owacja and the wild species *S. chacoense* and *S. maglia*. The influence of GLA on the growth of two highly aggressive for potato tubers strains of *Dickeya solani* and *Pectobacterium brasiliense* was tested in this study. Bacteria were adjusted to OD600 = 1, equivalent to 109 CFU/ml, and diluted 10 times in Luria Bertani Broth. GLA was added to bacterial suspension to final concentration 0.8 mg ml-1. The bacterial growth was measured after 0 and 24 h of incubation at 25°C and 150 rpm/min. The growth of bacteria was inhibited by all tested GLA extracts. The highest inhibition of both tested bacteria was observed for GLA obtained from *S. maglia* , DG 00-683 and cultivar Tajfun. *S. maglia* and cultivar Tajfun were characterized by high content of α-chaconine and α-solanine in equal proportions. The composition of GLA in DG 00-683 was more complexed, and the content differed from the highest to lowest as follow: α-chaconine > α-solanine > α-solamargine > α-solasonine. The inhibitory effect of GLA isolated from all tested potato genotypes was similar for *D. solani* and *P. brasiliense* (correlation coefficient r =0.98, $P < 0.05$).

9. Genetics & genetic resources

9.P01 Collection, maintenance, and use of tetraploid potato varieties in the Polish Potato in vitro Genebank.

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Potato Genebank, in vitro plants, variety, genetic resources of potato

Potato in vitro Genebank was established in 1981 in the Plant Breeding and Acclimatization Institute - National Research Institute in Bonin, Poland. The main task of the Genebank is collecting, maintaining, and long-term storage of tetraploid potato genotypes in form of in vitro plantlets.

Currently, the collection of potato genotypes includes 1621 varieties from around the world, of which 18% (288 varieties) are Polish and 82% foreign genetic objects, respectively. The oldest Polish genotypes in the Genebank are Marius from 1894 and Świteź from 1902, and the newest are Karat, Lenka and Meluzyna entered in 2022 to the National Register of Varieties.

The source of plants maintained in the in vitro Genebank are potato tubers, free from quarantine organisms like *Clavibacter sepedonicus* and *Ralstonia solanacearum*, as well as PSTVd. Before depositing in the Bank the potato plants are subjected to 3-week thermotherapy for virus elimination. Plantlets grown from meristems are 2-3 times controlled by DAS-ELISA assay for the presence of PVA, PVX, PVS, PVM, PVY, and PLRV. Only plants free of the quarantine objects and the potato viruses can be introduced into the Genebank collection. All stored gene resources are described in detail and valorized for the botanical and functional characteristic in field conditions during the annual identification.

The resources of the Genebank are a huge genetic wealth of the assembled features and starting base for potato breeding, research works, as well as for seed production.

The work was carried out under the task 1.2 Targeted Grant entitled "Ex-situ preservation of genetic resources of agricultural crop plants, financed by the Polish Ministry of Agriculture and Rural Development.

S9.P02 Characterization of the accessions of potato relatives preserved in Plant Breeding and Acclimatization Institute in Poland

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Solanum species, dormancy, flesh colour, enzymatic discoloration, resistance to P. infestans

In changing climatic conditions, potato relatives are sources of desirable agronomical traits as well as of resistance to biotic and abiotic stresses. The goal of this study was to evaluate the accessions of potato species from the N.I. Vavilov Institute for Plant Genetic Resources (VIR), Russia preserved in IHAR-PIB. We selected 29 seed-preserved accessions of 26 potato species and characterized 10 clones from each accession. Morphological traits such as plant habit, stem colour, leaf, flower, fruit and tuber shape and other traits were described for 281 clones. To test the *P. infestans* resistance, laboratory detached leaflet/leaf assays were performed in four years, on two different dates each year and in two replications on each date. After two growing seasons in greenhouse, the tubers were collected, counted and weighted. To estimate dormancy period, potato sprouts were measured by electronic callipers for 15 tubers of each clone before planting. Flesh colour was evaluated for 5 tubers using the Minolta CR-400 Colorimeter and assessed on a visual 1 – 6 scale. Enzymatic discoloration was estimated on a 1 – 9 scale, where 9 means a lack of discoloration. Dormancy, flesh colour and enzymatic discoloration were assessed in two years. The characterized clones varied in tested phenotypic traits between species and also within the accession numbers. The susceptible, resistant and accessions segregating for resistance to *P. infestanswere* noted. Results of the dormancy estimation were also diversified from lack of sprouts for the accessions of *S. stoloniferumand S. aemulansto* the longest sprouts (around 12 cm) in *S. microdontum*. Clones with white flesh colour dominated among tested potato clones. Majority of the clones showed lack of enzymatic discoloration. All of the tested clones were preserved in vitro and such preservation will allow using in the future the acquired knowledge to identify the genes controlling several traits. Further phenotyping is in progress. The clones were genotyped using genotyping-by-sequencing within the G2P-SOL (EU Horizon 2020, 677379) project. Well-characterized clonal accessions will be easier to exploit in potato breeding programs.

S9.P03 Potato collection in the Czech Republic

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potato, Solanum L., genetic resources, in vitro culture

The mission of the potato genetic resource collection of *Solanum* genus in the Potato Research Institute Havličkův Brod is assembly, documentation, long-term conservation and guarantee for potato genetic resources in the Czech Republic. A part of this involves systematic study, especially of new obtained materials, their description and evaluation with recommendation of suitable donors of agronomically valuable traits and characteristics, development of the national potato database with passport and descriptive data unification based on GRINCZECH system and providing of genetic resources to inland and foreign users. The potato collection involves 2.682 in vitro entries.

The collected wide biodiversity of *Solanum tuberosum* ssp. *Tuberosum* varieties, *S. tuberosum* tetraploid hybrids and dihaploids combined with conserved accessions of cultivated and wild species represents a wide option for selection of donors possessing important agronomic and breeding properties for breeders and researchers. The work was solved with the support of funds for the National Program for the conservation and utilization of genetic resources of plants, animals and micro-organisms important for nutrition and agriculture Ref. 51834/2017-MZE-17253/6.2.3 and the Czech Republic's NAZV QK1910277.

S9.P04 Application of the PotatoMASH genotyping platform to a large panel of diploid potato breeding lines to drive progress towards Fixation-Restitution Breeding.

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Potato Breeding, Diploids, Genotyping, GWAS,

The DIFFUGAT project proposes a new breeding system called Fixation-Restitution Breeding, which allows predictable accumulation and fixation of biotic and abiotic resistances with yield, quality, and nutritional traits. In this innovative potato breeding system, self-compatible diploids are used to accumulate favourable alleles via rapid backcrossing schemes. These lines are subsequently used to rapidly transfer and fix the traits into tetraploid breeding populations by virtue of the ability to produce unreduced diploid pollen, producing viable tetraploids when used in 4x X 2x crosses. Potato breeders commonly serve several markets with their variety portfolio, such as processing crisps, processing fries, table firm, table semi-firm, export, or starch markets, each requiring a different suite of relevant traits. The partners in the project have accumulated a set of over 600 diploid lines that will serve as the basis of future Fix-Res breeding clones, and are trialling these genotypes to assess them for 20 important agronomic and traits quality (collectively called „utility traits") for the different market segments.

We aim to map those traits in the panel of diploid genotypes and to develop genomic tools for the accumulation and fixation of those traits in the Fix-Res breeding program. To mediate this, we are using a platform called PotatoMASH (Potato Multi-allele scanning haplotags), a pooled amplicon-based genotyping-by-sequencing approach based on GT-Seq. PotatoMASH scans allelic variation at 340 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. In this poster, we describe the latest results in the application of the PotatoMASH platform to the panel of diploid material that forms the basis of the Fix-Res Project.

S9.P05 Marker imputation and high-density linkage map construction using a skim sequenced diploid potato population

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Skim sequencing, imputation, linkage map, heterozygous, diploid With the low cost of next-generation sequencing, genotyping-by-sequencing strategies have become increasingly popular. In potato, those approaches usually involve a step of genome complexity reduction such as capture baits, amplicon sequencing (potatoMASH) or restriction-site associated DNA sequencing (RAD-seq). We choose a whole genome sequencing approach at low depth.

However, in outcrossing populations with unknown linkage phase, a very low read depth complicates SNP calling and the imputation of missing values.

We skim-sequenced multiplexed barcoded libraries of 1536 full-sibs descending from heterozygous diploid parents to an average read depth of 1.5x.

We aligned the resulting sequencing reads to a reference genome and enforced SNP calling based on known variant positions, because parental clones were already re-sequenced at ~20x depth. We used the sparse SNP calls available, within 0.1 Mb regions, to calculate the genetic distance (Euclidean) between descendants. Clustering based on pair-wise distances created groups corresponding to the transmission of parental haplotypes, which were then converted into a genotype call. Marker positions were filtered against non-segregation, non-biological transmission distortion ratio and aberrant recombination patterns between adjacent bins. This filtering resulted in 4893 female and 4735 male segregating markers, giving an average of one female marker every 149 kb and one male marker every 154 kb. The algorithm Smooth Decent was then used to correct for imputation errors. The cleaned genotypic data allowed to generate parental linkage maps and to find association with traits of interest via single marker regression. Genetic distances were calculated and compared to the physical distances of the reference genome.

As expected, recombination is restricted to euchromatic chromosome arms, whereas large pericentromeric regions were excluded from recombination. More striking were two non-recombining regions on chromosomes 3 and 10 as well as a 6 Mb inversion on chromosome 3 which were not reported in the less dense linkage maps previously generated on the same population. We also observed highly skewed marker segregation on chromosomes *1* (S-locus and *StSIEL*), and 11. In subsequent studies, we will use this population to map a variety of traits valuable for potato breeding including plant architecture, tuber number, production of unreduced pollen and desynapsis.

S9.P06 Analysis of cytosine methylation in genomic DNA of *Solanum × michoacanum* (+) *S. tuberosum* somatic hybrids

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epigenetic, potato, somatic fusion, MSAP, HPLC

Interspecific somatic hybridization is a useful breeding strategy that allows the production of novel genetic variability when crossing barriers exist between two parental species. Somatic hybridization results in changes in the structure and sequence of DNA and affects the epigenetic regulation of gene expression. Although the genetic consequences of somatic hybridization have been well documented, little is known on its impact at the epigenetic level. Previous analysis of the genetic composition of S. × *michoacanum* (+) S. *tuberosum* [*mch* (+) *tbr*] somatic hybrids evaluated by diversity arrays technology (DArT) markers indicated that 13.9 to 29.6 % of the markers that were present in fusion parents were lost in hybrids. The explanation of this phenomenon may be the change in the methylation pattern in genomes of somatic hybrids. Digestion of genomic DNA in DArT technology is carried out with a methylation - sensitive PstI restriction enzyme. Changes in methylation pattern in somatic hybrids could change PstI enzyme digestion, resulting in different DArT patterns than in their parental forms. The aim of our research was to investigate the DNA methylation level of *mch* (+) *tbr* potato somatic hybrids. We used 96 interspecific somatic hybrids from five fusion combinations and their parents: diploid (2n = 2x = 24) clones of S. × *michoacanum mch*/8 and *mch*/39, interspecific potato hybrid DG 81-68, a dihaploid clone dHBard (2n = 2x = 24) derived from cv. Bard and a tetraploid (2n = 4x = 48) cultivar Rywal. Somatic hybrids from combinations mch/8 (+) dHBard; *mch*/39 (+) DG 81-68; *mch*/39 (+) dHBard are all tetraploid, and plants from mch/8 (+) cv. Rywal, *mch*/39 (+) cv. Rywal combinations have a ploidy higher than 4x.

To check the methylation changes in somatic hybrids methylation-sensitive amplified polymorphism (MSAP) and high-performance liquid chromatography (HPLC) methods were used.

Our results indicated that six MSAP primer combinations generated 622 unique bands, of which 295 were fully methylated. HPLC analysis showed from 15.5 % to 16.9 % of total cytosine methylation within parental forms. MSAP and HPLC methods indicated an increase of DNA methylation in somatic hybrids in comparison to their parents.

A lower degree of DNA methylation in the wild S. × *michoacanum* species than *S. tuberosum* was found. Our findings indicated that somatic hybridization changed the level of cytosine methylation in the studied potato somatic hybrids. The research was financed by grant UMO-2012/07/B/NZ9/01901 financed by the National Science Centre in Poland.

S9.P07 Genome sequence of the potato variety „White Lady" and its application in breeding

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bioinformatics, genome assembly, "White Lady", whole genome sequencing

Although large-scale sequencing of whole genomes has become routine, for most species with a reference genome, the reference represents no more than a few selected individuals, usually from one or a few breeds. Potatoe is one of the most important food crops worldwide, but its production is threatened by its sensitivity to biotic stressors. There are currently thousands of potato varieties, most of which are tetraploid, highly heterozygous. Sequence and structural differences between cultivars suggest that variety-specific reference sequences would be needed to make optimal use of the genome of a given variety. One of the results of the resistance breeding program in Keszthely, which has been running for about 60 years, is a variety called White Lady.

This variety contains the majority of resistance genes, such as PVY, PVA, PVV and extreme resistance genes against PVX, and *Phytophthora* resistance genes. Sequencing of the whole genomic DNA was performed on a NextSeq 500 (Illumina, USA) platform using a High-output 300 v2.5 sequencing kit at 40x coverage. Paired-end reads were assessed for quality using FASTQC and cleaned using Trimmomatic. Filtered paired-end reads were used with the SOAPdenovo2 assembler to generate an initial assembly. This assembly was fed to Chromosomer along with the SolTub 3.0 reference sequence to build pseudochromosomes. The initial assembly consisted of 448,469 contigs longer than 500 bp. While the total assembly size of 1.9 gigabases (Gb) was much larger than the estimated haploid genome size of ~844 Mb, it accounted only less than 60% of the tetraploid genome size indicating that a major portion of the genome collapsed during the assembly. The pseudochromosome sequence corresponding to all 12 chromosomes was assembled, with a total size of 1.4 Gb, more than one and a half times the reference size. This suggests that there may be significant sequence or structural differences between a reference and the White Lady genome. Less common potato breeds and local varieties are valuable sources of genes and alleles that affect tolerance to biotic and abiotic stress and other important traits. Given the key role of potatoes in world food production, the genomic sequence of such varieties and breeding lines provides a new resource. The resulting genomic information selection markers for already isolated resistance genes could be effectively developed.

On the other hand, the identification of yet unknown resistance genes and gene candidates becomes more efficient using the new genomic data.

S9.P08 Detection of genes for resistance to *Phytophthora infestans* in selected potato genotypes using PCR markers

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Rpi genes, resistance, late blight, Phytophthora infestans

Late blight, caused by the oomycete pathogen *Phytophthora infestans* (Mont.) de Bary, is one of the most economically damaging potato (*Solanum tuberosum* L.) and tomato (*Solanum lycopersicum* L.) diseases occurring worldwide. Resistance to *P. infestans* was the first trait that potato breeders searched for among *Solanum* species. Scientists identified and mapped more than 70 major resistance genes against late blight (Rpi genes), originating from *Solanum* spp. from Mexico, Peru, Argentina, Bolivia, Ecuador and Chile. These genes belong to the NBS-LRR gene family, and they are located in chromosomal clusters in the potato genome. The aim of the study was to use markers to diagnose the presence of 12 Rpi genes in selected potato genotypes. The material consisted of 223 potato genotypes including 110 potato cultivars, 60 breeding lines and 53 potato wild species. The PCR markers for the following genes- R1, R2 (R2-like, Rpi-blb3, Rpi-abpt), R3a, R3b, Rpi-phu1, R8, R9a, Rpi-chc1.1 (Rpi-ber1.1), Rpi-sto1, Rpi-pta1, Rpi-blb1 and Rpi-blb2 were taken from the literature or designed in this study on the basis of Rpi gene sequences available in databases. We used from 1 to 3 primer pairs for each gene. We confirmed the presence of Rpi genes in from 1 to 150 genotypes of the 223 tested ones, depending on the marker. We obtained 48 positive results for R1, 94 for R2, 118 for R3a, 122 for R3b, 14 for Rpi-phu1, 150 for R8, 1 for R9a and 77 for Rpi-chc1.1. For the Rpi 8_4F / R10 marker for the R8 gene, we got 150 positive results, but the band was weaker than the positive control. Such result for R8 may indicate the amplification of the product on the template of some homologue of the R8 gene. Similarly, a product of unexpected length was amplified using the marker for Rpi-blb2. Work is in progress as we continue scoring the presence of more Rpi genes, including Rpi-sto1 and Rpi-pta1.

S9.P09 StBBX24 affects the floral induction in cultivated potato

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The transition from vegetative growth to reproductive development is a critical developmental switch in flowering plants to ensure a successful life cycle and also has commercial significance for crop plants. However, while the genes controlling flowering are well-known in model plants, they are less well-understood in crops. B-box proteins named BBX comprise one of the essential family in plants. They play essential roles in regulating plant growth and development, including seedling photomorphogenesis, photoperiodic regulation of flowering, shade avoidance, and stress response.

In this work, we dissected the physiological function of StBBX24 in potato, a clock-controlled gene encoding a B-box protein located in the cytosol and nuclear chromatin fraction. We revealed that *Solanum tuberosum* lines silenced for *StBBX24* expression displayed much earlier flowering than WT plants. Conversely, plants overexpressing *StBBX24* mainly did not produce flower buds other than wild-type plants. Furthermore, RT-qPCR analyses of transgenic silenced lines revealed substantial modifications in the expression of genes functioning in flowering. It is noteworthy that genes promoting and repressing reproductive development exhibited up-and down-regulation at the transcript level, respectively. Altogether, these data reveal that StBBX24 participates in potato flowering repression.

S9.P10 Homologs of FAD7 encoding genes of *Solanum tuberosum*

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Solanum tuberosum, FAD7 encoding genes, adaptation mechanism, homologs, evolution Plants are known to be subjected to a wide range of temperatures. High temperatures increase the fluidity of the membrane, and the membrane lipids of plants are replaced by unsaturated fatty acids to maintain appropriate fluidity of the membrane. The previous studies have clearly demonstrated that fatty acid desaturase 7 (FAD7) greatly affects the composition of membrane lipids. At the same time plants with an altered saturation level of lipids show different temperature sensitivities at various stages of growth. FAD7 affects the composition of membrane lipids and responsiveness to temperature stress.

Solanum tuberosum is an important food crop, ranking fourth in the world in terms of growing. The actual yield of potatoes is significantly lower than its potential productivity. Decoding of the potato genome made it possible to use advances in molecular biology to study the role of individual genes and identify key proteins that can increase resistance to changing temperature. It is widely known that under the action of high temperatures, there is a phase transition of membrane lipids, which is accompanied by a decrease in membrane fluidity and loss of their barrier properties and, as a result, by inactivation of enzymes. In response to changes in physical properties of membranes, cells activate protection systems, among which an important role is played by the induced increase in the degree of unsaturation of fatty acids of membrane lipids. Therefore, one of the main goals of adaptation is the stabilization of membranes, for example, due to the work of enzymes, FAD7 encoded by genes FAD catalyzes the conversion of saturated FA into unsaturated.

The aim of the current study was to detect homologs of FAD7 encoding genes of *Solanum* using molecular phylogenetic analysis methods of Maximum Likelihood. As result, we obtained the phylogenetic tree of FAD7 encoding genes of *Solanum* which consisted of two clades. The first clade was formed by FAD7 encoding genes of *S. lycopersicum* and *S. pennellii*. The second clade of the tree included FAD7 encoding genes of *S. pennellii, S. tuberosum* and *S. pinnatisectum*. The results of our study display the evolution and biodiversity of FAD7 encoding genes and can be used in Solanum breeding in order to increase its adaptation mechanism.

S9.P11 Development of cryopreservation technology for implementation of the potato back-up collection

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A new method for long-term conservation of potato *in vitro* collection was developed at the Natural Resources Institute Finland (Luke). Through Luke's CryoPot project (Utilization of Cryotechnologies in the Implementation of a Cost-effective Potato collection), cryopreservation technology for potato was set up in 2019-2021.

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Potatoes have become even more important crop for human nutrition, and it is also introduced as a novel plant to guarantee food security in various parts of the world. Potatoes have recently been strongly featured in Finland to maintain national food security. Potato contains Vitamin C, and B and essential amino acids and proteins for human health. In addition, potatoes also have nutritional value as an important source of calcium, iron, phosphorus and potassium.

At Luke, the potato collection contains hundreds of varieties, breeding lines and research materials, which are maintained as microtubers *in vitro*. To keep them disease-free and genetically true-to-type, the microtubers are stored in test tubes in the dark at 4°C. The cultures, however, must be renewed each year. Cryopreservation, which is introduced as the latest method for preserving potato genetic resources, allows the materials to be kept deep-frozen in the cryobank for decades without separate maintenance efforts.

The management of cryo-methods at Luke is constantly being expanded for many plant species. The CryoPot project was designed to develop cryo-banking and to secure the management of national potato collection. Through the project, the method development of cryopreserving potatoes was started, and in 2021 the first varieties were frozen for the long-term preservation in a cryotank in Jokioinen. Sterile potato materials grown from micro-propagated shoots were pre-treated with appropriate cold pre-treatments before isolation of the meristems, and using antifreeze solutions before freezing. In the future, the cryo-banked material will be divided into two cryotanks located in two sites of Luke (Jokioinen and Haapastensyrjä) to maintain the storage security.

The results of the project can be used to increase national food security level in the long term. The further goal is to get additional potato genotypes into cryopreservation and to design more extensive use of cryopreserved potato material. Potato cryobank could be the basis of storing potato nuclear materials and for delivering them for other needs of use.

S9.P12 Identification of natural allelic variants associated with tolerance to water stress in diploid potatoes

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Aquaporin NIP 1-1, Aquaporin TIP, QTL-stress due to water deficit, aquaporin allelic variants

Potato is the first most important non-cereal food in the world and is fundamental in food security. One of the main abiotic problems that threaten the yield of this crop is stress due to water deficit. This problem is accentuated by the effect of climate change and climate variability.

Potato has been reported to be susceptible to water deficit; therefore, knowing its response at physiological and biochemical levels is very useful for understanding the trait in a more comprehensive way, as the same as for identifying allelic variants associated with these responses, which would allow identifying markers diagnosis of this type of stress. In this study, an association panel corresponding to the Potato Plant Breeding Program Working Collection was analyzed based on its response to stress due to water deficit, and these phenotypic data were associated with SNP-type molecular markers, with a matrix of 87,657 markers. Through the wide association of the genome and the candidate gene approach, allelic variants were found that identified candidate genes that encode proteins that act in response to abiotic stress, hormonal signaling regarding stomatal closure, and oxidative stress. From the Aquaporin NIP 1-1 and Aquaporin TIP aquaporin candidate genes, allelic variants associated with influence on the variables of stomatal conductance, relative water content, harvest index, and malondialdehyde content were identified. Information is generated from the discovery of genomic regions related to water deficit stress to continue identifying genes that code for proteins related to the hormonal, physiological and biochemical response to adverse environmental conditions that can be validated in potatoes and contribute to the understanding of this complex trait and can be used for future breeding programs.

10. Late blight

10.P01. Evaluation of different potato varieties and fungicide combinations for potato late blight (*Phytophthora infestans*) control in central part of Romania

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Potato, late blight (Phytophthora infestans), fungicides, varieties, yield

Late blight caused by *Phytophthora infestans* remains the greatest potential disease in Romanian potato crop. Late blight can destroy foliage prematurely and in short time, reducing production, while the tuber infections associated with rots can cause important crop losses during storage. National Institute of Research and Development for Potato and Sugar Beet Brasov is constantly working to create new varieties of potatoes adapted to changing climatic conditions, with high yield and disease resistance, according to the quantitative and qualitative requirements of consumers. Field experiments were carried out in the years 2018 - 2019 using a complete randomized block design with four replicates. Planting was made in 19 April 2018 and in 4 April 2019. In all cases, cultivation and maintenance was in line with current good agricultural practice. The eight potato varieties were examined regarding the foliage and tuber susceptibility to late blight and the disease development during the season. Late blight appeared on July 3, 2018, relatively late compared to previous years. The significant quantities of rainfall and the favorable temperatures of June, when an average of 18.1°C was recorded, provided the necessary conditions for the onset of the late blight epidemic.In 2019 the first late blight spots were observed very early, on May 30 at Brasovia variety. The relatively high volume of rainfall in May and June, together with the optimum temperatures, favored, besides the development of plants, the attack of foliar diseases, whose control was relatively difficult.In 2018, Christian variety showed the lowest level of resistance on foliage, followed by Brasovia variety. Castrum and Sarmis varieties have an medium attack. The varieties Sevastia, Asinaria and Marvis were situated towards the upper limit of the resistance. In 2019 from the studied varieties, Asinaria and Cezarina have the lowest level of attack, followed by Braşovia, Castrum and Sarmis varieties. Sevastia, Marvis and Christian varieties presented a higher level of attack. The aim of this work was to study the interactions between varieties resistance, fungicides application intervals and the specific climatic conditions.

10.P02. Metabolomics as a useful tool for breeders

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Phytophthora infestans, resistance markers

Late blight disease (*Phytophthora infestans* (Mont.) de Bary) (PI) significantly affects potato worldwide production. In cold and wet years, it can cause a reduction in tuber production of up to 90%. The main mechanisms of plant defence against fungal infections are structural defence mechanisms (mechanical barrier against penetration of the pathogen into the plant body) - higher thickness of cuticle, epidermis, and higher number of trichomes in resistant plants. The second type is biochemical defence reactions in plant cells and tissues after infection with the pathogen, resulting in the activation of compounds that inhibit the growth of the pathogen or are toxic to it. Targeting the search for specific molecules correlated with PI resistance in potatoes using metabolomic analyses may lead to a better understanding of the defence mechanisms of wild species. Initial experiments were aimed at searching for specific groups of compounds in leaves of susceptible/resistant genotypes. Analyses of these plant materials have found more than 50 metabolic markers positively correlated with resistance, including phenolic compounds and cysteamine, a compound with known antimicrobial activity. Continuing the metabolomic search for specific resistance molecules is proving to be a good way to select unsuitable breeding material *Solanum tuberosum* early. This work was supported by the Czech Republic´s NAZV QK1910045 project and the institutional support of conceptual development of research organization PRI Havlickuv Brod MZE-RO1622.

10.P03. The variability of *Phytophthora infestans* isolates collected from Estonian islands in the Baltic Sea

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Metalaxyl, late blight, mating type, virulence, SSR

Potato late blight caused by the oomycete *Phytophthora infestans* (Mont.) de Bary is on of the most destructive potato pathogen in the world. In this study populations of *Phytophthora infestans* from Estonian islands located in the Baltic Sea were characterized by mating type, sensitivity to metalaxyl, virulence on 11 potato R-gene differentials of Black and 12 SSR markers. Among the 193 tested *P. infestans* isolates from 2012 to 2014 from Estonian islands, 49% were A1 mating type, and 51% were of the A2 mating type. Isolates with both mating types were observed in each year and island. During the three years study period 2012–2014, 193 *P. infestans* isolates, collected from Hiiumaa, Saaremaa and Vormsi islands on 23 potato fields, showed quite a high and stable frequency of the A2 mating type, 53% of the total population, vary largely between islands 69% on Saaremaa, 49% on Hiiumaa and absent on Vormsi . In 87% of all sampled potato fields, both mating types were recorded, suggesting continuous sexual reproduction of *P. infestans* and possible oospore production. Metalaxyl-sensitive isolates prevailed in all three years (68 out of 99 isolates). Amongst the 95 isolates tested, 51 virulence races were found. The race structure was diverse and most pathotypes were unique, appearing only once; the two most common pathotypes, 1.2.3.4.6.7.10.11 and 1.2.3.4.7.10.11, comprised 35% of the population. The *P. infestans* population was genetically highly diverse and most of the multilocus genotypes (MLGs) appeared only once. Furthermore, all of the MLGs appeared in only one of the three sampling years. Our results confirm that the high diversity in the Estonian *P. infestans* population is most likely the result of frequent sexual reproduction, which benefits the survival, adaptability and diversity of the pathogen in the climate of North-Eastern Europe.

10.P04. Allelic variants of the NLR protein Rpi-chc1 differentially recognise members of the *Phytophthora infestans* PexRD12/31 effector superfamily through the leucine-rich repeat domain

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Late blight resistance gene, NLR cluster, Phytophthora infestans, RXLR effector, Leucine rich repeat

Phytophthora infestans is a pathogenic oomycete that causes the infamous potato late blight disease. Resistance (R) genes from diverse *Solanum* species encode intracellular receptors that trigger effective defence responses upon the recognition of cognate RXLR avirulence (AVR) effector proteins. To deploy these R genes in a durable fashion in agriculture, we need to understand the mechanism of effector recognition and the way the pathogen evades recognition. In this study, we cloned sixteen allelic variants of the Rpi-chc1 gene from *Solanum chacoense* and other *Solanum* species, and identified the cognate *P. infestans* RXLR effectors. These tools were used to study effector recognition and co-evolution. Functional and non-functional alleles of Rpi-chc1 encode Coiled-Coil Nucleotide Binding Leucine-Rich-Repeat (CNL) proteins, being the first representatives of the CNL16 family. These alleles have distinct patterns of RXLR effector recognition. While Rpi-chc1.1 recognised multiple PexRD12 (AVRchc1.1) proteins, Rpi-chc1.2 recognised multiple PexRD31 (AVRchc1.2) proteins, both belonging to the PexRD12/31 effector superfamily. Domain swaps between Rpi-chc1.1 and Rpi-chc1.2 revealed that overlapping subdomains in the LRR were responsible for the difference in effector recognition. This study showed that Rpi-chc1.1 and Rpi-chc1.2, evolved to recognize distinct members of the same PexRD12/31 effector family via the LRR domain. The biased distribution of polymorphisms suggests that exchange of LRRs during host-pathogen co-evolution can lead to novel recognition specificities. These insights will help future strategies to breed for durable resistant varieties.

10.P05. Influence of nitrogen supply on the susceptibility of potato germplasm to *Phytophthora infestans* in organic farming

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Nitrogen efficiency, Phytophthora infestans, Resistance, Organic Farming

Until today, late blight (*Phytophthora infestans* Mont. de Bary, P.i.) is of pivotal importance to potato (*Solanum tuberosum* L.) growers worldwide. This especially applies to organic farming where late blight control measures are restricted to the application of copper and to limiting plant density via crop management. Moreover, optimal nitrogen contents of the soil are more difficult to keep as compared to conventional farming. We thus started a project to analyse potential effects of nitrogen supply levels on the vulnerability of a panel of potato pre-breeding clones and current varieties. Our aim is to develop pre-breeding clones that exhibit adequate levels of resistance to *P.i.* under varying N supplies. The field trials will be carried out for three years at two locations in northern and southern Germany, respectively. The experimental approach includes the assessment of maturity-corrected late blight attack (ΔrAUDPC) in a randomized block design for three levels of nitrogen supply. Besides, a detached-leaf assay and tests on whole tubers and tuber slices will be conducted to record infestation of *P.i.* Field tests and detached-leaf assays started in 2020. A survey of first results indicates that both high and low nitrogen supplies favour infestation of *P.i.,* especially in susceptible breeding clones and varieties. These initial results suggest a need for potato cultivars in organic farming that come along with a genetically based resistance to late blight, which remains effective even under low nitrogen supply. With this in mind, JKI pre-breeding clones will be assessed.

10.P06. Late blight disease progress in Rpi-Smira/R8 potato plants

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late blight, Sarpo Mira, Rpi-Smira2/R8, resistance assessment, gene expression

Sarpo Mira, a Hungarian commercial variety, retains its high resistance to late blight (*Phytophthora infestans* (Mont.) de Bary) despite the high genetic variation of the pathogen and its ability to rapidly overcome new resistant varieties. Sarpo Mira has five major resistance *(R)* genes: *R3a, R3b, R4, Rpi-Smira1*, and the *Rpi-Smira2/R8* gene, the latter being a source of quantitative resistance that has been under further investigation since its discovery. Plants carrying only the *R8* gene and transgenic *R8* plants showed high and durable resistance in field trials, similar to that of Sarpo Mira. However, this was not the case when the *R8* plants were exposed to late blight under detached leaf assay conditions, where roots and meristems played an important role in the systemic resistance response. To further investigate this variation, we obtained *R8* plants from crosses between Sarpo Mira and four susceptible commercial cultivars (Rioja, Lusa, Colomba, Sylvana) to show the influence of genetic background on resistance levels. The R8 plants were transferred, maintained and propagated in in vitro cultures together with the parental lines. For the resistance tests, the *R8* plantlets were inoculated with several foreign and Slovenian isolates of *P. infestans* with different levels of aggression. Plantlets were visually inspected for the presence and development of late blight and scored using a 0 to 8 rating scale, with 0 representing no symptoms and 8 representing plant leaves completely covered with *P. infestans* mycelia and sporangia. The results obtained showed the susceptibility or resistance to late blight for each *R8* genotype, which was then compared with the susceptible and resistant parent cultivars. Several *R8* genotypes showed milder late blight symptoms after inoculation with aggressive *P. infestans* isolates than the corresponding parent cultivars. One *R8* genotype even showed similar resistance to late blight as Sarpo Mira. This particular *R8* genotype was selected for further analysis using RT-qPCR, where we monitored the expression patterns of the *R8* gene along with its counterpart, the effector gene AvR8, at two and four days after inoculation with *P. infestans*, with particular attention to the time before signs of infection were evident. This research will make a valuable insight to understanding the contribution of the *R8* gene to late blight resistance and further demonstrate the enduring potential of this gene and Sarpo Mira as an R8 gene donor in potato breeding.

11. Climate change (drought & heat resistance)

11.P01 Characterization of the effects of water shortage on potato

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1. INRAE APAALE,

Magnetic Resonance Imaging (MRI), Solanum tuberosum, water shortage, phenotyping, gene expression

Drought is a major problem affecting agricultural practices as a result of global warming.
Potato is considered as a drought sensitive crop, which results in loss of yield and tuber quality.
Further, water shortage may induce physiological disorders such as glassy tubers and internal rust spots. Potato response to drought is complex: it depends on cultivar, climatic and soil conditions and water stress timing within the growing period. Characterization of plant adaptive responses is a major issue in the field of phenotyping. There is therefore a demand for the emergence of analytical techniques that are non-invasive, allowing better performance of this phenotyping. This project aimed to benefit from innovative approaches in plant Magnetic Resonance Imaging (MRI) and molecular biology in order to evaluate the effects of water stress on plants during growing. For this purpose, plants were cultivated in pots under different water conditions. A variable water deficit (three water stress-rehydration cycles, with water stress corresponding to 20% of field capacity) was applied at different phenological growth phases (during tuber initialization and filling). The stress experienced by plant was evaluated through the monitoring of soil water potential and soil humidity. 3D morphological images of the underground part of the potato plant in pots were recorded on a 1.5 T MRI scanner (Avanto, Siemens). The number and the individual growth kinetics of potato tubers were extracted from the images acquired seven times during an eight-week growing period. Furthermore, to get an insight of the molecular adjustments in potato plants in response to external drought stimuli, expression patterns of selected drought-responsive genes were analyzed by qPCR. The approaches developed in the present study were shown to be effective to characterize plant response to water stress at different scales, from the tuber development to the gene expression. The results are discussed from the perspective of applying this methodology for phenotyping of plant under water shortage.

11.P02. Characterization of the effects of water shortage on four potato cultivars

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1. Agroscope
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Magnetic Resonance Imaging (MRI), Nuclear Magnetic Resonance (NMR) relaxometry, water shortage, phenotyping, Solanum tuberosum

The potato is the fourth most important food crop worldwide in terms of quantity produced after maize, wheat and rice with 370 million tons of potatoes produced in 2019. Potato is the most water-efficient crop, yielding 5600 kcal.m-3; over double that of wheat (2300 kcal.m-3). Nevertheless, potato is a drought sensitive crop, which results in loss of yield (over 60% in sensitive cultivar) and tuber quality (e.g., misshaping, glassy tubers, internal rust,…). Those loss are highly variable according to the cultivar. Characterisation of differences between susceptible and tolerant cultivar responses to water shortage is a major issue in the context of climate change. This project aims to seek whether innovative approaches such as Magnetic Resonance Imaging (MRI) and Nuclear Magnetic Resonance (NMR) relaxometry can be used to characterize the potato genotypic variability in plant adaptative responses to water shortage. For this purpose, four cultivars (Agria, Kennebec, Jule, Lady Claire) which represent a range of resistance to water shortage were cultivated in pots under different water supply conditions. A variable water deficit (two water stress-rehydration cycles, with soil dehydration corresponding to 20% of field capacity) was applied at different phenological growth phases (tuber initiation and filling). The stress experienced by plant was evaluated through the monitoring of soil water potential and soil humidity. The underground part of the potato plant was scanned at five times during a ten-week growing period using a 1.5 T MRI scanner (Avanto, Siemens). The number and the individual growth kinetics of potato tubers were extracted from the 3D morphological images acquired. Leaf water status was monitored by NMR relaxometry and water potential measurements at the start and end of the stress-rehydration cycles. Results will be discussed based on observed differences among sensitive/tolerant cultivars in term of tuber individual growth kinetics and leaf water status.

11.P03. The effect of drought and heat stress on potato tuber yield and quality

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potato, drought, heat, yield, genotype

During the growing season potato (*Solanum tuberosum* L.) plants are often exposed to soil drought, and often accompanying it heat stress which result in crop losses. In our experiment we assessed the impact of both stresses separately and simultaneously on tuber yield and quality. The following combinations were used: control -optimal irrigation and temperature 18/ 22oC, drought stress - without irrigation high temperature stress - maintenance of elevated temperature (38/25oC) and watering, drought + high temperature. Six potato varieties Aldona, Bojar, Irmina, Szyper, Mieszko and Otolia were tested. The plants were stressed 3 weeks after the tuberization process started.

Our results show that both stresses studied caused changes in tuber yield. Drought stress had greater impact than high temperature stress. The biggest changes, however, took place under of both stresses used simultaneously. There were significant varietal differences in response to both stresses.

The most reactive variety was Otolia, while the Bojar variety reacted the least. The applied stresses caused changes in the tuber size distribution and quality of the crop. The largest tuber diminution occurred under the stress of drought and both stresses simultaneously. A similar situation occurred with regard to tuber defects. Varietal differences were also noted. Each applied stress also decreased the dry matter and starch content in tubers. In general, drought stress had a greater impact on the tuber yield and its quality than the high temperature stress, while both stresses applied simultaneously caused the greatest losses in the yield.

11.P04. Agronomic and molecular analyses of drought stress in potato

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drought tolerance, physiological parameters, candidate genes

Water availability is probably the most important limiting factor in crop production and the potato is considered a drought sensitive crop causing significant yield losses. Therefore, the identification of water stress tolerant genotypes is a good strategy to deal with climate change. In this context, NEIKER has initiated a preliminary study to determine the behavior of potato varieties subjected to water stress. A field trial was carried out using 150 varieties in a randomized block design with two repetitions. The control plot was watered every week, while the plot under water stress was not irrigated. The irrigation doses were estimated using the model of the FAO56 dual coefficient. When the plants began to show the first stress symptoms, four physiological parameters were measured: Chlorophyll content (SPAD-502), Fluorescence (fluorimeter FP 100), Stomatic conductivity (Leaf Porometer) and Photosynthetically active biomass NDVI (RapidScan CS-45). Measurements were conducted at two different moments: 50 and 70 days after planting (DS). At postharvest also tuber yield and tuber number data were recorded. The ANOVA analyses for the physiological parameters revealed significant differences among varieties for all parameters except for SPAD. Average values for yield and tuber number were also higher in the control plots. For association mapping a total of 175 Candidate Genes (CG) were selected. After primer design a library of barcoded partial amplicons in exon regions of these CG was constructed for the 150 genotypes (GT) and sequenced. The obtained sequences were processed by in house developed software. GT and CG specific sequences were extracted and a list of CG specific haplotypes (“alleles”) was established and the allelic composition of each GT was determined. Each haplotype was converted into an “artificial” CG of presence/absence data (450 CG in total). These were used for association mapping using Proc GLM and Proc Stepwise with SAS. A total of 20 traits from control and drought stress plots were processed. Several parameters were evaluated which include effects of all CG alleles on all traits. Breeding values (BV) and model correlations between predicted and observed trait values were computed. Correlations ranged from 14 to 78% for CG alleles. Predicted progeny performance (PPP) matrixes were computed and the 100 top crosses were extracted from these matrixes. The obtained results are useful for performing promising crosses to accelerate breeding for drought tolerance and reduced sets of markers for validation.

11.P05. Spectral responses of greenhouse grown potato (*Solanum tuberosum* L.) cultivars to water restriction stress

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Abiotic stress, Potato, Cultivar differentiation, Spectral response, Remote sensing

Drought stress is one of the main abiotic factors reducing crop yields. It affects on several morphological, physiological and biochemical processes. Potatoes (*Solanum tuberosum* L.) are susceptible to water deficit, although some varieties show more drought tolerance. The objective of our research was to assess the spectral response of three potato cultivars with different drought tolerance in a greenhouse. Three potato cultivars were included in the study; KIS Krka (late, drought-tolerant), KIS Savinja (mid-early, moderately drought-tolerant) and KIS Vipava (early, drought-sensitive). The greenhouse experiment was carried out between April and August 2020 at the Agricultural Institute of Slovenia. Plants were divided in two groups, i.e. well-watered conditions (above 87 % of weight of saturated substrate) and water-restricted conditions (60-70 % of weight of saturated substrate). The treatment started approximately five weeks after planting and lasted for four full weeks. After that period all plants were watered to substrate saturation for four more weeks until the end of experiment. Tuber production in individual pots was assessed at the end of the experiment. Hyperspectral imaging in visible and near infrared (VNIR, 400-1000 nm) and shortwave infrared (SWIR, 1000-2500 nm) spectral regions were used to obtain spectral signatures of individual plants under control and water restriction treatment. Raw spectral data were radiometrically calibrated to radiance units. Reflectance data were smoothed by Savitzky-Golay gap smoothing, and 2nd order derivatives were calculated to remove scattering effect and emphasize spectral variations not evident in the reflectance data. By combining sparse partial least squares – discriminant analysis and support vector machines (sPLS-SVM) we achieved up to 100% classification accuracy for differentiation of cultivars, water regime and it's severity. Relevant wavelength bands were additionally identified by variable in projection scores (VIP). Several relevant wavelengths were identified for detection of water regime and cultivars; most of them in the SWIR region. The study demonstrated the usefulness of hyperspectral imaging for evaluating effects of drought and differentiation between cultivars. Findings are valuable for future work in breeding programmes. This study is also providing better insight into capabilities of remote sensing to assess abiotic stress in potato and the advantages of using it as a non-destructive method for phenotyping.

12. Post harvest & storage technology

12.P01. Changes occurring in potato tubers during storage in cultivars differing in soil drought tolerance

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potato, reducing sugars, respiration rate, storage, drought

Abiotic stresses during the growing season affect not only the level of the yield but also the commercial and processing value of the tubers. Processing quality has become increasingly important to the potato industry. The research was carried out on two potato (*Solanum tuberosum* L.) varieties with different tolerance to drought stress. Both varieties were cultivated in various moisture conditions: No stress, which uses the natural atmospheric conditions prevailing during the growing season and supplemented with water using drip irrigation and two combinations of drought conditions: 40 days stress at tuberizations, and intermittent drought (3 stress periods of 7 days). After harvesting, the tubers were stored at two temperatures, that is, 5°C and 8°C, for 39, 67, 143 and 164 days. The main aim of the research was the evaluation of the reaction of two potato varieties differing in drought stress tolerance to the accumulation of sugars and the respiration rate of tubers. It was found that tubers of drought stress-sensitive variety (Cekin) accumulated more glucose and fructose than tubers of drought-resistant variety (Tajfun), regardless of the type of drought applied during the growing season. The applied drought, both constant and intermittent, resulted in an increase in the content of reducing sugars compared with the control conditions. After applying both types of droughts during the vegetation period, the respiration rate increased during tuber storage. Larger changes were recorded in the case of an intermittent drought. At a higher storage temperature, in the variety resistant to drought stress, a decrease in glucose content was found after long-term storage, while in the sensitive variety, the content of this component increased, regardless of the moisture conditions during the growing season.

12.P02. Turning fridge unit around improves airflow in overhead-throw box stores

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Storage, airflow, box, refrigeration, uniformity

Ventilation is a key part of storage as it enables potatoes to be dried and cooled. In the UK potato stores, overhead throw ventilation is the most common type of box storage, especially for the fresh market which is served by many refrigerated stores of this design holding crop at 3-4°C. Typically, fans at one end of the store discharge air over the boxes using the store headspace to achieve circulation. Air then returns to the fridge via the pallet box slots. As this system is not positive, air returns by the easiest route, e.g. through the sides of the stack and top boxes, short-circuiting back to the fan. Recent R&D highlighted the inefficiency of these systems. A semi-commercial trial, funded by Innovate UK, showed only 31% of air reached the end of the store. Corners of the building were particularly prone to poor airflow leading to longer cooling time and poor evenness of temperature control, raising the risk of condensation. This can lead to disease and sprouting. Different box layouts were tested at the former R&D centre at Sutton Bridge. One such layout turned the fridge unit through 180° so the evaporator and return air intake faced the wall rather than the boxes. The trial showed better air distribution was achieved through the boxes across the width of the store, with less bias of air flow towards the centre of the store. Winters Lane Storage (WLS), a UK co-operative storing potatoes on behalf of its grower members, decided to test this set-up commercially. A comparison study between a conventional store and the new layout was assessed by Assimilate Systems and the former AHDB research team at Sutton Bridge Crop Storage Research (now closed). Airflow data showed the system with the reversed fridge worked better. It resulted in more uniform airflow through the boxes as the air returned along the pallet slots, compared with the conventional system. The difference was particularly striking in the central parts of the store with more event flow across the breadth of the building. Overall, commercial storage has been improved by the change in unit operation. Two further stores were fitted with the new layout in 2019/20 by WLS and a second business has reconfigured five stores during 2020/21 – see www.potatostorageinsight.com

13. Engineering, DSS & precision agriculture

13.P01 Agrotechnical procedures for establishing the potato crops in relation to water resource protection

Pavel Kasal, Ph.D.

de-stoning, weeds, mechanical cultivation, herbicide residues, nitrates

Limitation of using pesticides and fertilizers in water resource protection zones also applies to potato growers. Due to insufficient options of weed control with herbicides in potatoes working tools were designed and developed for mechanical weed management prior to emergence and at the beginning of potato crop emergence. The tools are intended for using in the de-stoning technology. Developing the working tools, an emphasis was placed to the gentle soil loosening in addition to weed destruction to prevent the support of soil mineralization processes, increase in CO2 emissions and soil water loss after more intensive soil aeration. The weed-killing efficacy of this measure was 6 % decreased compared to using of a pre-emergent herbicide. The combination of mechanical destruction and a post-emergent herbicide was 4 % increased compared to the conventional treatment. Similar results were also obtained for potato yield. Potatoes are often grown on sloped fields. To guarantee better retention of water from precipitation and erosion control small pits and tied ridges could be formed in the non-trail furrow and/or liquid mineral fertilizers could be applied into the potato root zone. This procedure results in reduced erosion risk and water resource contamination with herbicide residues, nitrates and other undesirable substances.

13.P02 Potato growing technology with using of drip irrigation

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Potato, drip irrigation, yield

Due to climate change irrigation becomes an important intensification factor in the potato growing technology. In the past, early potato areas situated in lowlands were only irrigated (via sprinklers), at present the lack of water has to be managed also in other regions. A possible option is using of drip irrigation system. Between 2016 and 2019 Potato Research Institute in Havlíčkův Brod (Czech Republic) realized a project directed to evaluation of new technological procedures for effective water management under drought conditions. Growing technology using drip irrigation combined with fertigation was verified. After the planting irrigation pipes were put under the soil surface on the ridge top. In years 2016 – 2018 two varieties differing in growing season duration were used for planting – early variety Monika and medium-early Jolana, Five variants of irrigation combined with N fertilization were established in four replications for each variety. A technique for irrigation management was determined based on soil conditions (M15 – from 15% soil moisture, M20 – from 20% soil moisture). N fertilization during the season was done in two variants: 120 kg N/ha prior to planting and 60 kg N/ha at planting + 60 kg N/ha in four irrigation rates (15 kg N/ha for each). In non-irrigated variant with fertilization during the season single N rate was spread on the soil surface in the same fertilizer. In the trials an effect of irrigation on all studied factors was detected. Potato yield was statistically significantly increased in variants with irrigation compared to non-irrigated variants. The results of recent years show that the potato yield was increased between non-irrigated variant and variants M15/M20 by 18.9 %/32.86 % (Monika) and 15.0/22.2 % (Jolana) in 2016. In 2017 a potato yield increase of 35.2 %/57.3 % (Monika) and 11.9 %/22.5 % (Jolana) was recorded, in 2018 the yield increase was 42.3 %/58.7 % (Monika) and 54.3%/54.6 % (Jolana). The way of nitrogen application (single rate or split rates) had no effect. The trial design was adjusted in 2019, namely different varieties were used (very early Rosara and medium-early Antonia). In this year no significant results were obtained and a negative tendency of the irrigation was determined. The reason was higher volume of precipitation, which highly exceeded long-term month normal in May, July, August and September.

13.P03 Detection of *Meloidogyne luci* infections in potato tubers using hyperspectral imaging and real-time PCR

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Meloidogyne luci, hyperspectral imaging, real-time PCR, Solanum tuberosum, latent infections

Root-knot nematodes (RKN, *Meloidogyne spp.*) are considered the most aggressive and economically important group of plant-parasitic nematodes, and are responsible for approximately 5% of global crop losses. They are also a limiting factor for potato production and tuber quality. *Meloidogyne luci* has a significant reproductive potential on potatoes. In this study we showed that *M. luci* can develop severe infection symptoms on tubers similar to those of quarantine pests *M. chitwoodi* and *M. fallax*. Furthermore, *M. luci* infection can result in latent infection (i.e without visible infection symptoms on tuber-surfaces), which may pose a high risk for uncontrolled spread of the pest via seed potato material. We developed two methods to detect *M. luci* in potato tubers. By using hyperspectral imaging and real-time PCR we were able to detect *M. luci* in both heavily infested potato tubers and tubers without visible symptoms, with high accuracy, up to 100%. In addition, these new methods were also able to distinguish between *M. luci* and *M. fallax*, with high accuracy. Identified relevant wavelengths for detecting *M. luci* infections indicate, that nematode infections alter the chemistry of potato tubers, and that plant immune response is systemic. We developed two methods for detection of potato tubers infected with *M. luci* based on hyperspectral imaging and real-time PCR, both of which can detect both latent and severe infestations, and are suitable for high-throughput screening. Testing of seed potatoes for presence of *M. luci* should be considered in phytosanitary surveillance programmes.

13.P04 Electrocution: a new way for potato haulm destruction

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Chemical alternatives, Electrocution, Haulm destruction

Introduction:
Haulm destruction of the potato crop is usually practiced to limit tuber damages during harvesting and the risk of bad evolution during storage (rots, weight losses, …). Due to prohibition of efficient chemicals (e.g. diquat), their replacement mainly by less effective ones and the wish to develop new agricultural practices less dependent on chemistry for better adaptation to consumer requirements, more or less innovative techniques have emerged to propose alternative solutions. Between optimisation of mechanical equipment (i.e. flailing, haulm pulling…), electrocution appears to be a real new approach for this operation.

Material and trials:
Since 2018, Zasso and Crop Zone companies have developed innovative machines combining electricity generator and application ramp for plants electrocution. Linked to the tractor PTO, the generator delivers a high voltage electricity (7000 to 15000 V) applied on the foliage via positive and negative electrodes. This electrocution damages the vascular tissues of stems and leaves which gradually witter. In collaboration with Nufarm, Crop Zone proposes to associate a preliminary spray of an electrolyte on the foliage to amplify the effect of the electricity (Nucrop system). This can also help to work on wider application ramp for an increased work rate. These two machines have been tested along the years on the experimental platform of ARVALIS-Institut du vegetal located in Picardy, North of France. Diverse varieties have been involved in these trials where main attention has been given on the following experimental conditions: advancing speed, number of passages and combination with a preliminary haulm topping.

Results and conclusion:
The observed efficacy on haulm destruction was mainly in relation with the initial importance of plant leaf development and the advancing speed. If one passage at around 5 km/h or more seemed sufficient for an acceptable result on a crop with a poor foliage development and near maturity, it seemed preferable to opt for a double pass or a pass after prior topping for an important and immature vegetation. Quality assessment made on tubers did not show any particular defects, internal or external, on the different tested combinations. If the effect of electrocution on soil biosphere needs to be completed, electrocution could become an interesting non-chemical alternative for potato haulm destruction due to its good efficiency. First of all, there is also the necessity to build an adequate economical approach for its use due to the expensive cost of the equipment.

13.P05 Use of drip irrigation with regard to the reduction of irrigation water in potato growing in the Czech Republic

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Drip irrigation, Soil moisture, Soil temperature, Water consumption, Moisture and temperature sensor

In the 2018/2019 season, field experiments with drip irrigation took place in the Czech Republic at two locations in the Vysočina Region (Valečov 49.643145, 15.497054 and Okrouhlice 49.625860, 15.505214). In the spring of 2018, the used agrotechnical procedures of soil preparation, work operations and other agrotechnical interventions on the established experimental plots were monitored. Measurements of physical soil properties were performed including sampling for soil analyses. Soil conditions, i.e. soil moisture and temperature in potato ridges, were being monitored starting from potato planting, during the whole vegetation period until harvest, especially in the root system of tubers. Other monitored parameters were the air temperature, rainfall and irrigation doses at the sites were monitored. The potato variety Antonia (medium early) was used on both experimental sites. At the Okrouhlice site, half of the experimental area was irrigated and half was left without irrigation. Irrigation was controlled using Virrib soil moisture sensors. Irrigation would be started when the soil moisture dropped under 15% vol. At the Valečov site, the monitored variants were 1) without irrigation with 120 kg/ha N before planting 2) irrigation at 15% vol. and with 120 kg/ha N before planting 3) irrigation at 15% vol. and 60 kg/ha N before planting and 60 kg/ha N before irrigation and 4) control variant without irrigation and without N. Irrigation regulation was controlled again by Virrib sensors. In both sites, drip hoses were installed and retrieved using burying and recoiling machine manufactured according to design by Research institute of agricultural engineering, p.r.i. The drip hose was placed to a depth of 5 cm from the top of the ridges and the tubers were at 15 cm. Moisture and temperature sensors TMS-3 and TMS-4 from company TOMST (Czech Republic), were used to monitor soil moisture and temperature on the experimental site. The sensors were installed in the upper and lower part of the ridge profile. The depths of the installations were 10 cm and 20 cm from the top of the ridge. The evaluation parameters of the quality of drip irrigation with regard to climatic conditions were the time intervals, frequency and the moisture in selected soil depths. From the trend of decrease in soil moisture after irrigation, it is possible to recommend lower irrigation doses around 4-5.5 mm, where the inefficient water consumption is lower than at doses higher than 6 mm.

13.P06 A new digital French fry quality assessment system for research

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Digital Assessment, French fry, Quality

Assessing baking quality of potatoes is a difficult topic. For research purposes a fine resolution of the baking colour in different segments for every single French fry within a sample is eligible. So far in most cases a visual scoring according to the USDA standard is done, which allows a differentiation between 0 = flawless and 4 = dark brown. The differentiation with only five classes is often not fine enough to detect small differences between variants in research. Furthermore human scorings always depend on environmental and subjective factors. Other approaches to rate baking quality are colorimeter measurements. Although these measurements itself are objective and steady, they are not suitable to depict a whole sample, as only spot measurements can be done with this technique. Here again biases can occur when selecting the spots for the readings. A few systems, which depict whole samples, are available on the market, but they only assess USDA scores with no further output.

In this poster a new assessment system will be presented, which is capable of recording whole French fries and output their baking colour in RGB values in different segments. The goal clearly was to neither work with a fixed assessment algorithm nor one acquired by AI. The reason therefor was that it again would be biased through the pre-set input data. Generating only an output of colour values allows every researcher to do their own calculations and scorings.

A photo box was built to enable standardised image taking. It is equipped with an industry camera, LED lightning and a drawer, in which samples - consisting of 20 French fries - are positioned on a removable tray. The camera is directly attached to a computer and a barcode reader. This enables seeing, naming and saving the picture at once. Pictures are taken from two opposite sides of the French fries to separate brown marks caused e.g. by bruises form physiological quality impairments.

In terms of image processing as first step an algorithm was trained to identifying French fry surface without the interference of visible potato skin or French fry edges. In a second step RGB values in means, medians and their standard deviations as well as min and max values of:
- whole French fry surface in the picture
- per French fry
- in lengthwise adjustable sections of every French fry were determined along with the length of every French fry. With the output as CSV file baking quality assessments can be done according to the needs of the research project.

13.P07 Defining new approaches for integrating remote sensing in on-farm-experiment potato research: results from a multinational experimental trials network

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High throughput phenotyping, NDVI, sensors, vegetation index, green fraction

Remote sensing technologies have been further developed and applied in recent decades for agricultural experiments. Those technologies can be used to evaluate experimental trials across multifunctional objectives, such as cultivar evaluation, irrigation strategies and crop nutrition. Previous studies have demonstrated the use of remote sensing in microplot experiments. However, remote sensing techniques represent a new way to characterize and analyse the interaction between experimental treatments and underlying spatial variability in field-scale on-farm experimental plots. The aim of this research was to develop a 'Protocol' for integrating high temporal and spatial resolution crop data for research experiments in microplot and field-scale on farm experimental trials. The 'Protocol' was developed from a programme of 'conventional' field experiments. Conventional plot measurements were compared with vegetation indices calculated from crop reflectance data. This data was acquired using different vectors (ULA, SpetrCam, ALPHI®) with a variety of mounted sensors (RGB or multispectral cameras) to provide information such as soil cover fraction, green fraction, vegetation indices (NDVI, etc.), height and leaf angle of the plant. As this data can be collected without damage to the crop, all these variables can therefore be acquired with a temporal kinetics. The 26 experimental trials on potatoes show the reliability of these technologies to identify different treatments, such as cultivar evaluation, nitrogen response curve, fertilizer evaluation The project has shown how analysis of crop sensing data can improve the efficiency of small plot and on farm research experiments. After three years of experimentation, consistent result and statistically significant correlations have been found between agronomical variables and vegetation indices. Moreover, trial results have allowed us to demonstrate a different way to phenotype the crop, according with the aims and budget of the experiment. For example, take one or two measurements at the beginning of the senescence phase and use a Vegetation Index directly linked to biomass in a non-saturated cover crop. This could be achieved with a simple Vegetation Index such as NDVI or CI-Green.

14. Processing (old & new products)

14.P01. Developing a new automatic tool for assessment of French fries colouration

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colouration after frying, French fries, algorithm, image analysis, machine learning

For more than seven years now, the amount of acrylamide in potato fried products is being closely monitored in the French fries industries as well as in the batches specifically marketed in the fresh market for home frying products. Acrylamide, a "probable" human carcinogen, forms in foods from a chemical reaction between asparagine, an amino acid, and reducing sugars such as glucose and fructose. This reaction is part of the Maillard reaction, which leads to colour, flavour, and aroma changes in cooked foods. Unlike other species, for potatoes, the acrylamide content of the fried products is closely related to the reducing sugar content in the tubers and to the colouration after frying. Therefore, these two parameters are particularly monitored by the operators and industrials for estimating in an easy approach the risk of acrylamide threshold exceedance. The colouration after frying also represents a quality standard which depends on the country where the French fries are marketed. Until recently the evaluation of the colouration after frying of French fries was made by experts only. Therefore, during the last two years, using machine learning and image analysis ARVALIS-Institut du vegetal has worked in the development of an algorithm to evaluate the colouration after frying of French fries after picture capture in a standardised photographic cabinet. Assessment was carried with the two main rating scales used in France. The first one is the USDA scale, used to range the colouration of the French fries in five classes (from 0 to 4, with three nuances of 0). The second one has been developed for the batches sold on the fresh market and presents six classes (from 0 to 5). From two datasets of 14 000 fries and 9000 fries respectively, the algorithm is now able to note as well as the experts with a R2 correlation from 85 to 88%. The equipment can also process a high quantity of images at once.

14.P02. Genotype-specific starch characteristics in relation to resistant starch formation in table potatoes

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Resistant starch, glycemic index, starch characteristics, pasting properties, warehouse potatoes

Table potatoes are important staple foods and rich in carbohydrates. Cooked potatoes have a higher satiety index but provide lower energy contents compared to other carbohydrate-rich products. However, potatoes also reach a higher glycemic index compared to rice, pasta and bread, leading to contradictory dietary recommendations regarding their consumption. It was the aim of this study to contribute towards resolving this contradiction by investigating molecular properties, pasting- and retrogradation characteristics of potato starches from table potatoes with a broad range of starch contents. Therefore, the table potato cultivar Huckleberry Gold, which was previously reported for a low glycemic index and five other common table potato varieties of different cooking types were used to investigate the starch digestibility after cooking of the tubers and molecular properties in isolated starches. First, the two varieties with the most divergent starch contents, estimated by under-water weight determination, were selected for cooking experiments. Fifteen tubers per variety were cooked until done. Subsequently, samples were kept at 4°C for up to 72 h. Determination of rapidly, slowly and total digestible starch, as well as resistant starch was carried out on freeze-dried raw tubers and cooked tubers directly, 24h and 72h after cooking. Based on these results, 24 h in the fridge at 4°C was selected as the post-cooking treatment for further investigations on the starch retrogradation properties of all six cultivars. In addition, starch from all six cultivars was isolated for characterization of important molecular properties, including granule size distribution, molar mass distribution, amylose/amylopectin ratio. Cooking was simulated on the isolated starches by pasting in a micro-visco-amylograph. The results show substantial differences in starch pasting and retrogradation characteristics among potato cultivars, also regarding the digestive characteristics, classified as rapidly or slowly digestible and resistant starch. Interestingly, the variety Huckleberry Gold formed resistant starch already shortly after cooking, whereas other varieties required longer cold storage to reach similar levels. This was also evident in the shift of molar mass distribution after pasting and during retrogradation. Hence, this study makes a valuable contribution towards a better understanding of the nutritional properties of potatoes.

14.P03. Oleogels as new alternative frying media for potato crisps and a replacement for conventional frying media

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Liquid oil structuring, rapeseed oil, sunflower wax, monoglycerides, sensory test

The deep-frying medium holds an essential role for deep-fried products. It transfers heat into the food and influence the formation of typical flavor, texture, rheological and sensory properties of final products. Deep-frying partially replaces the water present in the food with the frying medium. Consequently, the frying medium becomes an important component of the product. Texture and rheology of the frying medium are directly related to surface properties of the fried food and can be adjusted by using specifically optimized frying media based on palm oil or modified fats. A new alternative for reducing the proportion of saturated fatty acids (SFA) and replacing palm oil are structured oils, so-called oleogels, based on a liquid oil phase such as rapeseed oil combined with a structuring agent like sunflower wax (SFW) or monoglycerides (MG). Rapeseed oil is nutritionally valuable because it contains a high proportion of unsaturated fatty acids and is low in SFA. Melting the structuring agent in the oil and subsequent cooling cause it to form a 3-dimensional network in which the liquid oil is embedded. The liquid oil thus changes to a solid state and the nutritionally valuable fatty acid composition of the oil is maintained. The aim of this research is to replace conventional liquid oils or solid fats in deep frying process with oleogels consisting of structured rapeseed oil. This should improve the haptic properties, significantly reduce the content of SFA in the products and increase the content of mono- and polyunsaturated fatty acids. It was shown that the use of oleogels for deep frying is suitable for potato crisps and other food products. Oxidation stability of oleogels was comparable to that of conventional semi-liquid and liquid frying media. The firmness and oil holding capacity of oleogels were also comparable or higher than those of conventional semi-liquid frying media. In addition, the firmness and oil holding capacity remained constant over 40 frying cycles. However, the use of MG resulted in higher levels of polar compounds, a parameter for evaluating the condition of the frying media. With regard to the breaking strength and fat content of crisps, no clear effect could be determined by using oleogels as a frying medium. However, the color was affected positively, since a lightening of the crisps surface was measured. In terms of appearance, feel and mouthfeel, the crisps fried in oleogels were rated as less oily, representing an improvement in sensory quality.

14.P04. Quantification of nutrients, polyphenols and antioxidant activity in coloured potatoes by Raman and IR spectroscopy

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coloured potatoes, nutrients, antioxidant activity, quantification, vibrational spectroscopy

Coloured-fleshed potatoes become increasingly popular as a raw material in food processing and in human diet. They are characterized by a noticeably higher concentration of polyphenolic compounds (TPPs) than the more common yellow-fleshed ones. The content of nutrients and TPPs depends primarily on the plant variety but also on conditions of cultivation and storage. In potato originating products, the content of macronutrients and TPPs can be significantly affected by technological processes. From the other side, the properties and composition of potato tubers affect technological processes, yield and quality of the finished product. In potato industry, physico-chemical parameters and nutrients content are determined on the basis of separated, multi-stage protocols. They usually include extraction step, require dedicated analytical instrumentation and are laborious. In this report an effective procedure enabling simultaneous analysis of several components and parameters of lyophilized potatoes on the basis of their Raman, NIR and IR spectra is presented. Classification of the lyophilized potatoes was performed on the basis of their Raman and IR spectra using Principal Component Analysis (PCA) and clustering technique. Combining vibrational spectra and the results of reference analyses using AOAC methods, Partial Least Squares (PLS) regression models were built that enable protein, starch, total and reducing sugars, TPPs and ABTS antioxidant activity determination. To estimate quality of the constructed models and to compare them, relative standard errors of prediction were computed for the studied components and parameters. The obtained results demonstrate that infrared and Raman spectroscopy allow simultaneous determination of a number of parameters for the lyophilized potatoes based on their spectra recorded in 2-5 min. time. They can replace commonly used methods and effectively support raw material analysis in industry.

14.P05. Influence of blanching solution on quality of crisps from red- and purple-fleshed potatoes

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coloured potatoes, crisps, blanching, organic acids, bioactive compounds

The aim of this study was to determine the influence of type of blanching solution used in the processing of crisps made from coloured-flesh potatoes *(Solanum tuberosum* L.) on their quality. The content of bioactive compounds (total polyphenols, anthocyanins), antioxidant activity (ABTS and DPPH), colour, texture and organoleptic testing were made. The raw materials used were: three purple-fleshed potato cultivars (Königsblau; Blue Star; Blaue Elise) and three red-fleshed cultivars (Herbie 26; Königspurpur; Rote Emma). Potato slices were either blanched in water for three minutes at 80°C, or in 0.3% acid solution (citric acid or tartaric acid or acetic acid). The control sample excluded blanching. Technological treatments such as blanching and frying decrease anthocyanins content in crisps obtained from coloured-flesh potatoes. The use of suitable blanching solutions enables final products to be characterised by an attractive colour. Using organic acid solutions for blanching reduced the loss of polyphenolic compounds, including anthocyanins, during crisp production. Crisps obtained from potato slices blanched in organic acid solutions exhibited higher polyphenol content and antioxidant capacity compared with traditional processing. Acidic solutions positively influenced sensory attributes of resulting crisps such as taste and texture.

14.P06. Content of nitrogen compounds in potato tubers with red and purple flesh in juice and sprouts as a storage effect

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nitrogen, colour-fleshed potatoes, storing, juice, sprouts

The aim of the study was to determine the nature and magnitude of changes in total nitrogen, protein and non-protein nitrogen as well as amides in unpeeled potato tubers of five varieties with different flesh colour, in juice subjected to the process of elution adsorption, and in sprouts resulting from the storage of tubers for 4 months at 8°C. Samples of 20-30 kg of potatoes, five varieties: red-fleshed Herbie 26 (H26) and Highland Burgundy Red (HBR), purple-fleshed Olivia (O) and Vitelotte (Vi) from the test field at the station of the Central Institute for Supervising and Testing in Agriculture at Přerov nad Labem (The Czech Republic) from 2012 year were used for the research and yellow-fleshed Flaming (F) variety obtained from the Agricultural Experimental Station of the Wrocław University of Environmental and Life Sciences. Nitrogen compounds in the tested samples were determined by the Kjeldahl method. Protein nitrogen was precipitated with aluminum sulfate.

Regardless of the color of the potatoes examined, the content of nitrogen compounds in unpeeled tubers, juice and sprouts resulted from varietal features and different reaction of varieties to storage conditions. The impact of varietal variation on the content of tested forms of nitrogen in juice was much smaller than in tubers or sprouts. The highest total and protein nitrogen content was found in tubers of Vitelotte, Olivia and HBR cultivars, non-protein nitrogen in tubers of Vitelotte and HBR cultivars, while the most amides were found in tubers of HBR cultivar. The potato juice of Vitelotte variety had a higher content of protein than non-protein nitrogen and a higher content of amides than other samples. The potato sprouts of HBR variety contained the least nitrogen compounds, while the potatoes of Olivia variety had the most, especially non-protein nitrogen, including amide nitrogen. The storage of tested potato samples caused a decrease in the content of nitrogen compounds, especially protein nitrogen, to a greater extent in juice than in tubers. However, the content of non-protein nitrogen only slightly changed in tubers but decreased in juice, on average by about 12%. The share of amide nitrogen in non-protein nitrogen in the juice of the tested samples was 3 to 4 times smaller than in tubers. After storage of tested potato samples, an average of 3.74% of true protein content in tubers, 13.45% in the juice, and in sprouts of 13.91% this compound was found.

14.P07. Colour and flavour of potato protein preparations depending on the antioxidants and coagulants used

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Acidulants, chelating agents, potato protein preparation, volatile compounds

The aim of the work was to study the effect of the use of antioxidants, acidulants and calcium salts (for removing the pectin compounds) during the acid–thermal process to coagulate proteins on the colour and profile of the aromatic compounds of the obtained protein preparations. Fresh potatoes (Denar very early, edible variety) purchased in retail trade (Wrocław, Poland) and a commercially available potato fodder protein preparation (PPZ Niechlów S.A., Niechlów, Poland) were used in the experiment. The colour and profile of the aromatic compounds of potato juice (PJ) protein preparations were investigated following various process modifications. Several antioxidants (sodium bisulphate, tartaric acid, ascorbic acid), acidulants (tartaric, ascorbic and hydrochloric acids) and chelating agents (chloride, lactate and calcium hydrogen phosphate salts) used for pectin removal during the coagulation of the PJ proteins were evaluated. The use of NaHCO3 or ascorbic acid as antioxidants, in combination with CaCl2 or calcium lactate, followed by ascorbic acid in the acid–thermal coagulation of potato proteins, was the most effective at brightening the obtained protein preparations. Analysis of the volatile compound profiles of the potato protein preparations with the brightest colour showed differentiation between all tested variants. When compared with the industrial-type precipitate, we observed less impact of n-hexanal or total aroma composition on the odour-activity value (OAV). Considering n-hexanal as the most undesirable compound, we pointed out that the CaHPO4 variant, as well as ascorbate–lactate, led to the lowest impact on the off-flavour compounds.

14.P08. Potato consumption in Argentina: factors influencing preference for food safety attributes

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Consumers, Experimental Economy, Three-Way Tables

The Buenos Aires South-Earstern province is one of the most important potato production areas in Argentina (around 32,000 ha). In domestic market, fresh potato is sold mainly in greengroceries and in bulk, that is, without identifying the variety, the origin of the product or its nutritional content. Bearing this in mind, questions arise regarding our research: Do consumers value the quality attributes of potatoes related to food safety and nutrition? What demographic and socioeconomic factors influence? The aim of this work is to quantitatively analyze the association between consumer's characteristics and their preferences for potato food safety attributes. A Vickrey Second Price Experimental Auction was developed to analyze the willingness to pay for potatoes with lower agrochemical content and a complementary survey was carried out to collect information regarding their nutritional composition, among other aspects. Following other empirical investigations, students and employees of the Economics and Social Sciences School of Mar del Plata National University were recruited. The sample (n=155) was representative by sex and age, in according with the database of the School. In the Experimental Auction two potato varieties were used: Spunta -produced conventionally- and Frital INTA -produced with lower agrochemical content-. The statistical tests of Breslow-Day and Cochran and Mantel-Haenszel were applied to three-way contingency tables, which allowed analyzing the association between variables, stratifying by the groups in which the participants carried out the Auction and completed the survey. Among the main results, it should be noted that the nutritional composition and the lower agrochemicals content in potatoes, the information in this regard, the origin of potatoes and quality controls are issues that are affected by consumer's demographic and socioeconomic aspects. Although the results obtained are exploratory and cannot be extended to the population, this work is one of the few carried out in the country on potato consumption. It can guide the decisions potato sector stakeolders interested in differentiating the product and attracting new consumers, and for those in charge of formulating public policies on food and health. It is planned to continue the investigation, understanding the population of the City of Mar del Plata, increasing the number of cases and using other potato varieties and other production modalities.

14.P09. The influence of processing of red-fleshed potatoes onto dried diced potato and French Fries on the contents and the compositions of anthocyanins

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Red-fleshed potatoes, Dried diced potato, French fries, Anthocyanins

The aim of the work was to determine the impact of the technological process of dried diced potato and French Fries producing from potatoes of red-fleshed Herbie 26 variety on the content of the sum of anthocyanins and their profile. The material used for the study were potatoes of Herbie 26 variety with red flesh. Samples of potatoes were divided into three parts for analysis in the raw material, for the preparation of potato cubes and fries. The dry matter, starch content, total and reducing sugars as well as the sum of anthocyanins were determined in the raw material. Potato cubes were made from peeled tubers, after cutting them (10x10x10cm), blanching in water (75°C / 5min), pre-drying at 120°C / 1 hour. and final drying at 55-60°C to obtain 10-12% moisture level. French fries were prepared by two-stage frying in rapeseed oil at 175°C, after peeling the tubers, cutting them into 10x10mm strips, blanching in water (75°C / 5min.) and drying at 30°C. Quantitative and qualitative anthocyanin determination using HPLC-PDA and UPLC-q TOF-MS / MS was performed in samples taken during the production of potato cubes and French fries. Based on the conducted research, it was found that potatoes of Herbie 26 variety can be recommended for the production of dried cubes and potato fries due to the suitable chemical composition of tubers, especially the low content of reducing sugars (0.24%). Pelargonidin 3-feruloylrutinoside-5-glucoside accounted for the largest share in the sum of determined anthocyanins (50%). Processing of red-fleshed potatoes into cubes and fries affected the losses of the studied anthocyanins. The largest losses of these compounds were found after final production processes, i.e. pre-drying, drying or frying. Potato cubes contained 9% of the initial amount of anthocyanins, while fries only 1%.

15. Physiology

15.P01. New sights on 30 years-legacy database about potato nutrition trail network: climate trends and cultivar responses in France

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Climate change, Nitrogen Use Efficiency (NUE), cultivar, legacy data base, field trail network

Over recent years, in France, the first evidence of climate trends on agricultural yield can be observed since the middle of ‘90s. For the potato crop, these impacts can extend the duration of the potato’s growing season and frequency extreme events (heat and drought). Indeed, given sensitivity to these environmental factors, potato crop has implemented adaptation strategies, related to temperature and water availability. Within crop management, fertilization has to take in account these environmental factors and the adaptation strategies according to cultivars. Nitrogen (N) is an essential nutriment and plays a key role for both yield and quality. However, an exceeding quantity has a negative impact on tuber quality criteria and might drive to nitrate leaching and ammonia volatilization. Nitrogen use efficiency (NUE) is affected by environmental and genetic factors. Nitrogen use uptake and utilization efficiency (NUpE, NUtE) depend on physiological stages and cultivars. To study the impacts of recorded climate trends and varieties over NUE, we conducted the analysis over a legacy database about nutrient and irrigation management, with over 50 field trials, from the early ‘90s to 2019. The experimental trials studied 14 potato cultivars with different maturity characteristics in Nord and Centre of France, at around 30 different locations. Fertilization has been split from one to seven applications along the growing season. Each trial includes a Nitrogen Rate factor, most of the time along a nitrogen response curve, with different increasing applied nitrogen rates. Beside classical variance analyses, statistical processing includes models fitting of nitrogen response curve to determine optimal nitrogen amount. Further experimental studies are needed to better understand the interactions among climate, locations, and plant nitrogen management approaches. However, additional data can differentiate nitrogen management recommendations according to cultivar groups. This work could be implemented with the establishment of more differentiate cultivar panels to allow exploring further research protocol process.

15.P02. Assessment of physiological age of seed tubers of potato and the subsequent crop performance

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Potato (Solanum tuberosum L.), Physiological age, Metabolomics, Crop model, Decision support system

Physiological age is the physiological state of seed tubers of potato, which influences their productive capacity. It determines the potential for vigorous plant growth and delivering a high yield of the right quality. It is therefore of high agronomic and socio-economic importance. Physiological age is influenced by multiple interactive factors, primarily genotype, growth history, and storage conditions such as temperature. Physiological age is a trait of great complexity and lacks clarification of the environmental cues and understanding of the biochemical mechanisms. The main goal of this project is to study the development of physiological age of potato seed tubers and its impact on subsequent crop performance. We use four cultivars of contrasting maturity types and rates of physiological ageing, and store the seed tubers at different temperatures before planting. To study the physiological expression of ageing, we examine sprout growth of seed tubers during the storage season. To search for potential biochemical indicators of physiological age, we use two modern plant metabolomics platforms to analyse changes in the metabolite profiles of these cultivars in response to storage temperatures. After storage, the seed tubers are planted at multiple field locations in the Netherlands where both below- and above-ground crop performance throughout the growth season are assessed. Data collected will be applied in modelling 1) the development of physiological age depending on thermal scales during storage and metabolites dynamics, and 2) the impact of physiological age on crop performance and yield. We aim to account for Genotype × Environment interactions. We will evaluate the models developed during this project and apply them in decision support systems to improve crop management and reduce yield gaps in potato production.

15.P03. Influence of different nitrogen fertilization amounts combined with irrigation on the baking quality of French fry potatoes grown in Germany before and after storage

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Baking colour, Nitrogen fertilization, Irrigation, Storage

Baking colour of potatoes (*Solanum tuberosum* L.) is not only the basis for farmers´ payment, but also closely linked to acrylamide forming. As high quality raw material is easier to process, too, potato baking quality is an overall production chain issue from farmer to consumer. In Bavaria (South-East Germany) a serious French fry potato production started about 20 years ago. Since then different reports on quality impairment appeared. Nevertheless the effect of crop management on baking quality has never been examined in a scientific way under the unique Bavarian growing conditions. From previous research is known that potatoes are very sensitive to biotic and abiotic stress. Depending on the time, severity and duration of the stress occurrence, different baking colour related defects can develop. Two important abiotic factors are nitrogen fertilization and water availability. Facing climate change and stricter fertilizing regulations, their significance will become even more pronounced in the future. For those reasons field trials were conducted in 2019 and 2020 at the Research Station Roggenstein, Technical University of Munich, a site 20 km west of Munich, with the variety Innovator. The factors were (I) nitrogen application rates (0, 160 and 240 kg N ha-1) and (II) irrigation (rainfed / drip irrigated). Post-harvest yield and starch content were assessed, and quality was determined twice (two and five months after harvest) through opto-electronical assessment. For this of each plot 20 French fries of 20 tubers were fried for three minutes at 180°C. Bud and stem end were assessed separately in addition to the middle section. Overall frying colour was darker in 2020 than in 2019. Although 2019 was a very dry year, irrigation only had a small improving effect on potato baking colour after two months. After storage though frying colour of irrigated potatoes was significantly lighter than the rain fed ones, especially without N-fertilization. Yield increased significantly by 140 dt/ha and so did nitrogen efficiency with irrigation. 2020 on the other hand was marked by high precipitation in June (213 mm/m^2). For that reason, only a small positive effect on yield (+12 dt/ha) and no effect on quality due to irrigation was found. At the second quality assessment 2020 trial effects were overridden by senescence. In both years frying colour became lighter with increasing nitrogen application, especially at the stem end. Yield improved as well with higher nitrogen application but at the same time dry matter content declined.

15.P04. Biocomposite component for slow release of active soil minerals for plant nutrition

Andrea Svobodová

Potato, Biocomposite component, nutrition, soil

The basic function of any fertilizer is to supplement the supply of nutrients for cultivated plants. One of the disadvantages of fertilizers is loss due to abiotic transformation, reduction to an insoluble form or leaching due to high mobility. Sources of nitrogen and phosphorus can limit plant cultivation. Especially in the case of phosphorus, there are many forms, but in the insoluble mineral form it is unusable for the plant. Lithotrophic and autotrophic metabolism of some microorganisms affect the solubility of various mineral components. These microorganisms are characterized by colonization of the surfaces of solid inorganic substances. Based on these findings, a project was realized in the years 2019-2021 in cooperation with Teramed, s.r.o. and the University of Pardubice. The experiments were performed at Valečov Research Station in the form of pot trials. Two types of soils with different phosphorus content were included in the trials. The aim of the project was to develop and test a technical solution, which will be a biotechnologically produced component of mineral fertilizers based on the preserved form of lithotrophic microorganisms on the surface of particles of sparingly soluble mineral fractions. After application in the environment, reversible hydration activates the biofilm and triggers lithotrophic metabolism, the outputs of which are local production of small amounts of acids, which contribute to the slow release of phosphorous and nitrogenous components in dissolved form for plant root systems. The results show that the stability of the biological material was confirmed on the basis of taxonomic analyses. The final form of the material was formulated and supplemented with calcium chloride, thus demonstrably strengthening the colonization effect by creating more stable and larger forms of colonized biomass.