



**21<sup>st</sup> Workshop, Ourense (Spain)**

**18-21 May 2026**

# **Book of Abstracts**

Universidade de Vigo

**GISA**

Grupo de Investigación en Sistemas  
Agroambientais



# TECHNICAL DATA

## Title

21<sup>st</sup> EuroBlight Workshop – *A potato late blight network for Europe*

## Editors

Laura Meno, M. Carmen Seijo & Olga Escuredo

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## Edition

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## PREFACE

Welcome to the 21<sup>st</sup> EuroBlight Workshop, held from 18–21 May 2026 at the University of Vigo, Ourense Campus. We are delighted to gather researchers, advisors, Agro-industry representatives, breeders and students from across Europe and beyond to continue the collaborative efforts that define the EuroBlight network.

Since its establishment, EuroBlight has served as a unique international platform for the exchange of knowledge on potato late blight and potato early blight pathogen characteristics, epidemiology, prevention and control. The 2026 workshop reflects both the increasing scientific complexity and the growing practical urgency surrounding the sustainable management of *Phytophthora infestans* and *Alternaria* species under rapidly changing agricultural, climatic, and regulatory conditions.

The scientific programme highlights advances across a broad range of disciplines, including pathogen population biology, fungicide resistance, epidemiology, host resistance, decision support systems, aerobiology, biological control strategies, and genomic technologies. Contributions from Europe, Latin America, Asia, and other regions demonstrate the truly global nature of the challenges faced by potato production systems and the value of coordinated international surveillance and research.

A major theme throughout this workshop is integration: integrating phenotypic and genotypic approaches; integrating resistant cultivars with forecasting and monitoring systems; integrating biologicals and reduced-input strategies into practical crop management; and integrating scientific innovation with policy and regulatory developments. The programme further emphasises the importance of collaborative infrastructures and shared facilities, including networks for aerobiology, whole-genome sequencing, phenotyping laboratories, and living labs for sustainable disease management.



The workshop also reflects the evolving role of EuroBlight as a community-driven initiative that not only disseminates scientific knowledge but also establishes concrete actions and working groups to address future challenges. Discussions during the subgroup sessions are expected to shape new collaborative activities leading towards the next EuroBlight workshop in 2028.

We extend our thanks to all speakers, poster presenters, session chairs, sponsors, and participants for their valuable contributions. Special thanks go to the local organising team at the University of Vigo for hosting the meeting and for their dedication in preparing this event in the beautiful region of Galicia.

We hope that the EuroBlight Workshop 2026 will stimulate new ideas, strengthen existing collaborations, foster new partnerships, and contribute meaningfully to the development of resilient and sustainable blight management strategies for the future.

On behalf of the organising committee,

21<sup>st</sup> EuroBlight Workshop Ourense, Spain

May 2026



## ***SPECIAL MENTION***

Dear Jens,

A new and well-deserved chapter in your life is close to begin and all members of Euroblight family would like to express our deepest gratitude for everything you have contributed over the years to the EuroBlight community and to potato research across Europe.

Your scientific leadership, generosity, and commitment have helped shape EuroBlight into far more than a research network. Through your work, you created connections between countries, researchers, advisors, and growers, always with the common goal of improving sustainable potato production and understanding late blight better. Your contribution has gone far beyond data, models, monitoring systems, or scientific papers. You have inspired collaboration, encouraged young researchers, and built a spirit of openness and friendship that has become part of the identity of EuroBlight itself.

Many of us will remember not only your scientific excellence, but also your kindness, calm perspective, enthusiasm, and willingness to help whenever needed. Although we understand that this moment marks the beginning of a more relaxed and well-deserved pace, we sincerely hope that EuroBlight will continue to benefit from your experience, insight, and presence for many years to come. Thank you for your years of passion, commitment, and friendship.

With sincere appreciation and warmest wishes for the future,

The EuroBlight family



Participants at the EuroBlight workshop, 2026 in Ourense, Spain (Photo: David Cooke).



## **ORGANISING COMMITTEE**

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## TIMETABLE SESSIONS AND PRESENTATIONS

<b>Monday 18 May</b>	
<b>18:00-21:00</b>	<p><b>Registration and mounting of posters, University of Vigo, Campus Ourense</b></p> <ul style="list-style-type: none"> <li>• Registration at the Faculty of Sciences, University of Vigo, Campus Ourense</li> <li>• Poster mounting</li> <li>• Welcome reception "Get-together" (from 19.00), Faculty of Sciences</li> </ul>
<b>Tuesday 19 May</b>	
<b>08:00 -08:30</b>	<b>Registration and poster mounting, Hall of the Faculty of Sciences</b>
<b>08:30-08:55</b>	<p><b>Opening and organisational remarks, Marie Curie Auditorium, Faculty of Sciences</b></p> <ul style="list-style-type: none"> <li>• EuroBlight - Opening of the workshop / <i>Alison Lees</i></li> <li>• Local organiser, University of Vigo, Campus Ourense / <i>Laura Meno &amp; Carmen Seijo</i></li> <li>• Vice-rector Campus de Ourense, Universidade de Vigo / <i>Francisco Javier Rodríguez Rajo</i></li> <li>• Manager INORDE / <i>Emma González Diéguez</i></li> </ul>
<b>Session 1 Plenary</b>	<p><b>Late and Early Blight, Status in Europe and Beyond (Marie Curie Auditorium).</b> <i>Chair: Jens G. Hansen, Sub-chair: Mout De Vrieze</i></p>
<b>09:00-09:20</b>	Late blight and early blight in Europe in 2024 & 2025 / <i>Isaac Abuley, Geert Kessel &amp; Hans Hausladen</i>
<b>09:20-09:40</b>	Update on the population of <i>Phytophthora infestans</i> across Europe via EuroBlight monitoring / <i>David Cooke</i>
<b>09:40-09:55</b>	Building a continental picture of <i>Phytophthora infestans</i> : population structure and emerging dynamics across Latin America through coordinated genotyping / <i>Florencia Lucca</i>
<b>09:55-10:20</b>	Discussion
<b>10:20-10:45</b>	<b>Coffee break and poster session</b>
<b>10:45-11:00</b>	United against potato late blight: the power of working together on phenotyping / <i>Lawrence Veryser</i>
<b>11:00-11:15</b>	From species to strains: CRISPR-Cas-mediated detection of bioaerosol environmental DNA enables strain-level late blight monitoring / <i>Weili Guo</i>



<b>11:15-11:30</b>	A remote field-based LAMP assay early warning system for fungal plant pathogens / <i>Guido Drago</i>
<b>11:30-11:45</b>	Real-time detection of <i>Phytophthora infestans</i> and <i>Alternaria solani</i> & <i>A. alternata</i> in the field using the SwisensPoleno Jupiter / <i>Tomke Musa &amp; Erny Niederberger</i>
<b>11:45-11:55</b>	Towards a more integrated control strategy for potato late blight. The added value of more resistant cultivars and spore traps / <i>Geert Kessel</i>
<b>11:55-12:10</b>	A European network on aerobiology (Spore traps and DNA methods) targeted crop health and disease early warning / <i>Carsten Ambelas Skjøth</i>
<b>12:10-12:30</b>	Discussion
<b>12:30-13:30</b>	<b>Lunch</b>
<b>Session 2 Plenary</b>	<b>Epidemiology and Host Resistance (Marie Curie Auditorium).</b> <i>Chair: Geert Kessel Sub-chair: Alison Lees</i>
<b>13:30-13:45</b>	Integrating host-pathogen dynamics and quantitative resistance for sustainable blight management in Solanaceous crops / <i>Remco Stam</i>
<b>13:45-14:00</b>	Emergence and detection of virulence towards host encoded late blight resistance / <i>Jack Vossen</i>
<b>14:00-14:15</b>	R-gene rotation in combined new genomic technologies and ICM strategies / <i>Kim Hebelstrup</i>
<b>14:15-14:30</b>	Resistant cultivars and decision support systems as the tools to significantly reduce fungicide use in late blight control / <i>Stany Vandermoere</i>
<b>14:30-14:45</b>	Discussion
<b>14:45-15:15</b>	<b>Coffee break</b>
<b>Session 3 Plenary</b>	<b>Control Strategies (Marie Curie Auditorium).</b> <i>Chair: David Cooke Sub-chair: Rebecca Joynt</i>
<b>15:15-15:30</b>	Control of late blight and early blight in Denmark without PFAS pesticides / <i>Lars Bødker</i>
<b>15:30-15:45</b>	Drivers of <i>Phytophthora infestans</i> population change in Denmark as a result of fungicide strategy / <i>Jens G. Hansen</i>
<b>15:45-16:00</b>	Late blight resistance management strategies: are we ready for the future? / <i>Faye Ritchie</i>
<b>16:00-16:15</b>	Discussion
<b>18:00-23:00</b>	Guided visit to the old town and dinner at restaurant Agape in the old town



### Wednesday 20 May

Session 3	<b>Control Strategies - continued (Marie Curie Auditorium)</b>
Plenary	<i>Chair: David Cooke Sub-chair: Rebecca Joynt</i>
08:30-08:45	The emergence and management of CAA and OSBPI fungicide resistance in <i>Phytophthora infestans</i> : A five-year European surveillance study / <i>Lorenzo Borghi</i>
08:45-09:00	Sagropia, how to include biologicals into blight management / <i>Bert Evenhuis</i>
09:00-09:15	Framework and pipeline for test of biologicals and alternatives / <i>Mout de Vrieze</i>
09:15-09:30	Epidemiology of potato late blight in Galicia (NW Spain) and on-farm validation of the NEGFY model for sustainable disease management / <i>Jonathan Castaño-Serna</i>
09:30-09:45	IPMorama: better integration of varietal resistance into the deployment landscape is essential for the successful future management of late blight / <i>Dan Milbourne</i>
09:45-10:00	The Regulatory framework in the EU status update May 2025 / <i>Albert Schirring</i>
10:00-10:15	Discussion
10:15-10:45	<b>Coffee break and poster session</b>
Session 4	<b>Alternaria (Marie Curie Auditorium)</b>
Plenary	<i>Chair: Hans Hausladen Sub-chair: Laura Meno</i>
10:45-11:00	Elucidating population structure, genetic diversity and host specificity of section <i>Alternaria</i> from diverse regions and wild and domestic host plants / <i>Gonne Clasen</i>
11:00-11:15	Global and regional diversity in <i>Alternaria</i> causing potato early blight / <i>Laura Meno</i>
11:15-11:30	Studies on fungicide sensitivity and fitness characteristics of <i>Alternaria solani</i> isolates / <i>Claire Haumann</i>
11:30-11:45	Overview of the current sensitivity of <i>Alternaria solani</i> to fungicides in Europe / <i>Gerd Stammler</i>
11:45-12:00	Studying wild relatives of potato to develop early blight-resistant cultivars / <i>Pieter J. Wolters</i>
12:00-12:15	Early blight control strategies / <i>Martin Teichmann</i>
12:15-12:30	Discussion
12:30-13:20	<b>Lunch</b>



### Wednesday 20<sup>th</sup> May, Parallel Sessions

Session 5	<b>Parallel subgroup meetings</b>
13:20-13:30	Introduction to parallel subgroup discussions <i>Geert Kessel, Alison Lees, Mout De Vrieze and Jens G. Hansen</i>
Session 5 A	<b>Subgroup - Control Strategies / Marie Curie Auditorium.</b> <i>Chair: Bert Evenhuis Sub-chair: Faye Ritchie</i>
13:30-13:45	Characterization of new resistance mechanisms for CAAs and OSBPIs in <i>Phytophthora infestans</i> and their impact on Late Blight control in potatoes / <i>Jürgen Derpmann</i>
13:45-14:00	Orbi-SIMS imaging to observe the spatial distribution of Amisulbrom within potato leaves / <i>Fabrice Robin</i>
14:00-14:15	Metalaxyl-M (Mefenoxam) in potatoes against Late Blight: a critical review of its role in modern potato production systems / <i>Myriam Van Hecke</i>
14:15-14:30	Monitoring sensitivity to fungicide active ingredients in the GB population of <i>Phytophthora infestans</i> / <i>James Lynott</i>
14:30-14:45	Leaf wetness climatology and forecasting in The Netherlands / <i>Bert Heusinkveld</i>
14:45-15:00	Discussion
15:00- 15:30	<b>Coffee break</b>
15:30-15:45	National-Scale EBH risk mapping for potato late blight in Ireland using interpolated historical meteorology and ensemble forecasts / <i>Sen Yan</i>
15:45-16:00	From smallholder to Intensive farming: testing the CARAH Model for onset of Potato Late Blight epidemic in Galicia / <i>Laura Meno</i>
16:00-16:15	Integrated crop management and taskforce Phytophthora / <i>Geert Kessel</i>
16:15-16:30	Discussion
Session 5 B	<b>Subgroup - Pathogen Characteristics &amp; Host Resistance / Salon de Grados.</b> <i>Chair: David Cooke Sub-chair: Geert Kessel</i>
13:30-13:45	High-throughput virulence assessment using detached leaf disc assays: validation through Whole Plant Phenotyping / <i>Steve Bicko</i>
13:45-14:00	Taking effectormomics to the potato field / <i>Amanpreet Kaur</i>
14:00-14:15	Integrating predictive models and agronomy for late blight control: a global company's experience / <i>Adrian Crucis</i>



14:15-14:30	Evaluating the success of 3 R-Gene late blight resistant potatoes in the diverse agricultural landscapes of Indonesia / <i>Philip Wharton</i>
14:30-14:45	First report of <i>Phytophthora infestans</i> self-fertile genotypes in potato crop in India / <i>Sanjeev Sharma</i>
14:45-15:00	Discussion
15:00-15:30	<b>Coffee break</b>
15:30-15:45	Field trials in Sweden of potato with changed expression of resistance and susceptibility genes / <i>Erik Andreasson</i>
15:45-16:00	Effect of infection with <i>P. infestans</i> on the potato plant microbiome / <i>Mout de Vrieze</i>
16:00-16:15	Hidden effector diversity in <i>Phytophthora infestans</i> : uncovering population structure beyond SSR genotyping / <i>May Bente Brurberg</i>
16:15-16:30	Discussion
17:00-23:00	Visit to Ribeira Sacra Heritage Site, Winery and Workshop dinner
<b>Thursday 21 May</b>	
Plenum 08:30-08:50	<b>EuroBlight: Future Shared Facilities, Coordination and Support actions</b> / <i>Jens G. Hansen, Mout De Vrieze, Geert Kessel &amp; Alison Lees</i>
Session 5 08:50-10:00	<b>Parallel subgroup meetings continued A, B &amp; C</b>
Control strategies - Marie Curie Auditorium: <i>Moderator: Bert Evenhuis, Secretary: Ruairidh Bain</i>	
<ul style="list-style-type: none"> <li>• Review the value of the fungicide tables</li> <li>• Framework and pipeline for test of biologicals and alternatives. Establish a EuroBlight working group with a mission</li> <li>• Network of Living labs in Europe re late blight management with less pesticides. Establish a EuroBlight working group with a mission</li> </ul>	
Pathogen and host resistance - Salon de Grados: <i>Moderator: David Cooke, Secretary: Geert Kessel</i>	
<ul style="list-style-type: none"> <li>• Network of phenotyping labs. Concrete actions in 2026. Establish a EuroBlight working group with a mission</li> <li>• Whole genome sequencing and marker development. Establish a EuroBlight working group with a mission</li> <li>• Aerobiology - spore detection and DNA sampling. Establish a EuroBlight working group with a mission</li> </ul>	
Alternaria - Class room B3: <i>Moderator: Hans Hausladen, Secretary: Laura Meno</i>	
<ul style="list-style-type: none"> <li>• Review the value of the fungicide tables</li> <li>• Concrete actions on <i>Alternaria</i> in 2026 and until next workshop</li> </ul>	



10:00-11:00	<b>Coffee break</b>
Session 6	<b>Plenary session in Auditorium- Outlook and New Initiatives – Reports and Discussion (Marie Curie Auditorium) Chair: Jens G. Hansen Sub-chair: Alison Lees</b>
11:00-12:15	<b>Report from the subgroups</b> <ul style="list-style-type: none"><li>• <i>Alternaria</i> Subgroup (<i>Hans Hausladen</i>) / 10 +5 minutes.</li><li>• Control strategies (<i>Bert Evenhuis</i>) / 10 + 5 minutes</li><li>• Pathogen and Host resistance Subgroup (<i>David Cooke</i>) / 10 + 5 minutes</li><li>• Outline of the EuroBlight statement 2026 (<i>Jens G. Hansen</i>) / 15 + 15 minutes</li></ul>
12:15-12:40	<b>Introduction to EuroBlight workshop 2028 – TBD</b> <b>Closing of the workshop / Mout De Vrieze</b>
12:40-13:00	<b>Sandwich To Go and Departure</b>
13:30-21:00	<b>Post workshop tour to Santiago de Compostela</b>



## Poster presentations

Lead author	Title
<b>Anna Gerdts</b>	Economic results of control programs with different doses in potato varieties with different resistance to late blight in southern Sweden 2018–2025, and considerations regarding PFAS/TFA-pesticides
<b>Elisa Vilvert</b>	Selection in <i>Phytophthora infestans</i> driven by fungicide use in Sweden
<b>Ruairidh Bain</b>	Selection for a <i>P. infestans</i> genotype resistant to metalaxyl-M by some cultivars more resistant to foliar blight
<b>Marta Janiszewska</b>	Population structure of <i>Phytophthora infestans</i> in Poland
<b>Manuela Hermeziu</b>	Evaluation of potato late blight in current climatic conditions in Romania, using fungicides, <i>Beauveria bassiana</i> and Neem oil
<b>Lawrence Veryser</b>	Capturing fungicide resistance selection: Evaluating <i>Phytophthora infestans</i> selection dynamics in a lab-greenhouse based assay
<b>Clarissa Grell</b>	Genotype x Isolate Interactions Drive R2 Resistance Performance
<b>Olga A. Oxholm</b>	Do R Genes Still Work? Assessing the effectiveness of single R-genes against novel <i>P. infestans</i> strains in Denmark
<b>Elina Seim</b>	Characterisation of <i>Phytophthora infestans</i> isolates from Norwegian potato fields
<b>Jonathan Castaño-Serna</b>	Spatial model of potato early blight risk in Galicia (NW Spain) based on vegetative development, TOMCAST, and Random Forest
<b>Phillip Wharton</b>	Monitoring fungicide sensitivity in <i>Alternaria</i> populations in the main potato growing regions of South Australia and Victoria, Australia
<b>Jeanne Simon</b>	Late blight situation in northwestern France explained through three years of trials and a specific case study within the IPMorama project
<b>Lea Vexler</b>	Developing processing potato germplasm with stacked late blight resistance in a variety-centric IPM framework
<b>Gabriel Dessiex</b>	Late blight population in Switzerland: current picture, future plans
<b>Vikrant Singh</b>	Identification and functional characterisation of an Rpi-R3a-like resistance gene from <i>Solanum bulbocastanum</i>
<b>Iris Visscher</b>	PhytoAlert-EU: a practical tool allowing for monitoring of virulence and protection of R genes
<b>Jérôme Cogniaux</b>	Fluazinam and its importance in resistance management programs
<b>Victor de Amorin</b>	Efflux pump modulation as a complementary strategy for disease management

## **ORAL PRESENTATIONS**

## **Session 1**

# **Late and Early Blight - Importance and Pathogen Characteristics - Status in Europe and Beyond**

*Chair: Jens G. Hansen*

*Sub-chair: Mout de Vrieze*



## Late blight and early blight in Europe in 2024 & 2025

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### Abstract

A Europe-wide survey was conducted to document potato late blight (*Phytophthora infestans*) and early blight (*Alternaria* spp.) epidemiology, fungicide use, and resistance management strategies during the 2024 and 2025 growing seasons. Responses were provided by national experts and advisory organizations from major potato-producing regions, including Switzerland, Serbia, the United Kingdom, Sweden, Spain, Finland, Iceland, France, Norway, Estonia, Denmark, Scotland, Germany, Flanders (Belgium), and the Netherlands. Late blight pressure varied markedly between years and regions. In 2024, many northern and western European countries experienced exceptionally high and continuous late blight pressure, driven by wet and mild conditions, resulting in intensive fungicide programs with up to 14–19 applications. In contrast, 2025 was generally warmer and drier, leading to lower or more episodic disease pressure and reduced fungicide use. Early blight occurred mainly under warm conditions, with variable importance between regions and increasing relevance in some production systems. Across both seasons, control strategies increasingly emphasize strict mixing and alternation of fungicides with different modes of action to mitigate resistance risk in both pathogens.

## Update on the population of *Phytophthora infestans* across Europe via EuroBlight monitoring

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### Abstract

The population of the potato late blight pathogen, *Phytophthora infestans*, is genetically diverse and highly dynamic; demonstrating marked population change over time and space across European potato crops. The pathogen population adapts to management practices with aggressiveness, fitness, fungicide resistance and virulence against blight resistance in cultivars recognised as the major drivers of population change. Our sampling and genetic fingerprinting of almost 23K samples from infected crops across Europe since 2013 indicates a mixed population structure with many long-lived clonal lineages, some of which survive from crop to crop for decades, and other sexual populations with ephemeral multilocus genotypes (MLGs) that appear locally in a single season only. These two populations reflect asexual inoculum surviving in tubers and sexual oospore inoculum in soil, respectively. The data in the EuroBlight database ([www.euroblight.net](http://www.euroblight.net)) indicates recent spreading clonal lineages with resistance to fungicides in the CAA and OSBPBI FRAC groups (EU43 and EU46) but also a newer lineage spreading due to its ability to overcome host resistance genes (EU47). We report on the spread and management of these and other lineages and how changing populations and Integrated Pest Management practices interact.

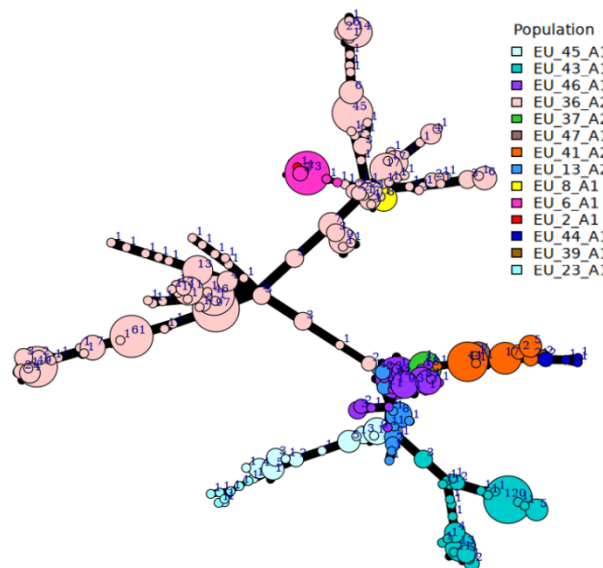


Figure 1. Minimum spanning network of 210 MLGs defined by SSR and representing 15 clonal lineages of *P. infestans* sampled from disease outbreaks in 2025 across Europe (1072 samples). Genetically diverse. Other types are not shown (571 samples).

**Keywords:** simple sequence repeat (SSR), population biology.

**Acknowledgements:** The EuroBlight consortium thanks the many commercial and academic research teams who have sponsored the monitoring program via the submission of samples and their metadata over the course of the program since 2013.

## Building a continental picture of *Phytophthora infestans*: population structure and emerging dynamics across Latin America through coordinated genotyping

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### Abstract

The Tizón Latino Network has consolidated a standardized regional strategy for the genotyping of *Phytophthora infestans*, using a common set of 12 SSR markers in multiplex format, fully aligned with the EuroBlight international protocol. Coordinated by INTA Argentina (EEA Balcarce and Biotechnology Institute, CICVyA, INTA Castelar), this initiative has enabled the analysis of more than 750 isolates collected from potato crops across 12 Latin American countries. The resulting continental dataset reveals a heterogeneous population structure. The clonal lineage EU\_2\_A1 appears predominant and stable in the Southern Cone, while Central America shows markedly higher genotypic diversity, including unique genotypes, the presence of US-7 and US-8 lineages, and reports of the A2 mating type (e.g. 13\_A2). These contrasting epidemiological scenarios point to different dynamics across the region. These findings provide key insights into potential migration routes, genotype displacement events, and inoculum flow within Latin America, while enhancing data comparability with global monitoring networks. Ongoing analyses incorporating newly collected isolates will further assess possible shifts in dominant lineages. An updated regional map and the latest results on population dynamics will be presented.

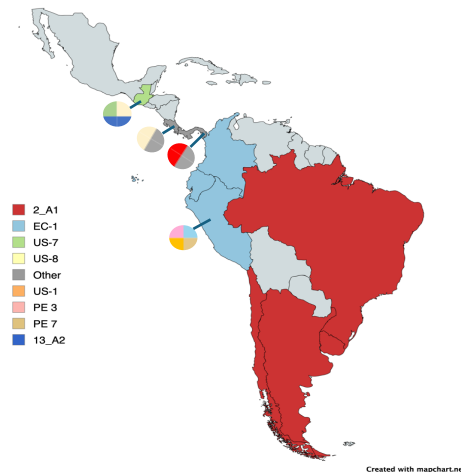


Figure 1. Genotypic distribution of *Phytophthora infestans* in Latin America based on 12-plex SSR genotyping (>750 isolates, Tizón Latino Network). EU\_2\_A1 predominates in the Southern Cone, EC-1 in the Andean region, and higher diversity is observed in Central America. Circles indicate genotype presence only (not proportional). Ongoing sampling aims to improve regional coverage.

**Keywords:** *Phytophthora infestans*, population structure, SSR genotyping, Latin America.

**Acknowledgements:** This work was carried out within the framework of the Tizón Latino Network and the FONTAGRO project ATN/RF-16678-RG. We thank all participating institutions and national potato programs for their collaboration in sample collection and technical support.

## Population Genetics and Fungicide Resistance of *Phytophthora infestans* in China: An Update

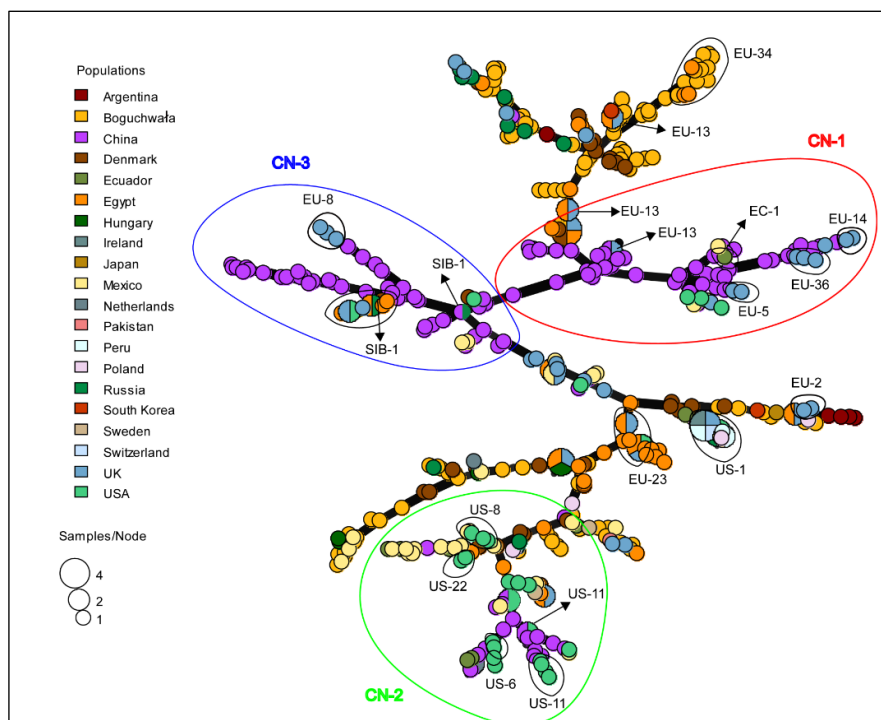
Chen, Han<sup>1</sup>; Zhang, Xinjie<sup>1</sup>; Wang, Xiao<sup>1</sup>; Zhang, Fan<sup>1</sup>; Zhang, Yiheng<sup>1</sup>; Guan, Tao<sup>1</sup>; Yin, Guoyu<sup>1</sup>; Song, Shengping<sup>1</sup>; Yu, Qianpeng<sup>1</sup>; He, Cheng<sup>1</sup>; Dang, Mingqing<sup>1</sup>; Dong, Suomeng<sup>1</sup>

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### Abstract

China is one of the world's largest potato producers globally, and late blight caused by *Phytophthora infestans* remains a persistent threat to food security. Current data indicate that the Chinese population comprises three distinct clonal lineages, with EU lineages predominating across major growing regions alongside the historically persistent SIB-1 lineage in northern China. The mating type distribution remains complex, with both A1, A2 and A1A2 types coexisting in several regions, indicating potential for sexual reproduction. Monitoring efforts reveal a widespread occurrence of resistance to metalaxyl. Notably, resistance to dimethomorph was detected only in 2023 in southeastern provinces. These strains exhibited reduced fitness and have since disappeared. Regarding OSBPI fungicides, resistant strains are emerging and spreading, conferred by point mutations in the target gene. These findings highlight the dynamic nature of the Chinese *P. infestans* population and the critical need for resistance management strategies. We present these updates to foster international collaboration on sustainable late blight monitor and control.



**Keywords:** China; population; mating type; fungicide resistance.

**Acknowledgements:** This research was supported by grants from the National Key Research and Development Program (2022YFD1400400, 2022YFC2601000 and 2022YFD1100202), National Natural Science Foundation of China (32488302) and earmarked funds from the China Agriculture Research System-potato (CARS-09-P20).

## United against potato late blight: the power of working together on phenotyping

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### Abstract

The rapidly evolving population of *Phytophthora infestans* continues to challenge late blight management across Europe, underscoring the need for coordinated, high throughput- phenotyping efforts. As new genotypes emerge through migration, mutation, and sexual recombination, gaining a detailed understanding of their phenotypic traits including, but not limited to, aggressiveness, virulence, and fungicide sensitivity—becomes essential for both research and industry. This initiative proposes the establishment of a collaborative, Europe-wide phenotyping network that unites academic institutes, industry partners, and existing national surveillance programs. By harmonizing methodologies and pooling datasets, the network aims to generate robust and comparable phenotypic profiles of *P. infestans* isolates, with a particular emphasis on dynamically shifting and understudied genotype groups. Such a shared framework will enable earlier detection of resistance development, strengthen genotype–phenotype associations, and support more informed agronomic decision-making. Beyond scientific outcomes, this initiative highlights the strategic value of collaboration: shared protocols reduce duplication, joint data interpretation accelerates learning, and cross sector engagement ensures that findings translate into practical, field relevant recommendations. Ultimately, a coordinated phenotyping network will provide EuroBlight participants with a powerful platform to monitor population changes, develop integrated control strategies, and collectively safeguard the sustainability of potato production across Europe.



Figure 1. Join the phenotyping network!

**Keywords:** Collaboration, Phenotyping, Late blight Management.

## From species to strains: CRISPR-Cas-mediated detection of bioaerosol environmental DNA enables strain-level late blight monitoring

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### Abstract

The increasing threat to European potato production posed by aggressive late blight strains (e.g., EU43) has intensified the need for effective tools capable of timely and accurate strain-level blight monitoring. Environmental DNA (eDNA) isolated from water, soil and air has emerged as a versatile and non-invasive tool for pathogen detection at both species and strain-levels. In particular, the detection of late blight (*Phytophthora infestans*) eDNA in bioaerosols enables tracking blight movement and implementing targeted interventions. In the AgSense project, we previously demonstrated a CRISPR-Cas assay for species-level blight detection with sub-femtomolar sensitivity. Building on this work, we established a strain-level assay capable of discriminating nucleotide-level mutation from wild-type sequences. Time-course optimization revealed that the assay distinguished mutant from wild-type strains on lateral flow strips within five minutes. To further enhance field deployability of the system, we integrated the species-level assay into multiple readout platforms. Lateral flow strips demonstrated the same level of detection capacity as fluorescence-based methods. Additionally, a single-tube colorimetric assay produced a distinct purple-to-pink visual shift of reagents in the presence of the target, with results verified using a UV imaging system. This single-tube platform potentially offers a more streamlined and cost-effective approach for point-of-need blight monitoring.

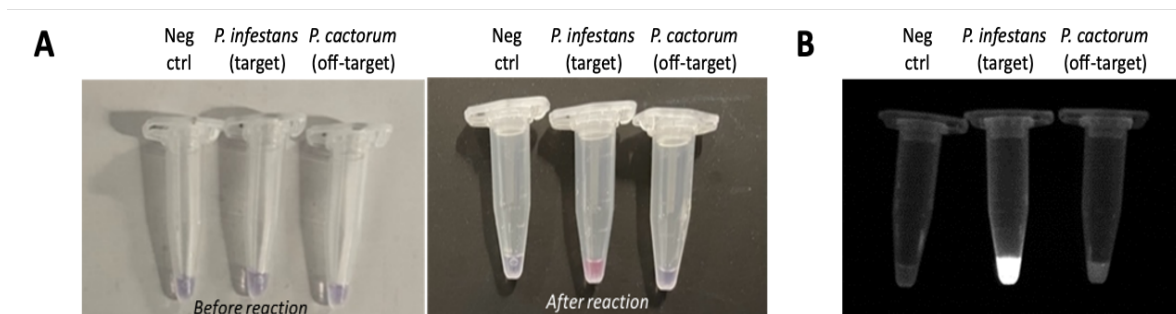


Figure 1. Development of the blight species-specific single tube assay (A) The reagent colour in the *P. infestans* (blight) tube changed from purple to pink after reaction. (B) A white glowing colour in the *P. infestans* (blight) tube under UV light verified the assay results.

**Keywords:** Strain-level, CRISPR-Cas, Bioaerosol, environmental DNA.

**Acknowledgements:** The research conducted in this publication was funded by Research Ireland National Challenge Fund under grant number [23/NCF/FF/11781].

## A remote field-based LAMP assay early warning system for fungal plant pathogens.

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<sup>1</sup>Polygenyn Ltd.; <sup>2</sup>Agri Samplers Ltd; <sup>3</sup>Plant Pathology and Aerobiology Lab; Rothamsted Research.

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### Abstract

In the European Union almost 1.3Mha of potatoes are grown, representing a value of close to 20 billion euros. Late blight caused by *Phytophthora infestans* causes annual losses (costs of control and damage) estimated at more than €1 billion euros. Chemical control is under pressure as fungal infections become increasingly aggressive. Here we report a field deployable instrument that samples air, captures oomycete and fungal spores and carries out LAMP diagnostic tests targeted to late potato blight remotely. Air is sampled at 200 Litres per minute over a 12-hour period. The instrument is primed with freeze dried stable LAMP reagents capable of carrying out multiple tests for different target pathogens, each day over a 7-day period without human intervention. LAMP assay results are assessable live via the internet. These LAMP assays detect less than 10pg of purified DNA, which is sufficient to provide an early warning of imminent infection in the field. This field instrument provides the farmer with an early warning system that enables targeted crop protection treatment only when required. The deployment of such technology will lead to reduced infection rates, increased crop yields and substantial monetary saving due to reduced crop treatment frequency.

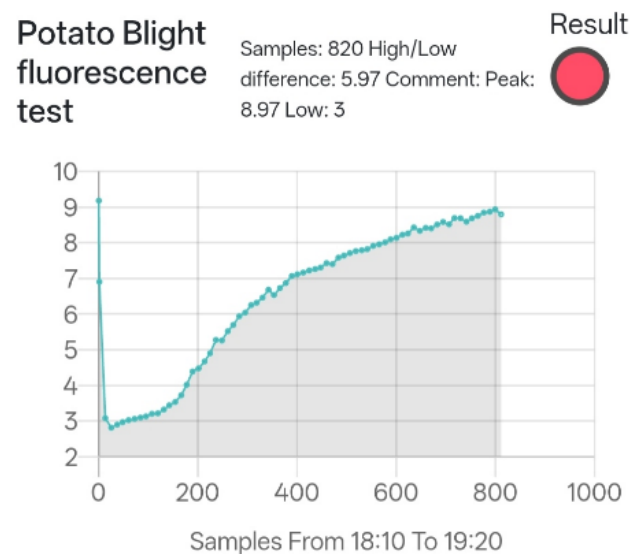


Figure 1. A representative positive LAMP assay result to late potato blight detected by a field deployed Auto Spore Trap.

**Keywords:** LAMP, airborne, fungal, pathogens.

**Acknowledgements:** This work has been funded by UKRI.

## Real-time detection of *Phytophthora infestans* and *Alternaria solani*/*A. alternata* in the field using the SwisensPoleno Jupiter

Musa, Tomke<sup>1,\*</sup>; Schwendimann, Andreas<sup>2</sup>; Zeder, Yanick<sup>2</sup>; Graf, Elias<sup>2</sup>; Gütlin, Haruna<sup>1</sup>; Kunz, Christa<sup>3</sup>; al Naser, Rafah<sup>3</sup>; Mascher, Fabio<sup>3</sup>; Lieberherr, Gian-Duri<sup>4</sup>; Erb, Sophie<sup>4,5</sup>; Clot, Bernard<sup>4</sup>; Bendinelli, Tommaso<sup>6</sup>; Dietler, Silas<sup>6</sup>; Niederberger, Erny<sup>2,\*</sup>

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### Abstract

Late blight (*Phytophthora infestans*) and early blight (*Alternaria solani*/*A. alternata*) are major potato diseases worldwide, spreading via airborne sporangia and spores. Late blight alone causes nearly €900 million in annual EU losses. Effective control requires timely fungicide applications. Current decision support systems (DSS) rely on meteorological data but lack real-time information on airborne pathogen abundance. The SwisensPoleno system can continuously monitor bioaerosols using digital holography, fluorescence, and AI-based classification. Field monitoring in Swiss potato fields (Zollikofen, Reckenholz) from 2023–2025 evaluated SwisensPoleno for detecting *P. infestans* sporangia and *Alternaria* spores, validated against Hirst-type traps. Detection succeeded, though low concentrations and variable morphology of *P. infestans* sporangia posed challenges. Best correlations were observed for *A. solani* ( $\rho=0.71$ ) and *A. alternata* ( $\rho=0.74$ ), while *P. infestans* reached  $\rho=0.65$  in 2024. Comparisons with SwissPollen rooftop stations operated by MeteoSwiss showed consistent regional correlations ( $\rho > 0.70$ ), indicating suitability for *Alternaria* monitoring. Further validation is needed for *P. infestans* and other SwissPollen sites. SwisensPoleno can reliably quantify *A. solani*/*A. alternata* in real-time and partially track *P. infestans* under favorable conditions. Real-time spore data could improve DSS like PhytoPRE and support an *Alternaria* DSS, but classifier accuracy, threshold definitions, and robust training datasets are needed for operational use.

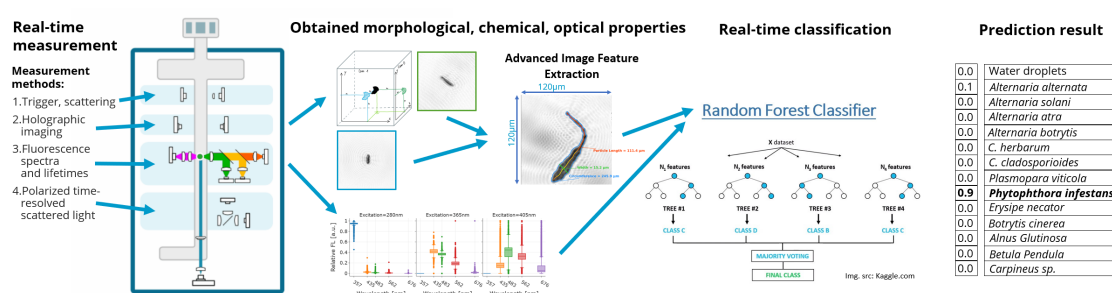


Figure 1. SwisensPoleno Jupiter air flow cytometer function principle (Sauvageat et al., 2020), showing two holographic images of a particle from different angles. The overall spore length is extracted using advanced image feature analysis. Below: Relative fluorescence data provide a chemical fingerprint of the particle (Erb et al., 2024). An example of the random forest-based model performing AI-driven classification in real time is shown. The classifier assigns each measured particle to a trained class with an associated probability.

**Keywords:** Airborne Plant Pathogen Detection, Automatic Spore Monitoring, AI, Classifier Validation.

**Acknowledgements:** Supported by FOAG, Fondation Sur la Croix, VSKP, Syngenta, the EU CHIPS Joint Undertaking, SERI, and the EU Horizon Europe project SYLVA (Grant No. 101086109).

## A European network on aerobiology (Spore traps and DNA methods) targeted crop health and disease early warning

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### Abstract

A number of plant pathogens, such as *P. infestans*, use the atmosphere as a vector and may episodically undergo long distance transport. An aerobiological network used for detecting these pathogens in the air can therefore be useful. Such a network may be part of an early warning system by detecting the pathogen before it is present in the crop. In the EU funded COST network ADOPT, a European-wide network for detection airborne spores was developed and demonstrated. Importantly, scaling from a single site to a network can make things that are trivial for individuals both a logistic and scientific challenge for the network -often dictated by the target organisms that and the resources at hand. By addressing challenges such as skills, infrastructure, sampling instruments and media, transport, ADOPT has created such a network covering North, South, East and Western parts of Europe. This network is designed for both optical and DNA analysis of the air, the later using both screening techniques such as metabarcoding and metagenomics and fully quantitative approaches based on digital PCR. The presentation will present recommendations for building a European Network and discuss current scientific challenges in analysing data from the network.



Figure 1. COST ADOPT campaign as executed in 2024. Left: Location of sites. Right. Multi-vial dry cyclone used for collecting material.

## **Session 2**

# **Epidemiology and Host Resistance**

*Chair: Geert Kessel*

*Sub-chair: Alison Lees*

## Integrating Host–Pathogen Dynamics and Quantitative Resistance for Sustainable Blight Management in Solanaceous Crops

Stam, Remco<sup>1\*</sup>; Einspanier, Severin<sup>1</sup>; Tominello-Ramirez, Christopher<sup>1</sup>; Ahmad, Farooq<sup>1</sup>; Delplace, Florent<sup>2</sup>; Raffaele, Silvain<sup>2</sup>; Witek, Kamil<sup>3</sup>; Chen, Yao<sup>1</sup>

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### Abstract

Historically, the management of both early blight (EB) and late blight (LB) in solanaceous crops has relied primarily on fungicide applications or, in the case of late blight, on dominant resistance genes. However, with the decreasing availability of permitted fungicides and increasing evidence of the rapid adaptation and evolution of the late blight pathogen *Phytophthora infestans*, and increased incidence of EB, there is an urgent need to develop alternative and sustainable strategies for disease control. We present a simple, low-cost phenotyping system designed to monitor disease progression under controlled conditions. Using detached leaf assays on crop wild relatives of tomato such as *Solanum chilense*, we demonstrate that plants can deploy multiple forms of quantitative resistance, including reduced infection frequency, prolonged lag phase (time until the first symptoms appear), and reduced pathogen growth rate against the EB pathogen *Alternaria*. These resistance mechanisms are genetically distinct and act independently. Through transcriptomic analyses, including weighted gene co-expression network analysis (WGCNA), we identify major quantitative disease resistance regulators associated with delayed symptom development and reduced lesion expansion. These findings reveal differential phenotypic responses, and thus different defense strategies among accessions. Screenings with different *Alternaria* isolates show strain-specific differences in pathogen-host interaction dynamics, which so far remain to be further investigated. Moreover, infection assays performed on these species and another wild relative, *Solanum americanum*, indicate a potential trade-off between resistance to late blight and increased susceptibility to early blight, suggesting underlying genetic and physiological constraints shaping disease resistance evolution. Finally, we discuss the relevance of this phenotyping system for advancing research on EB and LB resistance in potato and how our system can contribute to the development of data-driven decision support systems (DDS) to support more sustainable and targeted fungicide deployment. By integrating knowledge of host–pathogen interactions and quantitative resistance mechanisms, our approach aligns with the goal of exploiting host and pathogen biology for improved control strategies.

## Emergence and detection of virulence towards host encoded late blight resistance

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<sup>1</sup>Wageningen University and Research, Wageningen, The Netherlands.

\* Corresponding author: Vossen, Jack, E-mail: [jack.vossen@wur.nl](mailto:jack.vossen@wur.nl)

### Abstract

*Phytophthora infestans* is not only a plant- but also an *R* gene destroyer. Despite countless efforts to find alternatives, the immune receptors encoded by the *R* genes are still the only way to provide potato varieties with high levels of Late Blight resistance. Fortunately, since the beginning of this century, new insights and technology have emerged to deploy *R* genes in a durable way. An integrated approach of *R* gene stacking on the plant side, and monitoring virulence development on the *Phytophthora* side, through dedicated ICM strategies must be embraced to prevent resistance breakdown. In this presentation we will report about 20 years of virulence monitoring, which suggests the responses of the *Phytophthora* population to a changing potato variety set. As expected, variation in the sexual population seems to be a source of variation in virulence. But in recent years, the intra-clonal variation starts playing a major role as well. Over the years, virulent isolates for all late blight *R* genes that are currently deployed in varieties have been found and collected. We sequenced the genomes of these isolates to find the molecular changes associated with virulence development. Preliminary results will be presented, and an outlook will be provided as to how this research can lead to markers for the detect emerging virulent lineages.

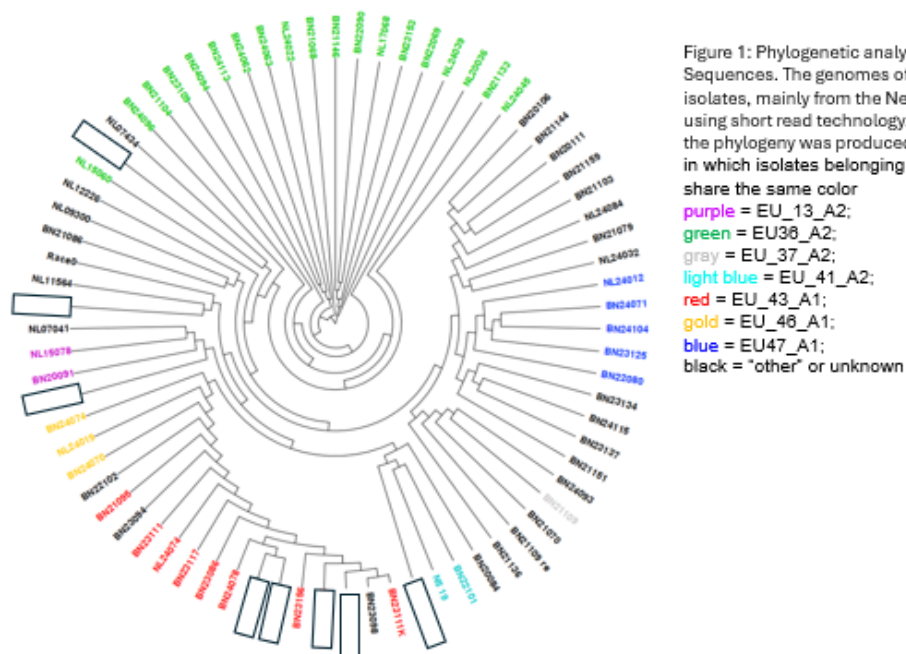


Figure 1: Phylogenetic analysis of *P. infestans* genome Sequences. The genomes of 75 well characterized isolates, mainly from the Netherlands were sequenced using short read technology. SNPs were called and the phylogeny was produced using Archaeopteryx, in which isolates belonging to the same SSR group share the same color  
purple = EU\_13\_A2;  
green = EU38\_A2;  
gray = EU\_37\_A2;  
light blue = EU\_41\_A2;  
red = EU\_43\_A1;  
gold = EU\_46\_A1;  
blue = EU47\_A1;  
black = "other" or unknown

**Keywords:** late blight *R* genes, virulence monitoring, genotyping.

**Acknowledgements:** IPMorama, funded by the European Union (GAP-101135348); TKI grant LWV24045, funded by the Ministry of AFFN in the Netherlands.

## R-gene rotation in combined New Genomic Technologies and ICM strategies

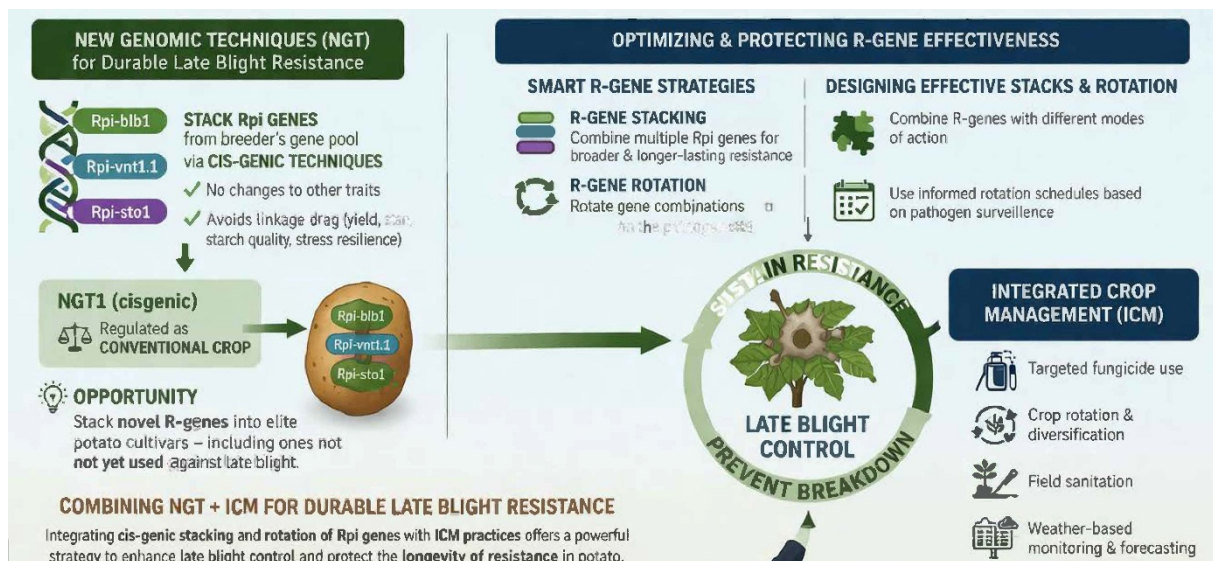
Hebelstrup, Kim H.<sup>1\*</sup>; Abuley, Isaac K.<sup>1\*</sup>

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### Abstract

The use of cis-genic techniques opens the possibility to stack Rpi genes from the breeder's gene pool into potato cultivars without disturbing other traits. This contrasts traditional breeding where the achievement of potato lines with new Rpi genes introduces changes in other traits due to genetic linkage of Rpi genes with genes that affect other traits, such as yield, starch qualities and resilience to abiotic stresses. In a situation where introduction of an Rpi gene is considered NGT1, and to be regulated equivalent to conventional crops, this opens a possibility to stack Rpi genes in existing potato cultivars, including new R-gene based resistances that have not before been used in the control of late blight. We suggest how to optimize the effect of Rpi genes by R-gene rotation and composition of R-gene stacks. We also suggest how this stacking and rotation of new R-genes should be combined with ICM to prevent the breakdown of new R-gene based resistance, as has been seen before when introducing R-genes by traditional breeding techniques.



**Keywords:** Biotechnology, genetic transformation, resistance mechanism, population dynamics.

**Acknowledgements:** Funding: GUDP - 'NGT Kuras' project (Green Development and Demonstration Programme no. 34009-22-2047).

## Resistant cultivars AND decision support systems to significantly reduce fungicide use in late blight control

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### Abstract

Reducing pesticide use has become a key challenge for agricultural production. In Flanders, potato late blight control accounts for almost 10% of all applied active ingredients, highlighting the need for more efficient management strategies. 26 years of experience with the Viaverda decision support system (DSS) for late blight control has demonstrated an average fungicide reduction of 11.7% compared with weekly spraying, in Flanders. To fully achieve the Green Deal objective of halving pesticide use, growing late blight-resistant potato cultivars presents a promising complementary strategy. Nevertheless, preventive fungicide applications remain necessary in these cultivars due to the high adaptive potential of *Phytophthora infestans*. To address this, Viaverda developed a modified DSS for resistant cultivars. Field trials conducted in 2024 and 2025 assessed the performance of this DSS and the added value of resistant cultivars. In 2024, under high disease pressure, the DSS for resistant cultivars reduced the treatment frequency index by 48%, while preventing any late blight infection. In 2025, characterized by low disease pressure, the DSS recommended no treatments for resistant cultivars, with no disease observed. These findings demonstrate that resistant cultivars are the primary driver of substantial fungicide reduction, while DSS-guided spraying remains essential to ensure sustainable R-gene protection.

Table 1. Treatment frequency indexes (TFI) and % disease observed in sensitive and resistant potato cultivars left untreated, treated following weekly applications, or treated following a DSS in the '24 and '25 growing seasons.

Cultivar	Application scheme	2024		2025	
		TFI	% Disease	TFI	% Disease
Sensitive	UTC				2
	Weekly	23	16,3	24	0
	DSS	25	6,9	17	0
Resistant	UTC				0
	DSS	13	0	0	0

**Keywords:** Potato late blight, Decision support systems, Resistance cultivars, Fungicide use.

**Acknowledgements:** The authors want to thank VLAIO - 'Flanders Innovation and Entrepreneurship' for funding this research project ([VLAIO LA HBC.2022.0927](https://www.vlaio.be/la-hbc/2022/0927)).

**Session 3**  
**Control Strategies**

*Chair: David Cooke*

*Sub-chair: Rebecca Joynt*

## Control of late blight and early blight in Denmark without PFAS pesticides

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### Abstract

In Denmark, the withdrawal of 33 PFAS-containing pesticides further reduces the already limited number of active ingredients available for managing potato diseases. From 2027 onwards, only mandipropamid, oxathiapiprolin, cymoxanil, and propamocarb will remain registered for late blight control, while difenoconazole and azoxystrobin will be the only options for early blight. Since 2023, preventive late blight strategies have relied on mixing and alternating fungicide modes of action using both full and variable doses (fig 1). Although this approach has been effective in 2023-2025, even without use of PFAS fungicide in 2025, a continued reduction in available MoAs is expected to accelerate the development of fungicide resistance and increase selection pressure for virulent strains capable of overcoming R-genes in new potato varieties. Reducing inoculum pressure is therefore essential to limit mutation, sexual recombination in late blight populations, and the emergence of new and better-adapted genotypes. The rapid evolution of late and early blight populations highlights the need for an integrated pest management (IPM) approach, including AI-based camera technologies for scouting, AI- and DNA-based aerobiology, new chemical and biological control agents, improved decision support systems (DSSs), and more robust varieties combining both major and minor resistance genes. Although oospores have generally been considered manageable since the early 2000s, they represent a significant and often underestimated risk due to their capacity for rapid adaptation through sexual recombination. Denmark and Norway show some of the highest genotypic diversity in Europe. This underlines the need for renewed focus on documenting the role of oospores and for implementing IPM/ICM approaches to ensure a long-term sustainable and viable potato production.

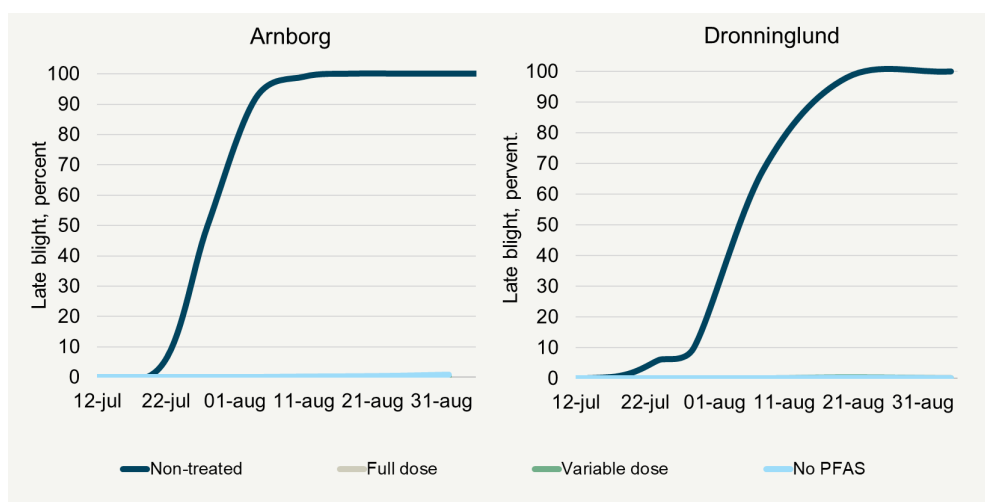


Figure 1. Development of late blight under preventive strategies using full and variable doses in a mixed and alternating fungicide program, with and without PFAS-containing fungicides.

**Keywords:** *Phytophthora infestans*, PFAS pesticides, crop rotation, oospores.

**Acknowledgements:** We gratefully acknowledge the continued support of the Danish Potato Levy Fund for their long-term funding of the development and testing of preventive strategies for the control of late blight and early blight.

## The emergence and management of CAA and OSBPI fungicide resistance in *Phytophthora infestans*: A five-year European surveillance study

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### Abstract

The emergence in 2021 of resistance to CAA and in 2023 to OSBPI fungicides in *Phytophthora infestans* posed significant challenges to European potato growers. We present here the response to the emergence of resistance and the new management strategies implemented from 2022. The presence of the cesA3\_1105S resistance-associated mutation in the previously unidentified EU43 clonal-lineage triggered CAA resistance across several EU countries. The situation has nowadays improved in regions with implemented new management strategies promptly communicated by Syngenta and FRAC. However, resistance to CAA still appears in areas without management intervention. The recessive nature of CAA resistance mutations, and the emergence of the EU46 clonal-lineage that, despite showing a sensitivity shift towards CAA in laboratory assays, has documented limited field impact, suggest that effective control can be achieved with the continued availability of differential fungicide classes. Managing OSBPI resistance is more challenging due to the multiple dominant mutations in the OSBP target gene, their co-occurrence within single strains in the prevalent EU36 clonal lineage, in addition to EU43 and EU46. However, recent mixture and alternation strategies successful in managing CAA resistance show promise for controlling OSBPI resistance. We present here the contribution of those strategies as recommendation to manage resistance.

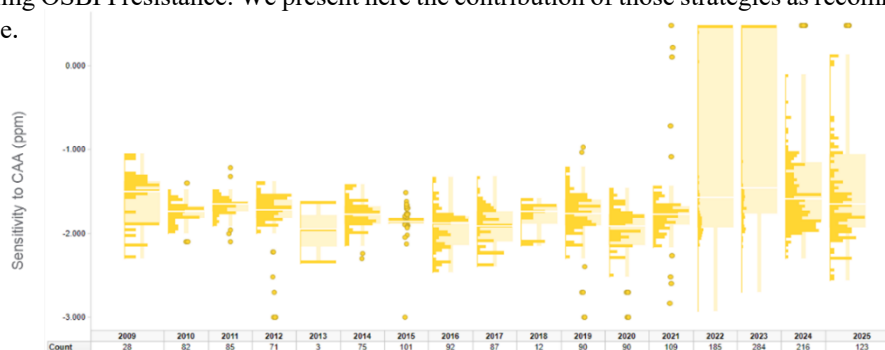


Figure 1. Boxplot representing the evolution of *P. infestans* sensitivity to CAA since 2008 ( $n$  of isolates = 2013). All samples tested up to 2020 showed complete sensitivity to CAA. In 2021, an outbreak of resistance to CAA was detected in Denmark, followed by the discovery of the mechanism of resistance by the Resistance Research Team in Syngenta. In 2022 we observed a spread of resistance to CAA across Europe: Syngenta wrote new recommendations for CAA resistance management with FRAC. In 2023 the application of new fungicide protocols with strict alternations and mixtures caused a decrease of resistance to CAA in Denmark. In 2024, such decrease could be quantified across Europe. In 2025 the levels of resistance to CAA across Europe are like 2024.

**Keywords:** CAA, OSBPI, resistance monitoring, resistance management.

**Acknowledgements:** We would like to thank our Crop Protection R&D colleagues, European technical specialists, product biologists and marketing colleagues. Boots on the field or hands on the budget, in the last years they allowed the strong increase of data generation for fungicide resistance monitoring presented in this work and the planning of new and successful fungicide resistance management strategies. Particular thanks go to Jesper Yngvesson (Technical Manager Nordics) and Roeland Kalkdijk (Technical Head BeNeLux) for the excellent work in increasing *P. infestans* sampling in their regions and for discussing new fungicide management strategies in the Nordics and Benelux, respectively. We would like also to thank David Cooke and the way that the Euroblight monitoring program contributes to the understanding of the generation and spread of the resistance within the population of *P. infestans*, to the benefit of the whole European potato industry.

## Sagropia, how to include biologicals into blight management

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### Abstract

SAGROPIA is dedicated to transforming plant protection in European agriculture through the introduction of thirteen biological and low-risk pesticides, which shall replace some “candidates for substitution” (CfS) and active substances that are currently in use. Specifically targeting potato and sugar-beet crops, the project aims to seamlessly integrate new and sustainable solutions to plant protection into comprehensive integrated pest management (IPM) strategies. The overall objective is to achieve a significant reduction in the reliance on chemical pesticides. This underscores the project’s strong commitment to mitigating adverse effects in crop production on natural resources, people, and the environment. To start with, Sagropia solutions were tested under greenhouse conditions to establish the efficacy to control pests and diseases. The results were used to develop IPM strategies for potato cultivation. Field experiments were set-up in different pedo-climatic zones. Trials consisted of 4 or 5 strategies depending on the location. A local reference strategy, including CfS was compared to three Sagropia strategies, with increasing level of conventional pesticide substitution. Finally, the strategies were compared to a local Best Agricultural Practice. Occurrences of pests and diseases were assessed. Yield and quality of the potato production was measured.



Figure 1. Sagropia field trial in Valthermond September 2025.

**Keywords:** *Phytophthora infestans*, *Alternaria solani*, IPM, environmental impact.

**Acknowledgements:** The Sagropia project (<https://sagropia.eu/>) was funded by the European Union it was carried out with the Sagropia partners Agroscope, AIT, Amoéba, Certis Biologicals, DTU, Rovensa Next, RTDS group, Südzucker AG, Verband Bayerischer Zuckerrübenanbauer e.V., Wageningen Research.

## Framework and pipeline for test of biologicals and alternatives

De Vrieze, Mout<sup>1,\*</sup>; Abuley, Isaac K.<sup>2</sup>  
Biologicals and alternatives Working Group

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### Abstract

The progressive withdrawal of active ingredients from plant protection products, combined with the emergence of more aggressive and virulent *Phytophthora infestans* populations, underscores the urgent need for alternative late blight control strategies. Biological approaches, including the use of microorganisms, plant extracts, essential oils, and other bio-based compounds, have been widely explored due to their diverse modes of action, such as inducing plant defenses or directly inhibiting pathogens. However, despite promising research outcomes, only a limited number of these solutions have reached practical application, often due to inconsistent efficacy and limited reliability under field conditions. One key limitation may lie in the way biologicals are evaluated, as current testing frameworks largely mirror those used for chemical pesticides and may not fully capture the context-dependent nature of biological control. Integrating these alternatives into broader disease management strategies, accounting for factors such as cultivar susceptibility, disease pressure, and pathogen population dynamics, could improve their performance and adoption. Rethinking evaluation and deployment approaches may therefore be essential to unlock the full potential of biologicals in sustainable late blight management.

## Epidemiology of Potato Late Blight in Galicia (NW Spain) and On-Farm validation of the NEGFY model for sustainable disease management

Meno, Laura<sup>1,2\*</sup>; Castaño-Serna, Jonathan S.<sup>1,2</sup>; Seijo, Carmen<sup>1,2</sup>; Escuredo, Olga<sup>1,2</sup>

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### Abstract

Over four years, the epidemiology of potato late blight (*Phytophthora infestans*) was studied in Galicia with the aim of improving disease management and reducing fungicide use. During the first three years, late blight epidemics were characterized under experimental field conditions, and the NEGFY decision support model was evaluated for its ability to predict infection risk. Model outputs were compared with observed disease development to assess their reliability under local climatic conditions. In the subsequent year, the NEGFY model was implemented on commercial potato fields in collaboration with local farmers, representing real production scenarios. Fungicide applications were scheduled according to model recommendations and compared with conventional farmer practices. The results showed a clear reduction in the number of fungicide treatments using the model-based strategy, and this did not result in significant yield losses. These results highlight the importance of testing and validating decision support systems directly with farmers under real field conditions, as a key step to ensure their practical applicability, adoption, and contribution to more sustainable disease management strategies.

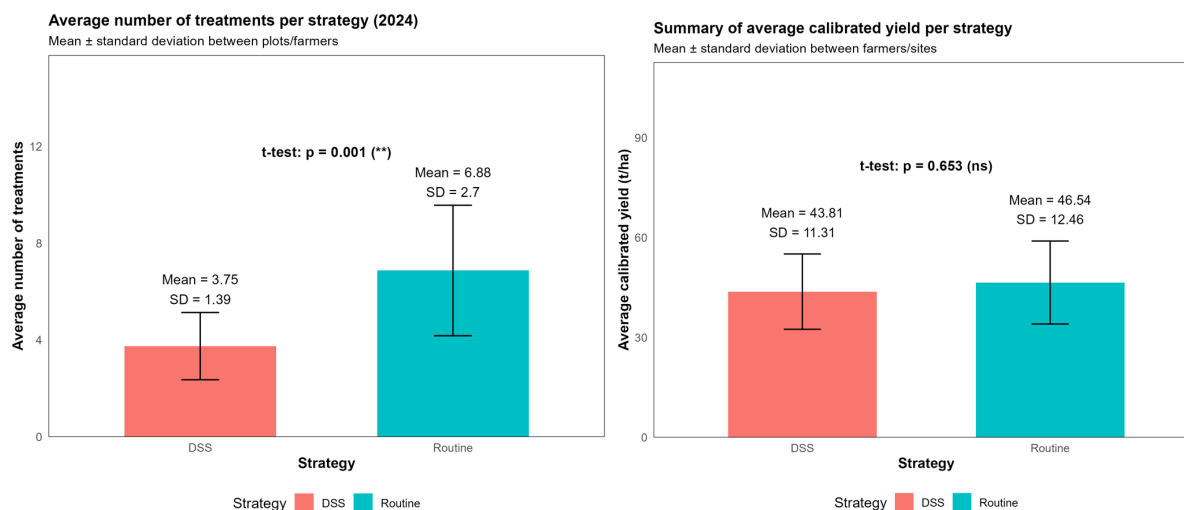


Figure 1. Average number of treatments per strategy (2024). Figure 2. Summary of average calibrated yield per strategy.

**Keywords:** Potato late blight; *Phytophthora infestans*; NEGFY; decision support systems.

**Acknowledgements:** Funding by “Sustainable strategy for integrated disease management in potato crops” with reference FEADER 2023/013B. Thanks also to the collaborating farmers. Laura Meno holds a postdoctoral fellowship (ED481B-2023-023) funded by Xunta de Galicia (Galician Government, Spain).



## **IPMorama: better integration of varietal resistance into the deployment landscape is essential for the successful future management of late blight**

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### **Abstract**

Disease and pest resistant potato varieties should form an integral part of integrated pest management approaches but are frequently poorly integrated into existing agronomic systems. As part of the Horizon Europe project IPMorama (Grant no. 101135348), we are proposing a three-component strategy to develop what we call a “variety-centric” integrated pest management (IPM) approach that will make best use of available plant protection products (PPPs) and genetic resistance. This approach is based on: (1) Genome-based breeding tools and strategies that allow the combination of multiple R-genes of known pathotype-specificity with the quality and agronomic traits that will drive uptake of new varieties; (2) Disease surveillance networks based on an understanding of the ability of the pest or pathogen to overcome both the specific R-genes that are currently deployed (and those in breeding pipelines) and the available PPPs; (3) Specific practicable management approaches that maximally combine the efficacy of the R-gene and PPP components, based on easy-to-use decision support systems. We’ll review the current state of play in the project with respect to late blight and propose how Euroblight members can contribute to successful outcomes. Further information can be found at the project website [www.ipmorama.eu](http://www.ipmorama.eu).

## The regulatory framework on crop protection in the EU status update May 2026

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### Abstract

Compared to the rest of the world, European potato growers lack access to innovative crop protection solutions to efficiently control pests and diseases. At the same time growers are confronted with a strong reduction in the availability of crop protection products with different modes of action. The innovation gap is the outcome of the European regulatory system. It requires the generation of extensive, research based regulatory dossiers that require time-consuming reviews and alignment processes on regional, zonal and country level. Target review times as set forth in EC guidance 1107/2009 exceed 4 - 5 times the original timelines (e.g. 8- 10 years instead of 2 years). The new EU Commission, taking office in November 2024, recognized the need to simplify the regulatory framework and to restore global competitiveness of European growers. It launched the Omnibus initiative, a structured process to review the regulatory constraints engaging a broad range of stakeholders, including growers, input providers, value chain partners, NGOs, and other civil society organisations with the aim to jointly identify opportunities to remove administrative hurdles. In December 2025 the EU Commission presented a draft proposal which is currently under review by the European Council and the European parliament. The European Commission anticipates announcing a simplified legislative system at the beginning of 2027 with amendments of the regulation of crop protection products (EC 1107/2009), the regulation for maximum residue levels (MRL, EC 396/2005) and the Sustainability guideline (Directive 2009/128/EC). Options to accelerate innovation can be achieved with provisional mutual recognition, National Provisional Authorizations (NPA) once a positive Draft Assessment Report (DAR) is available and re-registration based on data call in. Options to avoid further reduction of the toolbox, e.g. loss of active ingredients and or unique modes of action, can be achieved through the support of emergency registrations and maintaining critical uses where no alternatives have been identified while safety and transparency is maintained.

**Keywords:** Crop protection regulation in Europe, Omnibus, innovation.

## **Session 4**

### ***Alternaria***

*Chair: Hans Hausladen*

*Sub-chair: Laura Meno*

## Elucidating population structure, genetic diversity and host specificity of section *Alternaria* from diverse regions and wild and domestic host plants

Clasen, Gonne<sup>1\*</sup>; Ivanovic, Zarko<sup>2</sup>; Janiszewska, Marta<sup>3</sup>; Stam, Remco<sup>1</sup>

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### Abstract

*Alternaria* spp. are cosmopolitan, ubiquitous necrotrophic pathogens responsible for early blight and leaf spot diseases, causing substantial harvest losses in solanaceous crops. To investigate their diversity, spread, and adaptive potential, we collected *Alternaria*-infected leaves from potato, tomato, and wild solanaceous hosts across three climate zones and multiple farm types in Estonia, Poland, Serbia, and Germany. Molecular identification using the markers Alt a1 and RPB2 revealed that infections were dominated by small-spored species of section *Alternaria*, primarily *A. alternata*, findings further confirmed by morphological examination. Sequencing of the two markers revealed five widespread haplotypes with similar frequencies across host plants, farm types, and climate zones. Comparative diversity analyses ( $\pi$ , Tajima's D) likewise showed no significant genetic differentiation among isolates from different hosts. These results suggest that, based on these markers, small-spored *Alternaria* populations exhibit considerable genetic heterogeneity at the continental scale and a remarkable ability to colonise and infect across diverse environments. However, phenotyping using detached-leaf assays revealed significantly higher virulence in isolates originating from wild host plants, highlighting the importance of wild hosts as reservoirs that may contribute to pathogen spread. To further characterise population structure, admixture, and adaptive potential, we generated whole-genome sequences for 320 *A. alternata* isolates, enabling high-resolution analyses of gene flow and recombination. In addition, we are assessing fungicide resistance profiles, with a particular focus on the emergence and spread of resistance in wild host populations. Together, our results provide an integrative view of the ecology, population biology, and adaptive capacity of small-spored *Alternaria*, with direct implications for disease monitoring and sustainable management strategies in Europe.

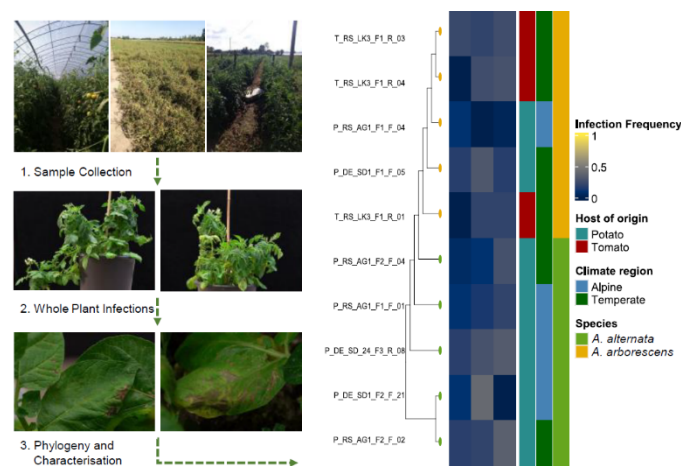


Figure 1. Workflow and Maximum-likelihood phylogeny of all phenotyped isolates of two Section *Alternaria* species from different climate zones paired with a heatmap of infection frequencies on three solanaceous hosts.

**Keywords:** Section *Alternaria*, Population Genetics, Infection Assay, Fungicide Resistance.

**Acknowledgements:** This work was funded by the DFG (Project number 403835372) and the Serbian-German joint research project 2023-2024 (Serbian Project number 337-00-19/2023-01/10, DAAD project number: 57656586).

## Global and regional diversity in *Alternaria* species causing potato early blight

Meno, Laura<sup>1,2,\*</sup>; Castaño-Serna, Jonathan S.<sup>1,2</sup>; Seijo, Carmen<sup>1,2</sup>; Escuredo, Olga<sup>1,2</sup>; Fejer-Justesen, Annemarie<sup>3</sup>; Wharton, Phillip<sup>4</sup>; Abuley, Isaac. K.<sup>3</sup>

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### Abstract

Early blight is an important potato disease caused by several species of the genus *Alternaria*. For many years, the disease was mainly attributed to *Alternaria solani*; however, recent studies have shown that early blight is a more complex pathosystem involving a high diversity of *Alternaria* species. Although resistance to several fungicide active ingredients has been reported in this genus, the response of different *Alternaria* species to fungicides remains poorly understood. The aim of this study was to compare the diversity and fungicide sensitivity of *Alternaria* species at both regional and global scales. Leaf samples showing early blight symptoms were collected from potato crops in different regions worldwide. Species identification was performed through genetic characterization based on two molecular markers, EF (Elongation Factor) and RPB2 (RNA Polymerase II Subunit B). Subsequently, colony morphology and conidia characteristics of each identified species were evaluated. In addition, dose–response assays were conducted using two fungicides with different modes of action: Azoxystrobin and Difenconazole. Four species were identified: *A. alternata*, *A. infectoria*, *A. protenta*, and *A. solani*. Greater species diversity was detected in Spain compared with Denmark, indicating regional differences within Europe. Fungicide sensitivity also differed among species, particularly for Azoxystrobin, where *A. alternata* and *A. infectoria* showed low sensitivity even at high doses. These findings highlight the importance of identifying the *Alternaria* species present in each region to optimize fungicide recommendations and reduce the risk of resistance development.

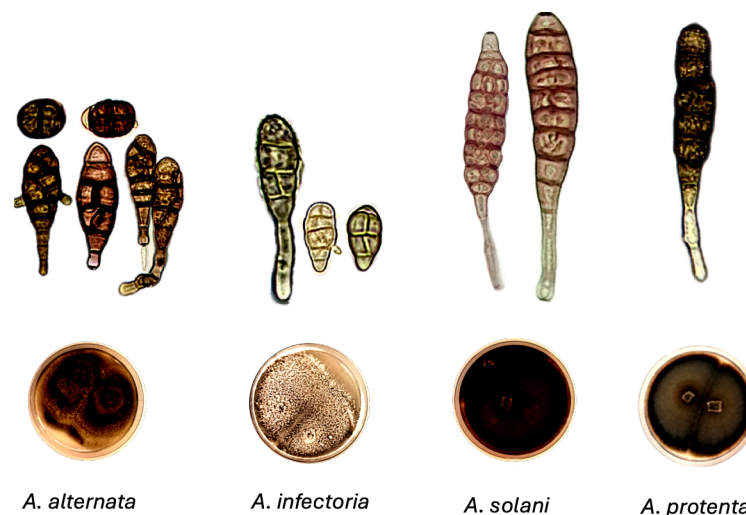


Figure 1. *Alternaria* species found in potato leaf samples. Conidia shape and colony of each species are shown in the figure.

**Keywords:** molecular characterization, *Solanum tuberosum*, colony growth, conidia.

**Acknowledgements:** Laura Meno holds a postdoctoral fellowship (ED481B-2023-023) funded by Xunta de Galicia (Galician Government, Spain).

## Studies on fungicide sensitivity and fitness characteristics of *Alternaria solani* isolates

Haumann, Claire<sup>1,\*</sup>; Stammler, Gerd<sup>2</sup>; Hausladen, Hans<sup>3</sup>

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### Abstract

Potato is an important food crop worldwide and is threatened by early blight caused by *Alternaria solani*. Management often relies on demethylation inhibitor (DMI) fungicides, which target sterol 14 $\alpha$ -demethylase encoded by the *CYP51* gene. Resistance-associated *CYP51* mutations have been reported in various regions, yet their impact on pathogen fitness remains unclear. This study examined field isolates from southern Germany to assess whether *CYP51* mutations influence infection ability and DMI sensitivity. The most frequent mutations detected were G462S (single) and L143F + G446S (double). Greenhouse infection assays showed that isolates carrying *CYP51* mutations generally caused lower infection levels than wild-type isolates under fungicide-free conditions. EC<sub>50</sub> measurements indicated moderate, compound-specific reductions in sensitivity to DMI fungicides, including difenoconazole, mefenftrifluconazole, and prothioconazole. *CYP51* mutation patterns were widespread, largely site-specific, and did not clearly correspond to pre-treatments. Taken together, these findings suggest that azole-resistant genotypes are already established in field populations, are associated with moderate DMI adaptation, and show costs in fitness-related parameters. As a result, resistant isolates are unlikely to spread rapidly in the absence of fungicide pressure.

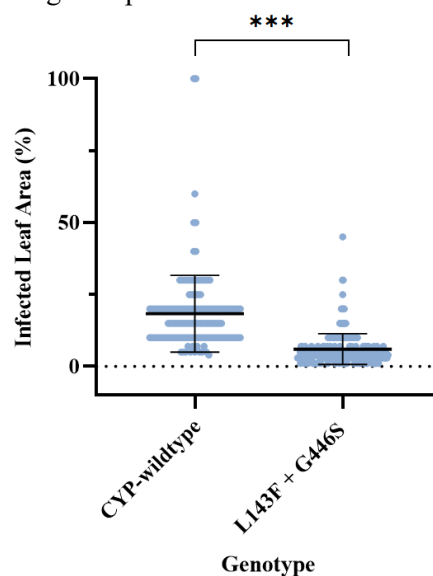


Figure 1. Infected leaf area (%) of *A. solani* isolates from a single field site by *CYP51* genotype. Black: wild-type; grey: mutants (L143F + G446S). Each dot = biological replicate ( $n = 144$  wild-type,  $n = 213$  mutants). Horizontal lines = mean  $\pm$  SD. Mann-Whitney test; \*\*\*  $p < 0.0001$ .

**Keywords:** *Alternaria solani*, *CYP51* mutation, Fitness parameters.

**Acknowledgements:** We acknowledge the TUM Plant Technology Center (PTC) and the Chair of Phytopathology, TUM School of Life Sciences, Technical University of Munich, especially Prof. Ralph Hückelhoven, for providing infrastructure and expertise that supported this study. We further acknowledge BASF SE for their support.



## Overview of the current sensitivity of *Alternaria solani* in Europe

The *Alternaria* Subgroup of Euroblight

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### Abstract

At the 2023 Euroblight meeting, the *Alternaria* subgroup of Euroblight agreed to collaboratively monitor fungicide sensitivity. Several laboratories participated by providing samples, isolates, sensitivity data, and genetic analyses focused on QoIs, SDHIs and DMIs. The data revealed that adaptation to QoI fungicides is mostly due to the F129L mutation in the cytochrome *b* gene. There are two genotypes (I and II)<sup>1</sup> that vary by region. In most current isolates, genotype I features F129, while genotype II has L129. Individual isolates carry one genotype or the other, but mixed genotypes are often found in field samples, identified using genotype-specific PCR. SDHI resistance is now widespread across Europe, mainly characterized by the mutation H134R in the *sdh-C* subunit (C-H134R). Isolated cases of B-H278L and C-N75S were observed, and B-I280V was regionally relevant in Bavaria. The mutations C-H134R and B-H278L have the greatest impact on SDHI sensitivity with some differences for different SDHIs. Due to frequent adaptation to QoIs and SDHIs, DMI fungicides have become a main option for controlling Early Blight. Two haplotypes showing slight adaptation to DMIs (L143F+G446S and G462S) have been identified<sup>2</sup>, displaying regional frequency differences. These haplotypes affect different DMIs differently, typically producing resistance factors around 10. While effects on field efficacy continue to be assessed, prior results indicate that alternating different DMIs in spray programs supports disease and resistance management.

**Keywords:** QoI, SDHI, DMI.

**Acknowledgements:** The *Alternaria* subgroup thanks all contributing laboratories and Biotransfer for excellent sensitivity analysis of a part of the samples.

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## Studying wild relatives of potato to develop early blight-resistant cultivars

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### Abstract

Early blight, caused by large-spored *Alternaria* species such as *A. solani*, is a disease that affects several Solanaceous crops including potato. Potato cultivars can display varying levels of susceptibility to the disease, but none are truly resistant. Warm temperatures and drought periods can be inductive to early blight development, leading to increasing problems with the disease in Northern Europe. Fungicides are used to effectively manage early blight in the field, but this can have negative effects on the environment and it can lead to the emergence of insensitive pathogen isolates. In search for a more sustainable solution, we look at wild relatives of potato as a source of resistance. We screened a large collection of wild potato relatives and identified various species with strong resistance to *A. solani*. More detailed analyses showed that resistance to early blight can often be linked to the production of specific glycoalkaloid variants and we are investigating whether such compounds can be used in breeding of disease-resistant varieties. In addition, we are looking into alternative resistance mechanisms found in wild potato to help the development of potato cultivars with a durable early blight resistance.

**Keywords:** Early blight, wild *Solanum*, *Alternaria*, glycoalkaloids.

**Acknowledgements:** This research was funded by the J.R. Simplot Company and the Top Consortium for Knowledge and Innovation (TKI) (LWV20.239).

## **Session 5**

**(A Subgroup) Control strategies**

*Chair: Bert Evenhuis*

*Sub-chair: Faye Ritchie*

## Characterization of new resistance mechanisms for CAAs and OSBPis in *Phytophthora infestans* and their impact on Late Blight control in potatoes

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### Abstract

The late blight disease, caused by the pathogen *Phytophthora infestans*, poses a significant threat to potato crops (*Solanum tuberosum*), with rapid field progression leading up to complete crop loss under favorable conditions. Integrated management strategies include the use of tolerant varieties and fungicides. However, for both technologies, resistance developments remain a critical challenge. Recent findings indicate the emergence and spread of resistance to Carboxylic Acid Amides (CAAs) and Oxysterol-Binding Protein Inhibitors (OSBPis) caused by mutations in *cesA3*- and *osbp*-genes. Since 2023, up to high frequencies of field isolates carrying mutations either in one or both target genes are detected in different sub-populations of *P. infestans*. Furthermore, a loss of heterozygosity after exposure to CAA-fungicides is shown for triploid isolates belonging to the EU\_46\_A1-EuroBlight-type sub-population resulting in a stable disruptive CAA-resistant phenotype. The implications of this double resistant fraction of the population on current resistance management strategies are discussed, emphasizing the cautious use of these modes of action at the beginning of the season. Translating scientific findings into applicable strategies and effective communication to officials, advisors and other multipliers is key for implementation in potato cultivation systems of farmers, thereby ensuring a sustainable potato production in Europe and beyond.

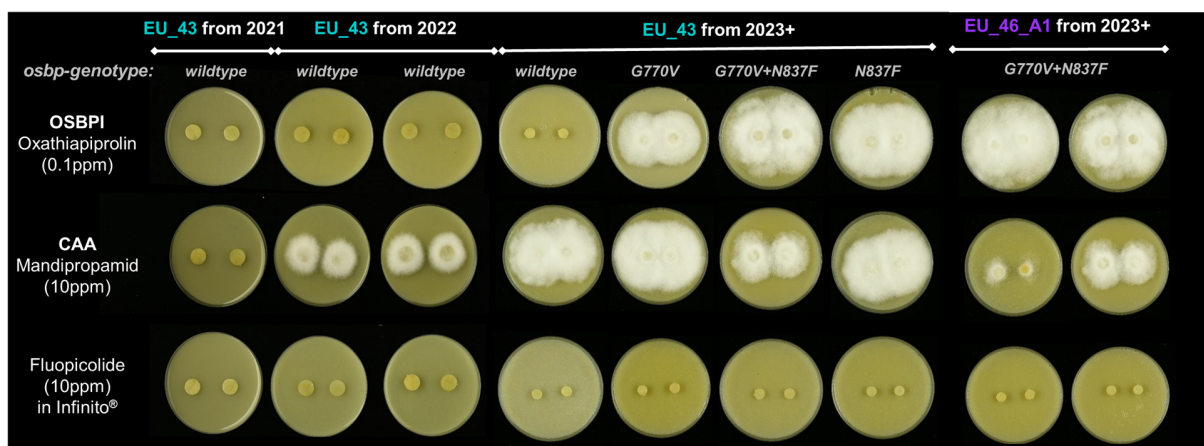


Figure 1. Petri-dishes illustrating evolution of OSBPI- and CAA-sensitivity of *P. infestans* strains in sub-populations characterized as EU\_43\_A1 as well as EU\_46\_A1 from 2021 to 2025.

**Keywords:** Late blight, fungicide resistance management, oxysterol binding protein inhibitor (OSBPI), carboxylic acid amides (CAA).

**Acknowledgements:** The authors would like to thank Geert Kessel and Trudy van den Bosch from Wageningen University for providing the Dutch *P. infestans* isolates, David Cooke from the James Hutton Institute for conducting the EuroBlight-typing and discussions on *P. infestans* evolution. This research received no further funding.

## Orbi-SIMS imaging to observe the spatial distribution of amisulbrom within potato leaves

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### Abstract

Studying the distribution within the leaf of agrochemicals applied on the leaf surface helps understanding the product efficacy. An optimized method for preparing leaf tissue sections suitable for mass spectrometry imaging (MSI) was established, enabling Z-directional visualization of agrochemicals penetration using a secondary ion mass spectrometer equipped with an Orbitrap mass analyzer (Orbi-SIMS). Potato leaves were cryo-sectioned using cryo-film and freeze-drying, which preserved the tissue structure, in contrast to conventional preparation methods that caused vacuum-induced damage. Detection limit studies demonstrated that Orbi-SIMS provided higher sensitivity than TOF-SIMS. MSI analysis revealed clear formulation-dependent penetration behavior, with amisulbrom distributing within the leaf while the reference formulation remained on the surface, consistent with bioassay results using late blight (*Phytophthora infestans*) on potato leaves. These findings demonstrate that the combination of Orbi-SIMS MSI with optimized sample pretreatment enabled reliable visualization of the penetration of amisulbrom within the leaves at field-practical concentrations. Confirmatory biological efficacy trials demonstrate the translaminar efficacy of amisulbrom on potatoes at registered rate.

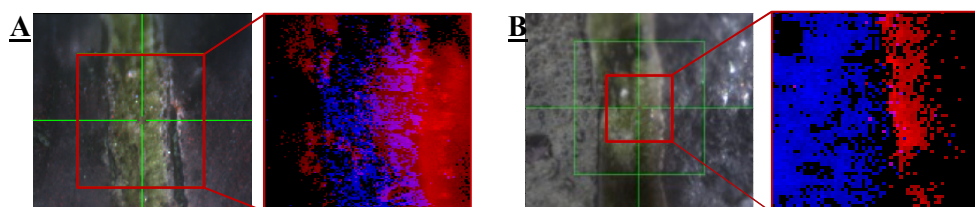


Figure 1. Orbi-SIMS images of potato leaf cross sections treated by (A) Amisulbrom and (B) formulation B. The red signal is for each formulation; the blue signal is for the potato leaf.

**Keywords:** Orbi-SIMS mass analysis, amisulbrom, translaminar distribution, potato late blight.

## Metalaxyl-M (Mefenoxam) in potatoes against late blight: A critical review of its role in modern potato production systems

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### Abstract

Metalaxyl-M (mefenoxam), an enantiomer of metalaxyl, represents a crucial systemic fungicide in the management of late blight (*Phytophthora infestans*) in potato production systems worldwide. This comprehensive overview examines its mode of action, efficacy, and role in disease management strategies. Metalaxyl-M belongs to the phenylamide class (FRAC code 4) and specifically targets RNA polymerase I in oomycetes, inhibiting ribosomal RNA synthesis. This interference disrupts protein synthesis, ultimately affecting hyphal growth, haustorium formation, and sporulation. The compound exhibits strong systemic activity through both acropetal and basipetal translocation within the plant tissue. Rapid uptake and translocation within plant tissues, preventive and early curative activity, protection of new growth through systemic movement results in effective control in various developmental stages of *P. infestans*. The fungicide is applied as foliar application (recommended in mixture with protectant fungicides). Due to its single-site mode of action, resistance development is a significant concern. Key management strategies include: Limited number of applications per season; Mandatory mixing with protectant fungicides; Integration within fungicide programs and Monitoring of pathogen sensitivity. Mefenoxam gives excellent control of late blight when used preventively, protection of both existing and new growth with good rain-fast properties enhancing reliability. Metalaxyl-M serves as a cornerstone in integrated late blight management programs, particularly during periods of rapid crop growth and high disease pressure. Its effectiveness is maximized when: Used preventively and applied according to anti-resistance strategies, combined with disease forecasting systems and integrated with cultural control measures (ICM).

**Keywords:** Metalaxyl-M, *Phytophthora infestans*, ICM.

## Monitoring sensitivity to fungicide active ingredients in the GB population of *Phytophthora infestans*

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### Abstract

Monitoring the late blight outbreaks in Great Britain in combination with knowledge of the efficacy of available fungicides against the *P. infestans* genotypes present, is essential for effective late blight control and integrated pest management (IPM). Between 2019 and 2025, representative isolates of dominant and newly emerging genotypes of *P. infestans* were sampled from GB crops through the Fight Against Blight campaign and tested for sensitivity to a range of commonly used fungicide active ingredients. The active ingredients selected for testing each year was informed by industry sponsors of the Fight Against Blight campaign and based on compound usage, as well as any resistance concerns reported in GB or continental Europe. The efficacy of active ingredients against different genotypes of *P. infestans* was assessed using detached leaf assays, floating leaf disc assays, and zoospore motility assays according to FRAC guidelines. Dose–response curves based on lesion area (mm<sup>2</sup>) were generated from detached leaf assays, and EC<sub>50</sub> values were calculated. These results enable the identification of emerging fungicide resistance, as well as the monitoring of temporal trends. In parallel with the detached leaf-based studies, resistance to mandipropamid and/or oxathiapiprolin has also been monitored during the growing season using molecular methods to detect the single nucleotide polymorphisms (SNPs) known to be associated with resistance. This has been achieved using Sanger sequencing and, more recently, digital droplet PCR (ddPCR) assays. These molecular techniques enable in-season detection of any resistance to mandipropamid or oxathiapiprolin which can be reported to growers rapidly. The recent GB sampling of genotypes EU\_46\_A1 and EU\_43\_A1, with reported resistance to these actives has highlighted the importance of timely advice in support of IPM. This paper provides an overview of the methods and findings from this ongoing monitoring, which represents an essential component of late blight IPM.

**Keywords:** late blight, fight against blight, fungicide resistance, Integrated Pest Management.

**Acknowledgements:** The Fight Against Blight campaign was previously funded by AHDB (Agriculture and Horticulture Development Board) Potatoes until 2021 and by The Scottish Government in 2022. Since 2023 it has been funded by industry sponsors including Certis Belchim, UPL Ltd, BASF, Bayer, Corteva, Syngenta, Gowan, Albert Bartlett, FMC, Agrovista, Frontier, Hutchinsons, GB Potatoes, McCain, Scottish Agronomy, ProCam, SAC, Agrico, Agrii, Branston, PepsiCo, SRUC. Funding for late blight research at the James Hutton Institute from the Scottish Government Rural and Environment Science and Analytical Services Division (RESAS) is also acknowledged.

## National-Scale EBH risk mapping for potato late blight in Ireland. Using interpolated historical meteorology and ensemble forecasts

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### Abstract

Late potato blight remains a major threat to Irish potato production because its development is strongly favoured by mild and humid weather. Using more than 30 years of hourly meteorological observations, this study first analyses blight-favourable conditions through Effective Blight Hours (EBH). The results reveal a persistent southwest-to-east spatial gradient, mainly associated with sustained humidity and precipitation, alongside clear seasonal patterns across monitoring stations. EBH conditions were also detected outside the core growing season at several locations. Building on this analysis, a national-scale EBH risk assessment framework was developed. Spatially continuous historical meteorological fields are reconstructed through interpolation, enabling EBH to be initialised with non-zero conditions before forecasting. Multiple interpolation methods are evaluated for their effects on EBH magnitude and threshold exceedance. These initial conditions are then combined with ECMWF ensemble forecasts to produce probabilistic EBH risk maps for low, medium and high risk levels. The findings highlight the importance of initialisation and interpolation choices for operational EBH-based decision support. Ongoing work is integrating *Swisens Poleno* bioaerosol classification, landcover information and in-field microclimate observations to improve localised and field-relevant disease risk estimates.

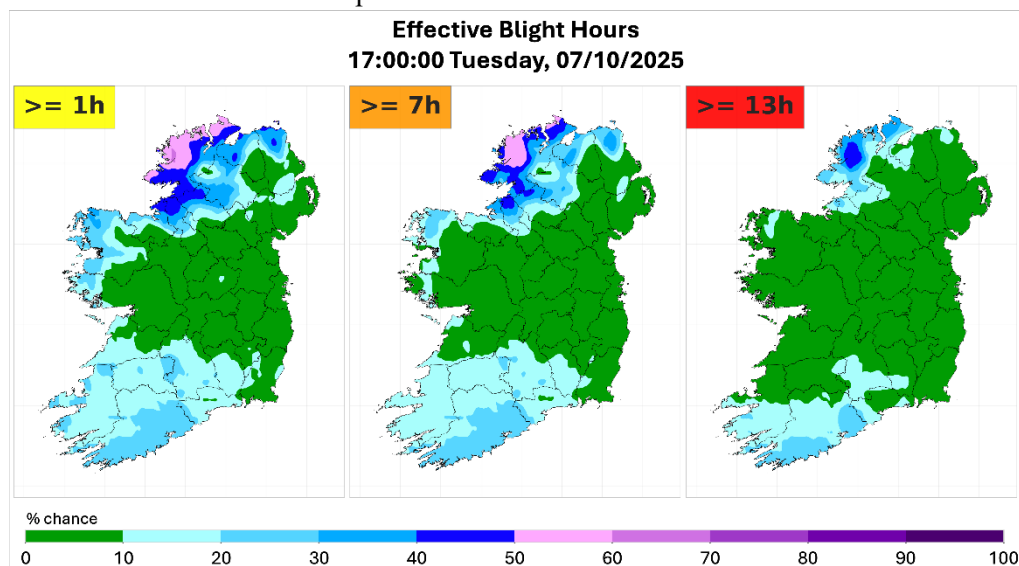


Figure 1. Probability of forecast EBH exceeding the thresholds of 1, 7, and 13 hours.

**Keywords:** Effective Blight Hours, Probabilistic Risk Mapping, Bioaerosol Classification, Artificial Intelligence.

**Acknowledgements:** This research was financially supported by Research Ireland through the National Challenge Fund under grant number 22/NCF/FF/11781 for the AGSENSE project.

## From smallholder to intensive farming: testing the CARAH model for onset of potato late blight epidemic in Galicia

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### Abstract

Late blight is one of the most destructive diseases affecting potato crops worldwide, causing significant yield losses each year. Disease management has become increasingly challenging due to the emergence of fungicide resistance, stricter legislation aimed at reducing pesticide use, the withdrawal of active substances, and the lack of fully resistant potato cultivars. Therefore, disease warning systems represent an important tool for sustainable crop protection. The aim of this study was to evaluate the epidemiology of potato late blight in two contrasting farming systems in NW of Spain: smallholder and intensive farming, and to assess the usefulness of the CARAH model for epidemic prediction during 4 crop seasons. Disease development, airborne sporangia concentrations, and the relationship between symptom onset and pathogen generations were analysed. Results revealed clear differences in late blight behaviour between the two farming systems. In intensive farming, aerobiological monitoring provided valuable predictive information for epidemic development, whereas in smallholder systems the aerobiological signal appeared too late to provide an effective early warning. In both systems, the first disease symptoms were consistently detected between the fourth and fifth pathogen generations of CARAH model. These findings suggest that the CARAH model could be a useful decision-support tool for predicting late blight epidemics around in both potato production systems.

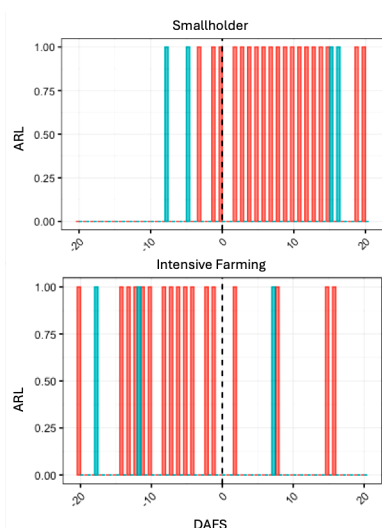


Figure 1. Daily aerobiological risk level (ARL) in two potato production systems. Day 0 represents the first disease symptom; negative and positive values indicate days before and after symptom onset, respectively.

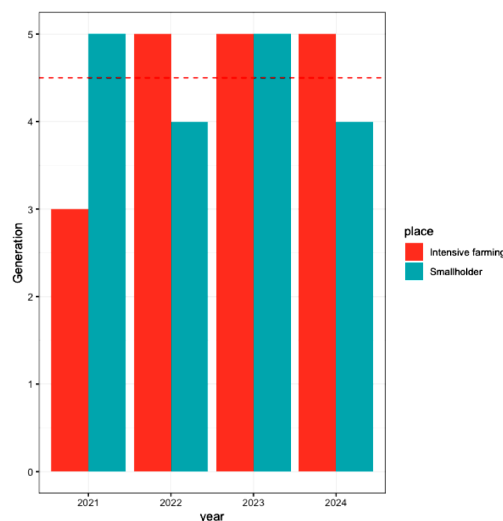


Figure 2. Generation according to CARAH model in which the first symptoms appeared in the potato crops grew in two different farming systems.

**Keywords:** *Phytophthora infestans*; VIGIMAP®; decision support systems, Aerobiology.

**Acknowledgements:** Laura Meno holds a postdoctoral fellowship (ED481B-2023-023) funded by Xunta de Galicia (Galician Government, Spain).

## **Session 5**

**(B Subgroup) Pathogen characteristics & host resistance**

*Chair: David Cooke*

*Sub-chair: Geert Kessel*

## High-throughput virulence assessment using detached leaf disc assays: validation through whole plant phenotyping

Juma, Bicko<sup>1</sup>; Oxholm, Olga<sup>1</sup>; Vossen, Jack<sup>2</sup>; Hebestrup, Kim<sup>1,\*</sup>; Abuley, Isaac K.<sup>1</sup>

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### Abstract

Potato late blight, caused by *Phytophthora infestans*, is one of the most devastating diseases of potato, leading to significant yield losses. Disease management largely relies on repeated applications of chemical fungicides during the growing season. However, the evolution of *P. infestans* has led to fungicide-resistant strains. And environmental concerns related to fungicide residues, such as trifluoroacetic acid (TFA), in groundwater have increased interest in genetic resistance via the deployment of resistance (*Rpi*) genes. To date, more than 70 *Rpi* genes from wild *Solanum* species have been cloned and introgressed into cultivated potato varieties. Assessment of the resistance spectrum of these genes traditionally involves agroinfiltration with cognate *PiAvr* effectors, detached whole-leaf assays, whole-plant assays in controlled environments, and field trials. However, these approaches are time-consuming and often limited to testing a small number of *P. infestans* genotypes. We present a rapid detached leaf disc assay (DLDA) for screening *Rpi*-mediated resistance against multiple *P. infestans* genotypes and compared it with the conventional whole-plant assay (WPA). DLDA results closely matched WPA outcomes. Lin's concordance correlation coefficient indicated excellent agreement (CCC = 0.974; 95% CI: 0.935–0.990), with minimal deviation from the 1:1 concordance line (Cb = 0.986). We show that DLDA provides a reliable and efficient method for screening *Rpi*-mediated resistance in potato and could be used without the WPA confirmation.

Table 1: Lin's concordance correlation coefficient of detached leaf disc assay versus whole plant assay.

Comparison	CCC	95% CI	Bias correction (Cb)
DLDA vs WPA	0.974	0.935–0.990	0.986

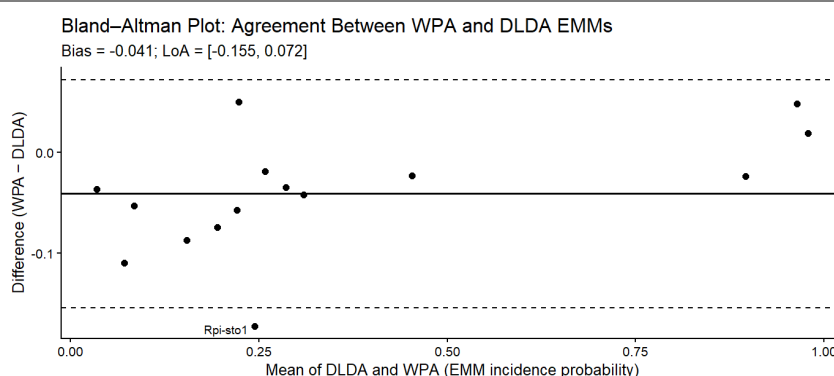


Figure 1. Bland-Altman plot showing the limit of agreement between DLDA and WPA.

**Keywords:** Late blight, *P. infestans*, Detached leaf disc assay, *Rpi*.

**Acknowledgements:** We are grateful to DEWAEGENEIRE Pauline (Inov3PT) for providing the French isolates for this study. This project received funding from the NovoNordisk Foundation grants (NNF) [grant numbers NNF19OC0056580 and NNF22OC0078898], and the Green Development and Demonstration Programme (GUDP) Denmark [grant number 34009-22-2047].



## Taking effectoromics to the potato fields

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### Abstract

*Phytophthora infestans*, the causal agent of potato late blight, remains a major threat to global potato production and is largely controlled through repeated fungicide applications. The increasing risk of fungicide resistance and tightening regulatory restrictions highlight the need for alternative, knowledge-driven disease management strategies. Effectoromics provides a valuable framework for understanding pathogen virulence and supporting durable resistance deployment; however, effector studies traditionally rely on establishing pure pathogen cultures, which is time-consuming and limits large-scale field analyses. Here, we present a pathogen enrichment sequencing (PenSeq) based approach enabling direct effector diversity studies from potato field samples. Samples were collected across Ireland on FTA cards and stored at room temperature before processing after 3 years to demonstrate capability of PenSeq to accurately identify effectors from degraded samples. An effector profile comparison between PenSeq results from FTA card and mycelium-derived DNA showed a strong correlation, demonstrating efficiency of PenSeq to reliably capture pathogen effector diversity from the field samples. This approach enables rapid, scalable effectoromics without the need for pure culture establishment, significantly accelerating pathogen surveillance and population-level analyses. The ability to directly study effector variation from field samples provides a practical tool for monitoring *P. infestans* populations and supports more informed resistance breeding and late blight management strategies aimed at reducing reliance on fungicides.

**Keywords:** Population genetics, effectors, disease resistance, informed breeding.

**Acknowledgements:** This work was supported through a Research Leaders 2025 fellowship funded by European Union's Horizon 2020 research and innovation programme under Marie Skłodowska-Curie grant agreement no. 754380. The authors acknowledge the Research/Scientific Computing teams at The James Hutton Institute and NIAB for providing computational resources and technical support for the "UK's Crop Diversity Bioinformatics HPC" (BBSRC grant BB/S019669/1).

## Integrating predictive models and agronomy for late blight control: a global company's experience

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### Abstract

Managing late blight across diverse production systems requires integrated and adaptable management approaches. This contribution presents the experience of a global food company in implementing an integrated late blight management strategy across diverse potato-growing regions. The strategy combines predictive disease models, agronomic decision-making, varietal development, and continuous optimization to support robust and scalable decision-making at farm level. Predictive models are a central pillar of the strategy and include a simple and an advanced forecast tools. Both based on Wageningen University Research late blight models. These two tools allow growers and advisors to select decision-support tools aligned with their level of technical adoption and data availability. Model outputs are complemented by local weather data, crop development stage, varietal susceptibility, and field observations to refine recommendations. Beyond short-term forecasting, the strategy integrates the continuous evaluation and deployment of potato varieties with improved resistance profiles. In parallel, fungicide programs are regularly optimized with a strong focus on resistance management, including mode-of-action rotation and risk-based application timing. Emphasis is placed on aligning control measures with actual infection risk rather than calendar-based programs. Implementation across multiple regions highlights the importance of grower engagement, technical alignment, and ongoing feedback. This integrated framework illustrates how predictive models, agronomy, varietal resistance, and resistance management can be combined to support sustainable late blight control at scale.

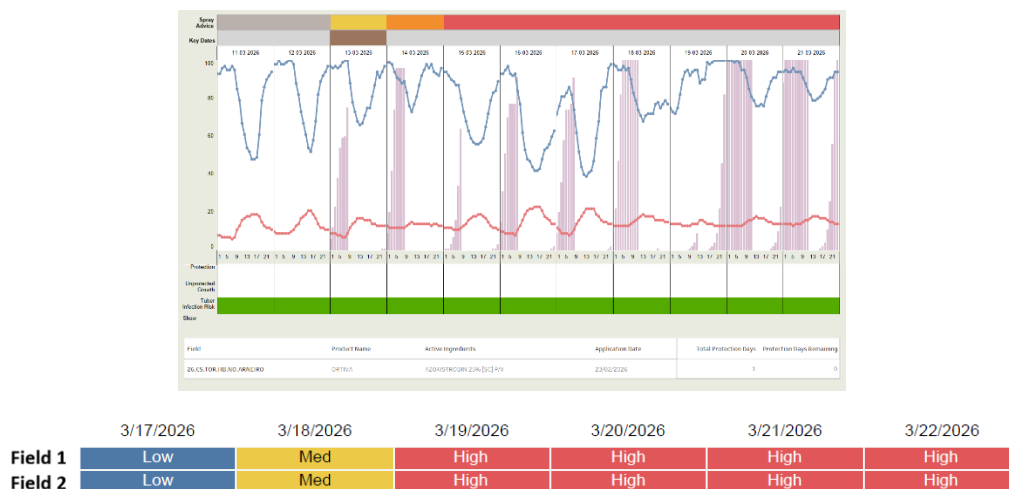


Figure 1. Pepsico Late Blight Forecast.

**Keywords:** *Phytophthora infestans*, predictive models, varietal resistance, resistance management.

**Acknowledgements:** The late blight strategy presented here is the result of cross-functional collaboration across several PepsiCo departments. Forecast is a joint initiative between PepsiCo and Wageningen University. The James Hutton Institute has also played a key role in resistance management.

## Evaluating the success of 3 R-gene late blight resistant potatoes in the diverse agricultural landscapes of Indonesia

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### Abstract

The USAID Feed the Future Global Biotechnology Potato Partnership has developed bio-engineered potatoes with 3 R-gene late blight resistance. To study the efficacy of this Rpi-gene stack in the local Indonesian variety Granola, randomized complete block variety x fungicide, confined field trials were carried out at four different locations in west, central and east Java. In these trials Granola 3 R-gene late blight resistant lines were compared to non-genetically modified Granola varieties in fungicide sprayed and non-sprayed plots. Late blight is endemic to Indonesia and the disease appeared in buffer rows two weeks after planting. Late blight ratings were started when the first symptoms were observed in the non-sprayed control plots and carried out weekly until harvest. No late blight lesions were found in any of the 3 R-gene lines in either the sprayed or non-sprayed plots throughout the whole trial up to harvest. After harvest, tubers were kept for 30 days and then assessed for late blight tuber symptoms. No tuber late blight was found in any of the treatments. These results showed that the 3 R-gene stack was able to provide complete resistance to infection by the *P. infestans* strains present in Indonesia. This data, combined with regulatory information, be used for the development of dossiers to be submitted to the national biosafety authorities of Indonesia for commercial release of the 3 R-gene potato.

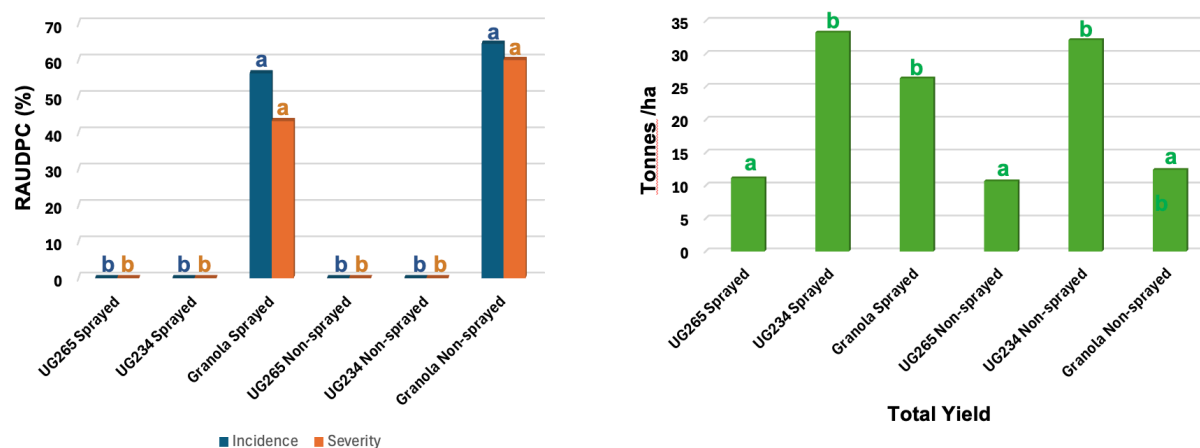


Figure 1. Disease incidence and severity of late blight (left) and total yield in field trials in Pangalengan, Indonesia.

**Keywords:** *Phytophthora infestans*, R-genes, cisgenics.

**Acknowledgements:** This work was funded by the United States Agency for International Development (USAID) as part of the Feed the Future Global Biotech Potato Partnership.

## First report of *Phytophthora infestans* self-fertile genotypes in potato crop in India

Sharma, Sanjeev<sup>1,\*</sup>; Oraon, Sourav<sup>2</sup>; Chakraborty, Ashis<sup>2</sup>; Lal, Mehi<sup>3</sup>; Sagar, Vinay<sup>1</sup>; Bist, CM<sup>1</sup>; Maharana, Chandan<sup>1</sup>

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### Abstract

Knowledge of mating type frequency and its spatiotemporal distribution is essential to understand mating history of pathogens population and for sustainable management of resistance genes and fungicides. With this aim, in the present study, a total of 280 isolates of *P. infestans* collected from different potato agro-ecologies of India during the crop season of 2021-22 to 2023-24 were purified on rye B medium. Isolates were mated individually with the reference isolates Jal 21-1(A1) and HP 21-86 (A2) maintained in the laboratory. Isolates that produced oospores with the A2 tester were designated as A1 mating type, with A1 tester were designated as A2 mating type and those forming oospores with both tester isolates and on their own were designated as self-fertile i.e. homothallic. The results revealed that 57 (56.43%) out of 101 isolates collected from West Bengal were homothallic belonging to A1 mating type. Similarly, in Punjab, 10 (37.03%) out of 27 and in Pune (Maharashtra), 2 out of 2 were homothallic belonging to A1 mating type. On the other hand, the isolates collected from Jharkhand and Bihar (one from each location) and Haryana (03), Rajasthan (02) and Uttar Pradesh (07) were A1 mating type and heterothallic while 17 (12.5%) out of 136 from Himachal Pradesh were homothallic and belonging to A2 mating type. Besides, isolates were also genotyped using SSR multiplex and results yielded only EU\_13\_A2 clonal lineage. There are reports of occurrence of homothallic isolates, belonging to both A1 and A2 mating types, that constitute a new threat to potato and tomato crops in China, Mexico, and Brazil. To our knowledge, this is the first report of the occurrence of homothallic isolates of *P. infestans* belonging to A1 mating type in commercial potato crop in India. This information is important for planning strategies for the effective management of late blight in India.

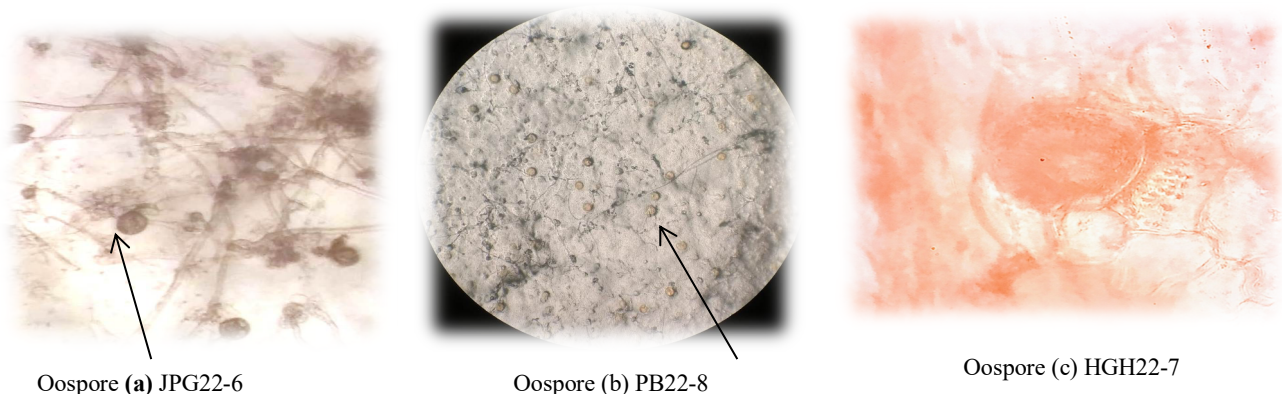


Figure 1. Formation of self-fertile oospores in Petri dish in media (a & b) and on detached leaf (c).

**Keywords:** Mating type, Homothallism, Heterothallism.

**Acknowledgements:** This work was supported by grants from the Indian Council of Agricultural Research (ICAR), India. The help rendered by Dr DEL Cooke, JHI, Scotland in scoring SSR peaks is duly acknowledged.

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

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### Abstract

Potato cultivation is threatened by various disease and abiotic stresses that could increase with climate change. Plant breeding approaches implementing knock-out of susceptibility genes (S-genes) are of growing interest, in addition to the use of resistance genes (R genes, immune receptors). S-genes are generally more robust than R-genes and can confer broad-spectrum disease resistance but are usually not as effective as R genes. Late blight, caused by *Phytophthora infestans*, is the most devastating disease in potato production. Here, we show strong late blight resistance in a location in southern Sweden with a genetically diverse pathogen population with the use of GM potato stacked with three R genes over three seasons and relative new *Solanum americanum* genes. In addition, we demonstrate that in-the-field-intervention among consumers led to change for more favorable attitude generally towards GM crops. We also present field evaluations of known CRISPR/Cas9 S gene potato mutants, during four consecutive years that indicate increased resistance to late blight without any significant trade-off in terms of yield penalty. Furthermore, the field trials showed increased resistance to common scab, and the mutant lines exhibit increased resistance to early blight pathogen *Alternaria solani* in controlled conditions. In order to find new resistance mechanisms, we studied immune responses of potato plants using quantitative proteomic techniques and identified a protein with an unknown function, named Parakletos. *Parakletos* silencing increased both the reactive oxygen species (ROS) and cytosolic calcium (Ca<sup>2+</sup>) bursts induced by flg22. In *Parakletos*-silenced plants, transcript analysis revealed increases in expression of defense-related genes in response to flg22. We also assessed the effects of CRISPR/Cas-mediated knock-out in potatoes. *Parakletos* mutant plants offer improved resistance to *P. infestans*, *Alternaria solani* and *Pseudomonas syringae* as well as increased plant tolerance to salt stress. Moreover, field trials corroborated that *parakletos* mutant lines have enhanced resistance to *P. infestans*, with significant yield increase.

## Effect of infection with *P. infestans* on the potato plant microbiome

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### Abstract

Plant-associated bacterial communities form a dynamic interface between the host and its environment, modulating plant responses to both abiotic factors and pathogen invasion. The “cry for help” hypothesis<sup>1</sup> states that these communities may contribute to plant defense through the recruitment of beneficial microbes under stress. The present study investigated whether *Phytophthora infestans* infection-driven microbiome shifts in the susceptible cultivar Bintje and the rather tolerant cultivar Innovator could reveal beneficial bacteria with potential for biocontrol for late blight. Plants of both cultivars were exposed to the pathogen for two consecutive generations. While the bacterial communities of both cultivars were initially similar, foliar infection induced clear divergence in the rhizospheric communities, with Bintje exhibiting markedly stronger community shifts. The taxonomic groups *Burkholderiales*, *Flavobacteriales*, and *Bacillales* were repeatedly affected. From these groups, 163 bacterial isolates were obtained and screened for antagonistic activity against zoospores and sporangia from *P. infestans*, revealing biocontrol potential for bacterial strains from *Advenella*, *Nocardioides*, and *Phyllobacterium*. No clear correlation was observed between infection-driven ASV abundance shifts and the inhibitory capacity of the corresponding isolates. Nonetheless, strains derived from Innovator consistently showed greater overall activity than those from Bintje.

### References:

Rolfe, S.A., Griffiths, J., Ton, J. (2019). Crying out for help with root exudates: adaptive mechanisms by which stressed plants assemble health-promoting soil microbiomes. *Curr Opin Microbiol*, 49: 73–82. doi:10.1016/j.mib.2019.10.003.

## Hidden effector diversity in *Phytophthora infestans*: uncovering population structure beyond SSR genotyping

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### Abstract

The late blight pathogen *Phytophthora infestans* delivers a diverse arsenal of effector proteins into the apoplast and host cells to suppress plant defence responses and facilitate infection. Variation in effector gene sequences and in the composition of effector repertoires is thought to influence the pathogens' virulence and aggressiveness. However, *P. infestans* is typically characterized using neutral short sequence repeat (SSR) markers, which do not capture any information about effector gene diversity. To address this gap, we developed Effector Amplicon Sequencing (EASe), a targeted, high-resolution genotyping approach designed to capture variation in effector genes, particularly in populations where sexual reproduction contributes to ongoing genetic diversification. Using long-read sequencing data, we identified coding sequences for approximately 70 effector genes from 384 *P. infestans* isolates. We further developed an open-source, modular analysis pipeline to process EASe data and created a population scale database describing genetic variation across these effector loci. EASe analysis revealed the expected strong conservation of effector repertoires within clonal lineages, differing by 10-20 % within a genotype. In contrast, effector repertoires differed by 35% on average between randomly selected isolates, highlighting substantial diversity at the population level. Notably, we also detected effector gene profiles shared across distinct clonal lineages and putatively sexually derived isolates, as well as profiles unique to sexually reproducing groups. Together, these results demonstrate that EASe captures biologically meaningful variation in effector genes that is invisible to SSR-based genotyping, providing new insights into *P. infestans* population structure and a framework for linking effector diversity to pathogen virulence and epidemiological risk.

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

# POSTERS

## **Economic results of control programs with different doses in potato varieties with different resistance to late blight in southern Sweden 2018–2025, and considerations regarding PFAS/TFA-pesticides**

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### **Abstract**

Annual field trials for controlling potato late blight have been conducted in southern Sweden at two nearby locations. In 2018–2019, untreated plots and 100%, 75%, and 50% of the annual control program were compared; in 2020–2021 the comparison was untreated, 100%, and 75%, all in the susceptible variety Folva. From 2022–2025, a control program in a susceptible variety ( Bintje or Folva) was compared with resistant varieties (Twister, Tinca or Jacky). Across 16 trials (2018–2025), a full-dose program (10–11 sprays) generated about 2762 €/ha in net return (based on 0.3 €/kg potato price). In eight trials including both susceptible and resistant varieties, untreated resistant varieties achieved the highest net returns—about 571 €/ha more than treated susceptible varieties and resistant varieties treated at 60–75% rates. This indicates that resistant varieties can be grown with reduced doses or even without fungicide treatments, especially when supported by forecasting tools. Fluazinam was not used from 2018–2022, but after the 2023 ban on cyazofamid, fluazinam products were reintroduced (2023–2025). Concerns about fluazinam as a PFAS and potential TFA formation have increased scrutiny of its use. A future reduction in fungicide options especially if more substances like oxathiapiprolin or fluopicolide are banned without replacements would make resistance management more difficult and increase vulnerability to late blight.

**Keywords:** late blight, control strategies, resistant varieties, PFAS.

## Selection in *Phytophthora infestans* driven by fungicide use in Sweden

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### Abstract

*Phytophthora infestans* is a major constraint in potato production worldwide, with control largely dependent on fungicides. In Sweden, the high genetic diversity of *P. infestans* and the intensive fungicide use increase the risk of resistance development. This study investigated the impact of fungicide use on the pathogen population using samples collected from a field trial testing different spraying programs. The PiCesA3 gene was sequenced to detect the mutation associated with mandipropamid resistance. The samples were also genotyped using SSRs. Live isolates were assessed for sensitivity to mandipropamid, oxathiapiprolin, and fluazinam. Field results showed that repeated applications of fluazinam or mandipropamid resulted in loss of disease control, whereas combining both fungicides minimized disease incidence. All samples were classified as ‘Other’ (unique genotypes) or as EU43 lineage. Mandipropamid-associated mutations were confirmed only in samples collected from mandipropamid-treated plots, and resistance was confirmed in live isolates carrying the mutation. These isolates also exhibited resistance to fluazinam, while all isolates remained sensitive to oxathiapiprolin. Most resistant samples belonged to EU43, with one classified as ‘Other’. The genotyping analysis showed that all EU43-resistant samples were clustered together. However, the ‘Other’ resistant sample was genetically distant from EU43 but closely related to the ‘Other’ susceptible samples.

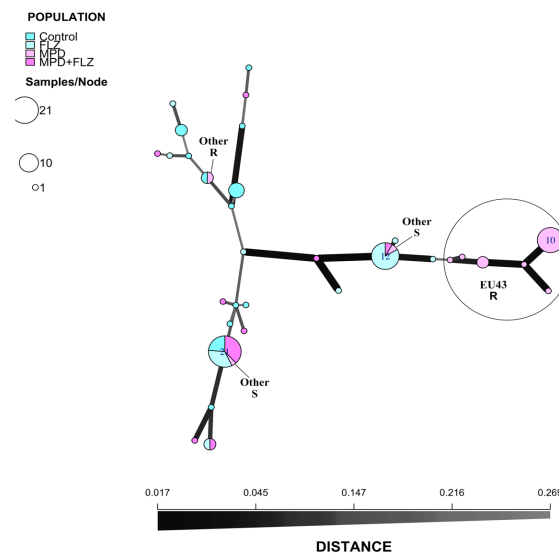


Figure 1. Minimum spanning network of *Phytophthora infestans* based on SSRs. The black circle indicates all the EU43 genotypes detected only in the mandipropamid treatment. The three extra genotypes from the mandipropamid treatment classified as ‘Other’ are indicated with black lines. R indicates the mandipropamid-resistant samples, and S indicates the mandipropamid-sensitive samples.

**Keywords:** *Phytophthora infestans*, fungicide, mandipropamid, resistance.

**Acknowledgements:** The funding for this project was provided by the Swedish farmers foundation for agricultural research, grant number O-23-20-890. We also acknowledge Syngenta for allowing sampling in their field trial.

## Selection for *P. infestans* genotypes with resistance to fungicides by some cultivars more resistant to foliar blight

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### Abstract

It has been hypothesized that ‘the use of cultivar resistance will reduce the rate of selection for fungicide insensitivity because growth rate limiting host resistance will slow the growth rate of both sensitive and insensitive strains.’ This will be true in general but with exceptions. Stellingwerf *et al.* (2018) reported that potato cultivars categorized as having medium to high resistance to foliar blight had a high percentage of samples with EU13 (metalaxyl-M resistant) (35.3 to 47.6%) compared with those in the low-resistance group (2% approx.). SRUC’s blight trial site contained mixtures of *P. infestans* genotypes for 3 consecutive years and was used to investigate the impact of cultivar resistance on the frequency of fungicide-resistant *P. infestans* on leaves. In all 3 years the dominant genotype was EU36 (not fungicide resistant). In the first year the less-sensitive genotype was EU37 (to fluazinam). In 2023 and 2024 the fungicide-resistant genotype present was EU13 (to metalaxyl-M). The two more-resistant cultivars were Royal (rated 5) and Innovator. Innovator proved to be more resistant than Royal in 2022 and 2024; the cultivars were of similar resistance in the middle year. These two cultivars were considerably more resistant than the very susceptible cultivars used: Shepody (2) in 2022 and King Edward (3) in the two other years. The experiments were not inoculated. Fluazinam and metalaxyl-M were not used at the site in 2022 or the subsequent years respectively. The experiments had at least four replicate plots. Leaflets with single lesions were collected. Often the number of lesions on the more-resistant cultivars was very limited. FTA cards were prepared and sent to The Hutton for genotyping. In four out of five experiments there was significant selection by the more-resistant cultivars for genotypes which happened to be less sensitive to fungicide; metalaxyl-M in three experiments and fluazinam in one. The lack of a statistically significant result from a fifth trial was most likely because of sparse numbers of Innovator lesions in that experiment. The study by Stellingwerf *et al.* (2018) and the 2022-2024 one suggest that fungicide usage is not the only driver of increased fungicide resistance. For some combinations of cultivar resistance and *P. infestans* phenotype a higher level of host resistance can inadvertently select for fungicide resistance. The frequency of this is not known. New genotypes of the late blight pathogen can sometimes combine fungicide resistance with the virulence genes that significantly reduce the resistance rating of cultivars, thereby diminishing the protection by host resistance against selection for fungicide resistance. The relatively recent trend for resistance to the same FRAC group to appear in a greater number of *P. infestans* genetic backgrounds may also negatively impact the protection against fungicide resistance afforded by some more-resistant cultivars.

**Keywords:** late blight, fungicide resistance, selection, host resistance.

**Acknowledgements:** Funding by RESAS is gratefully acknowledged. Thanks to the staff based on Auchincruive Estate for conducting the experiments: Claire Kennedy, Donald Kiltie, Adam Wallace & Billy Harrison.

### Reference:

Stellingwerf, J.S., Phelan, S., Doohan, F.M., Ortiz, V., Griffin, D., Bourke, A., Hutten, R.C.B., Cooke, D.E.L., Kildea, S., Mullins, E. (2018). Evidence for selection pressure from resistant potato genotypes but not from fungicide application within a clonal *Phytophthora infestans* population. *Plant Pathol*, 67: 1528-1538. <https://doi.org/10.1111/ppa.12852>

## Capturing fungicide resistance selection: evaluating *Phytophthora infestans* selection dynamics in a lab-greenhouse based assay

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### Abstract

Fungicide resistance in *Phytophthora infestans* remains a major challenge for sustainable late blight management. Increasing regulatory stringency and emerging resistance continue to limit available effective fungicides, making strategies reducing selection pressure increasingly important for long-term control. This work presents an experimental setup designed to quantify how repeated fungicide exposure selects for resistant *P. infestans* genotypes and the resulting impact on fungicide efficacy. The method integrates preventative sprays, controlled infections, and laboratory-based sensitivity and efficacy assessments to monitor changes in the pathogen population across sequential selection cycles. Mixed genotypes inoculum is applied to greenhouse-grown plants treated with a fungicide program reflecting field practice. At the end of each ‘application + infection’ cycle, lesions are harvested, counted, and sporangial germination rates are determined to monitor sensitivity and identify early trends in population shifts. This experimental design enables detection of quantitative changes between sensitive and resistant subpopulations, differences in selection strength among products, and potential efficacy loss associated with resistance selection. By capturing resistance selection as it develops, the assay provides a robust, repeatable platform to compare fungicide programs and anticipate selection risks. The approach supports preventive strategies, tankmix evaluations, and more sustainable fungicide use against potato late blight.

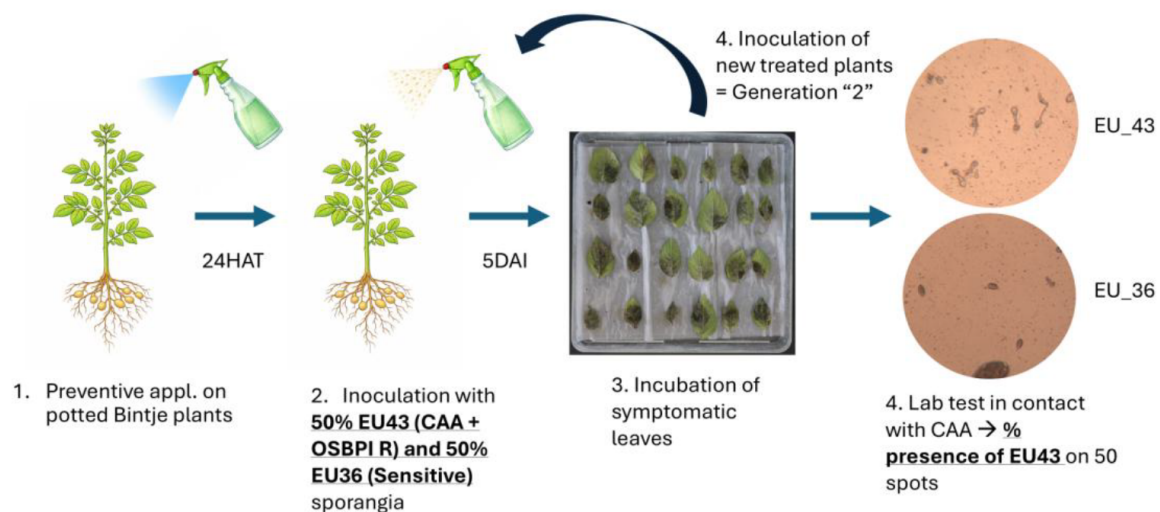


Figure 1. Schematic representation of the trial setup, potato plants were infected 24HAT (hours after treatment) and leaflets were isolated 5 DAI (days after infection). Isolated sporangia were used to determine the percentage of resistant spores using a discriminant fungicide dose rate. These spores were pooled to infect the next generation of new treated potato plants.

**Keywords:** Resistance selection, Fungicide programs, Method explanation.

## Potato genotype × *P. infestans* isolate interactions drive R2 gene resistance

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### Abstract

Late blight (*Phytophthora infestans*) remains a destructive threat to potato production. While the R2 gene is widely utilized, its efficacy is lineage-dependent, showing high effectiveness against genotypes like EU36 but vulnerability to others like EU43. This study utilized a Kuras (R2) × Aventra (non-R2) biparental population to dissect the inheritance of resistance against a total of five *P. infestans* isolates. PCR screening allowed for a direct comparison of R2-present vs. R2-absent genotypes. While R2-presence is highly significant for a resistant phenotype ( $p = 0.0001$ ), the interaction between R2 status and *P. infestans* isolate is a far stronger factor ( $p = 1.62 \times 10^{-14}$ ). Within R2-carrying genotypes, the genetic background became the dominant factor for resistance ( $p < 2.2 \times 10^{-16}$ ). A clear ranking gradient demonstrated that despite carrying the same R gene (R2), potato genotypes exhibited phenotypes ranging from highly resistant to susceptible. Furthermore, a significant potato genotype × *P. infestans* isolate interaction highlights that background support is not universal. These data confirm that the host's genetic environment acts as a crucial modulator of efficacy. Future experiments with Near Isogenic Lines are required to determine if this modulation stems from specific modifier loci or general plant robustness.

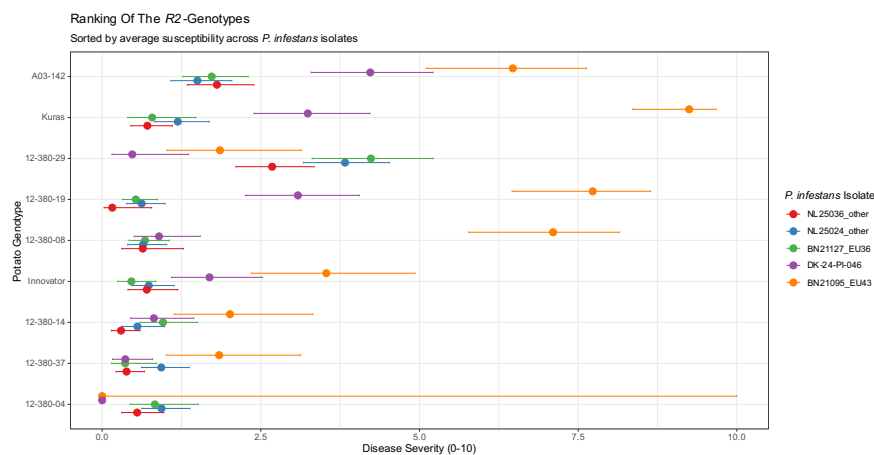


Figure 1. Ranking (based on estimated marginal means) of the resistance of the different potato genotypes towards the *P. infestans* isolates. EU43, EU36, and other indicates the genotype of the *P. infestans* isolates.

**Keywords:** R2 gene, genetic background, genotype x isolate interaction, robustness.

**Acknowledgements:** We thank the technical staff at Wageningen University and Research for greenhouse support and plant care. This work was supported by GUDP / 34009-24-2267 and IPMOrama which received funding from the European Union's Horizon Europe research and innovation programme under grant agreement GA / 101135348.

## Do R-genes still work? Assessing the effectiveness of single R-genes against novel *P. infestans* strains in Denmark

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### Abstract

The emergence and rapid spread of novel *Phytophthora infestans* strains continue to challenge late blight management in Europe. Although deployment of host resistance is a key control strategy, the high mutation rate of the pathogen threatens the durability of single late blight resistance (Rpi) genes due to potential resistance breakdown. In this study, we assessed the resistance of nine transgenic potato lines, each carrying a single Rpi gene in an otherwise susceptible cultivar background, against a panel of 28 *P. infestans* isolates representing the recent EU43 lineage and other clonal lineages. Resistance was evaluated using detached-leaf assays under laboratory conditions and whole-plant assays in the greenhouse, enabling comparison of disease incidence and severity. Several Rpi genes, most notably Rpi-vnt1.1, Rpi-blb2, and R9a, conferred strong resistance to the majority of tested isolates, whereas R3a and Rpi-blb3 showed partial loss of effectiveness. However, no single Rpi gene was able to defeat all tested *P. infestans* isolates. These results indicate that plants relying on the single Rpi genes may be vulnerable to emerging pathogen strains. Overall, our findings highlight the importance of deploying effective Rpi genes, preferably in combinations, to achieve durable late blight control, particularly in the context of increasing fungicide resistance in *P. infestans* populations.

**Keywords:** DLA, R-genes, resistance, breaking of resistance.

**Acknowledgements:** We would like to thank Inov3PT (France) for providing the French isolates for this study, and Anne-Pia Larsen for propagation of the isolates. The project has received founding from GUDP - 'NGT Kuras' project (Green Development and Demonstration Programme no. 34009-22-2047) and IPMOrama project under European Union's Horizon Europe research and innovation programme No.101135348.

## Characterisation of *Phytophthora infestans* isolates from Norwegian potato fields

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### Abstract

Late blight control primarily relies on fungicides; however, there is a growing emphasis on reducing chemical pesticide use due to environmental and sustainability concerns. Additionally, current and emerging genotypes may exhibit fungicide resistance, adding further pressure to develop new strategies and tools for managing late blight. Mapping the presence of pathogens and investigating genetic variation is an important aspect of developing new approaches. Over 250 samples from Norwegian potato fields have been collected on FTA cards during 2025 and genotyped at the James Hutton Institute using 12-plex SSR markers. Genotyping revealed the presence of named clonal genotypes EU\_41, EU\_43, and EU\_46. However, more than 80% of the isolates belonged to “others” with unique or locally distinct clusters of identical multi-locus genotypes. The EU\_43 genotype is associated with resistance to mandipropamid, and a real-time PCR SNP-test has been developed to detect the presence of a SNP associated with mandipropamid resistance. Work is ongoing to test a selection of *P. infestans* isolates for sensitivity to a range of fungicides using detached leaf assays and microtiter plate assays.

**Acknowledgements:** This project is a part of the “NoBlight: New challenges with old potato diseases: IPM to control early- and late blight” project, funded by the Research Funds for Agriculture and the Food Industry (FFL/JA).

## Spatial model of potato early blight risk in Galicia (NW Spain) based on vegetative development, TOMCAST and Random Forest

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### Abstract

The risk of early blight of potato (*Alternaria* spp.) is estimated from meteorological metrics conducive to infection, such as leaf wetness and mean temperature during the leaf wet period, which are combined in the TOMCAST model (Abuley & Nielsen, 2017). Epidemic outcomes also depend on crop phenology and planting date (Meno et al. 2024). We developed a spatial risk mapping framework for Galicia (northwest Spain) that integrates daily severity values (DSVs) from TOMCAST, dynamics related to thermal-temporal development (Pdays), and field disease observations. We take hourly meteorological data from the regional network of stations to quantify the occurrence of DSVs and simulate the crop development by accumulating Pdays under three planting date scenarios, suggesting different susceptibility depending on the host's vegetative stage. We trained a Random Forest using field data (disease and phenology) with risk periods and Pdays metrics. We interpolate the Station-level risk estimates to generate weekly risk heat maps for Galicia. The results showed strong spatial gradients and temporal shifts in epidemic risk windows. Planting-date scenarios substantially modify the correlation between infection climate and host phenology, highlighting differential host susceptibility across planting dates. The number of stations spread throughout the territory limits the possibility of making an extended map.

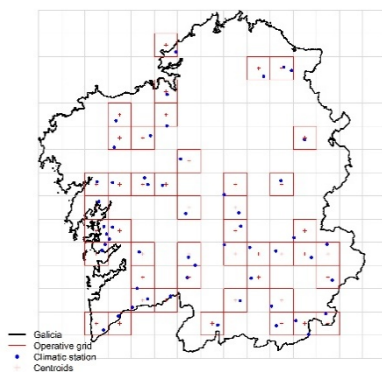


Figure 1. Methodological approach.

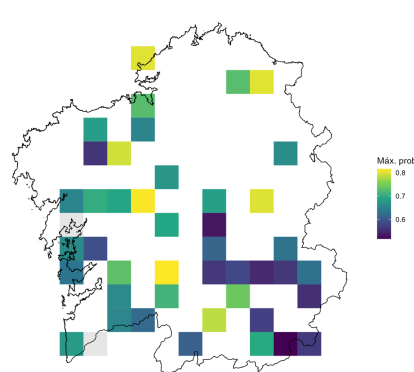


Figure 2. Maximum probability of disease for Kennebec on 2° trial planting 15/5/2025.

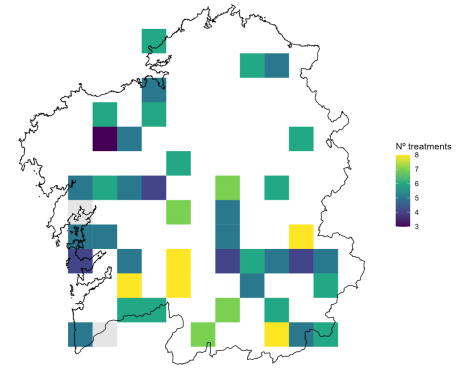


Figure 3. Treatments number for Kennebec on 2° trial planting 15/5/2025.

**Keywords:** risk, map of early blight.

**Acknowledgements:** Funding by “Sustainable strategy for integrated disease management in potato crops” with reference FEADER 2023/013B. Thanks also to the collaborating farmers.

## Monitoring fungicide sensitivity in *Alternaria* populations in the main potato growing regions of South Australia and Victoria, Australia

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### Abstract

Early blight caused by the fungus *Alternaria solani*, is an important disease on potato in all potato growing regions of southern Australia. In recent years a number of new fungicides have entered the market for the control of target spot. In summer 2024/25 a preliminary survey was carried out to screen *A. solani* isolates for resistance to the new and commonly used fungicides as there is no data currently available as to the efficacy of these products against Australian isolates of *A. solani*. Potato leaves with lesions characteristic of target spot were collected from commercial potato paddocks in all the main potato growing regions in SA and Victoria. Leaves were transported to the laboratory and pressed between filter papers to dry. Leaves were then sent to the University of Idaho (UI) potato pathology lab for fungicide sensitivity testing. In the UI lab to obtain isolates, a small piece of dried tissue was excised from the center of a lesion and streaked across the surface of tap water agar. After incubation overnight at 25 °C, single germinated spores were transferred aseptically to acidified potato dextrose agar and incubated at 25 °C in the dark for 5-7 days. Fungicide sensitivity testing was done using spiral plate dilution gradients. Fungicide solutions were applied to PDA in a 2.5-log dilution in a continuous radial concentration gradient using a spiral plater. Fungal inoculum was placed in radial lines across the gradient. Fungicide sensitivity was expressed as an EC<sub>50</sub>, the fungicide concentration at which a fungal isolate's radial growth was equal to 50% of the average growth of the isolate on non-amended PDA. The results showed that 93% of isolates tested were insensitive to azoxystrobin, 96% were insensitive to boscalid and 66% were insensitive to fluopyram. All isolates were sensitive to fluopyram + pyrimethanil, difenoconazole and fludioxanil + pydiflumetofen. This is concerning because Velum (a.i. fluopyram) has just been registered for use on potato in the past two years. Results from this study will be used to compare any differences in susceptibility between the *Alternaria* isolates and will be used to develop a more sustainable potato early blight control program for Australian potato growers.

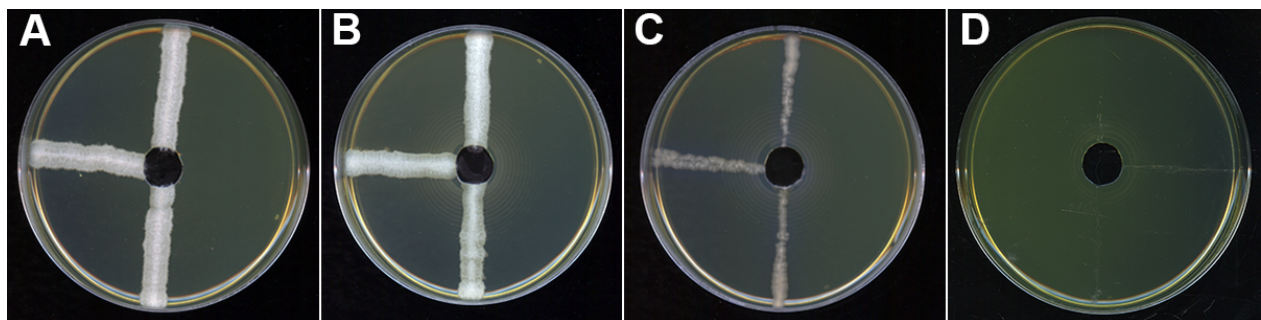


Figure 1. Fungicide sensitivity of *Alternaria solani* isolates to fluopyram and fluopyram+pyrimethanil. (A) Control. An *A. solani* isolate growing on a control plate free of fluopyram. (B) A fluopyram insensitive isolate growing on a spiral gradient plate containing fluopyram. The maximum inhibitory concentration at the center of the plate is 10,000 ppm. (C) A fluopyram sensitive isolate of *A. solani* growing on a fluopyram plate. (D) A fluopyram sensitive isolate of *A. solani* growing on a plate with fluopyram + pyrimethanil.

**Keywords:** early blight, *Alternaria solani*, fungicide resistance.

## Late blight situation in northwestern France explained through three years of trials and a specific case study within the IPMorama project

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### Abstract

The oceanic climate of Ploudaniel (northwestern France), characterized by wet summers with relatively low temperatures, is highly conducive to late blight development. First, we document the consistently high disease pressure observed in this area using several years of field trials aimed at characterizing genetic resistance within a genomic selection panel of potato genotypes. We then present preliminary results from a 2025 trial conducted under these high-pressure conditions, within the framework of the IPMorama EU project. Despite interannual climatic variability, late blight pressure remains consistently high, ensuring reliable disease expression each year. Phenotyping for resistance can therefore be carried out under naturally optimal conditions, without artificial inoculation and with no gaps in annual data series. The stability of responses is illustrated using five repeated control cultivars. In this context, we evaluated Integrated Pest Management (IPM) strategies for late blight control, focusing on resistant varieties. A conventional approach based on local practices was compared with an IPM strategy in which fungicide applications were guided by a Decision Support System (DSS). Results show that fungicide applications can be delayed depending on varietal resistance. Combining resistant cultivars with DSS-based management significantly reduced the Treatment Frequency Index while maintaining negligible levels of disease.

**Keywords:** late blight, resistant varieties, IPM, Decision Support System.

**Acknowledgements:** This project has received funding from the European Union's Horizon Europe research and innovation programme under grant agreement GA No.101135348. Associated country partners funded by SERI & UKRI. However, the views and opinions expressed are those of the author(s) only and do not necessarily reflect those of the European Union or the European Research Executive Agency (REA). Neither the European Union nor the granting authority can be held responsible for them.

## Developing processing potato germplasm with stacked late blight resistance in a variety-centric IPM framework

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### Abstract

IPMorama promotes a variety-centric integrated pest management (IPM) strategy by strengthening the link between resistance breeding, pathogen dynamics, and sustainable crop deployment. A key objective is the development of potato germplasm with well-defined and durable late blight resistance profiles that can be integrated into commercially relevant production systems. Within this framework, a foundation breeding population is being developed to introduce and combine late blight resistance (R) genes into modern potato processing backgrounds. An initial population of approximately 5,000 F1 progeny has been generated by crossing up to ten elite processing varieties with late blight resistant ware varieties covering a total of ten different R genes. This population provides a diverse genetic base for resistance stacking in a processing relevant context. During the first project year, activities focused on the initial accumulation of late blight resistance genes using marker-assisted selection (MAS) using KASP assays targeting known R-genes. This first round of MAS enables the identification of progeny carrying single resistance genes and preliminary resistance stacks, forming the basis for subsequent crossing and selection cycles. Planned activities include additional rounds of crossing and selection to further stack resistance genes, combined with selection for processing quality, and genotyping of selected progeny using a modified PotatoMASH array. These data will support the development of genomic prediction models for processing traits and the implementation of integrated marker-assisted and genomic selection strategies. The expected outcome is a set of advanced breeding lines combining processing quality with single and stacked configurations of two to four late blight R genes, together with genomic tools to support informed resistance deployment and stewardship within variety-centric IPM strategies.

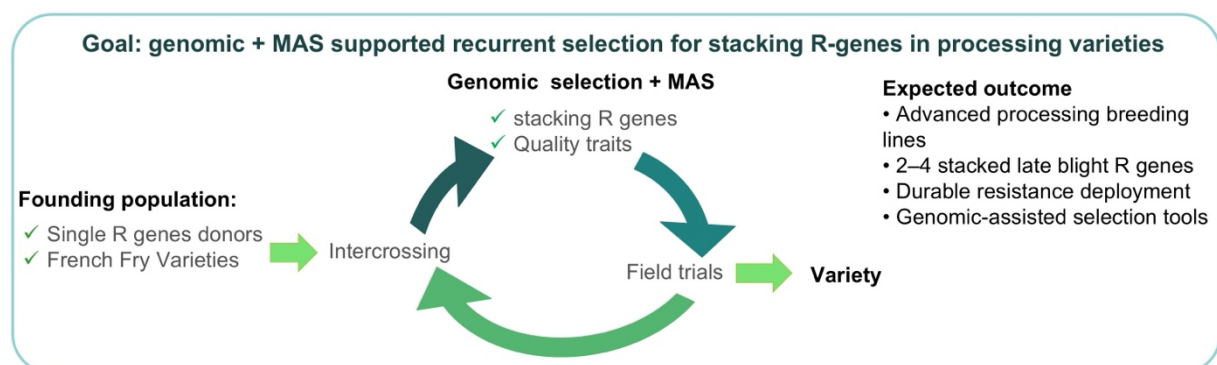


Figure 1. schematic overview of the IPMorama breeding strategy integrating marker-assisted and genomic selection for stacking late blight resistance genes in elite potato processing germplasm.

**Keywords:** late blight resistance; potato breeding; marker-assisted selection; genomic selection.

**Acknowledgements:** The project is funded by Horizon Europe Project IPMorama, Grant No. 101135348.



## Late blight population in Switzerland: current picture, future plans

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### Abstract

With an average of 6–7 fungicide applications per year, and over 14 in 2024, potato remains Switzerland's most fungicide-intensive arable crop. National policy aims to reduce pesticide risks by 50% by 2027, while the potato sector plans to expand the cultivation of robust varieties to 25% by 2028 and 80% by 2050. However, these efforts are challenged by the rapid evolution of *Phytophthora infestans*, with increasingly virulent and genetically diverse strains, such as EU43 and EU47, already present in Switzerland and potentially capable of overcoming resistance and reducing fungicide efficacy. Despite these developments, knowledge of the Swiss late blight population remains limited. This project seeks to address this gap by establishing a nationwide sampling network across diverse agroclimatic regions, from dry to humid zones, with strong farmer participation. The objectives are to characterize and better understand pathogen population structure and dynamics, evaluate the impact of agronomic practices on selection pressure, and assess interactions with cultivars and fungicides. In addition, the project aims to develop tools for the early detection of high-risk strains. Results will be integrated into the decision support system PhytoPRE platform to improve decision support and tailor disease management strategies and tested in a network of pilot farms to ensure rapid knowledge transfer and practical implementation.

## Identification and functional characterisation of a Rpi-R3a-like resistance gene from *Solanum bulbocastanum*

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### Abstract

Late blight, caused by *Phytophthora infestans*, remains one of the most destructive diseases of potato worldwide. Resistance breeding has historically relied on resistance (R) genes introgressed from wild *Solanum* species, including the well-characterised gene Rpi-R3a from *Solanum demissum*, which recognises the pathogen effector Avr3a. Understanding the evolutionary conservation and functional diversity of Rpi-R3a-like genes across wild relatives is important for broadening resistance resources for breeding. Here, we report the identification and characterisation of an Rpi-R3a-like gene, Rpi-R3ablb7645, from *Solanum bulbocastanum* accession 7645 using diagnostic Resistance gene enrichment Sequencing (dRenSeq). Sequence analysis revealed strong conservation within the coiled-coil and nucleotide-binding domains, with five amino acid substitutions located in the leucine-rich repeat region. Functional assays demonstrated that Rpi-R3ablb7645 recognises Avr3aKI with activity comparable to wild-type Rpi-R3a. In addition, the encoded protein localised to endosomes upon effector recognition, consistent with previously described Rpi-R3a behaviour and supporting conservation of immune function. Genomic and synteny analyses suggest that Rpi-R3a represents an ancient and evolutionarily conserved resistance gene lineage shared across divergent *Solanum* species. These findings expand current understanding of Rpi-R3a evolution and highlight wild germplasm as a valuable source of functionally conserved late blight resistance genes for future breeding strategies.

**Keywords:** *Phytophthora infestans*, *Solanum bulbocastanum*, dRenSeq, Rpi-R3a.

**Acknowledgements:** This work was supported by the Rural & Environment Science & Analytical Services (RESAS) Division of the Scottish Government through project JHI-B1-1, the Biotechnology and Biological Sciences Research Council (BBSRC) through awards BB/S015663/1; BB/X009068/1. The authors acknowledge the Research/Scientific Computing teams at The James Hutton Institute and NIAB for providing computational resources and technical support for the “UK’s Crop Diversity Bioinformatics HPC” (BBSRC grant BB/S019669/1).

## Graph-based pan-genome reveals the global spread and adaptation of *Phytophthora infestans*

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### Abstract

Late blight caused by *Phytophthora infestans* is a globally epidemic and devastating disease. Understanding its spread and adaptation is crucial to predicting impacts on potato production. To address this, we collected 237 global isolates to construct a graph-based pan-genome of *P. infestans*, and identified 5,130,254 SNPs and 31,293 SVs. Using these high-quality molecular markers, population genetic analysis revealed significant population differences across countries. Particularly, in China, *P. infestans* was divided into three geographically associated groups (CN-1, CN-2, CN-3). STRUCTURE analysis showed that *P. infestans* originated in Mexico and then spread globally with specific population structures. Notably, all Chinese populations are alien-derived, with the invasions of BLUE13, US-1, and SIB1 leading to the formation of the CN-1,2,3 groups respectively. In addition, we found that SV markers outperformed SNPs in resolving Chinese populations, indicating that SVs are the major driver of *P. infestans* population differentiation in China. Our work provides a high-resolution framework for decoding its global spread and local adaptation.

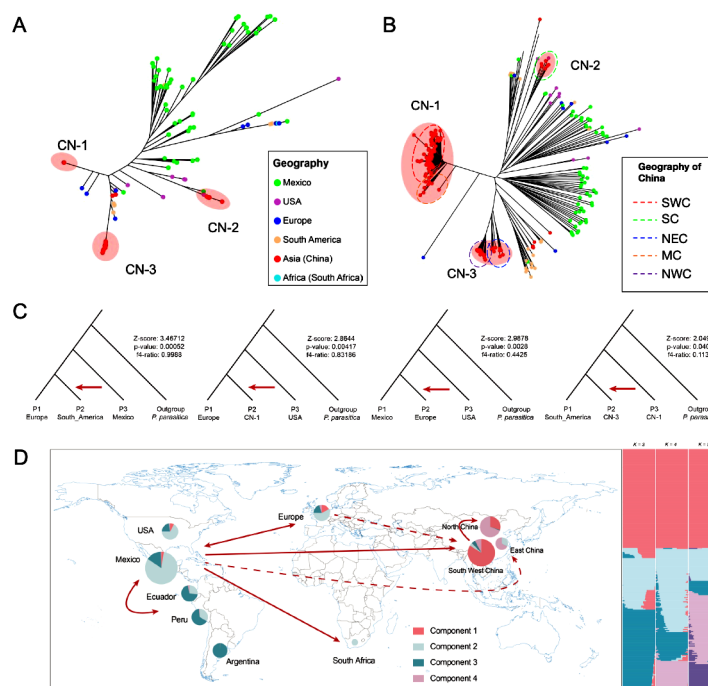


Figure 1. Analysis of the genetic structure and spread of *Phytophthora infestans* populations based on pan-genome.

**Keywords:** pan-genome, population, China, structure variation.

**Acknowledgements:** This research was supported by grants from Jiangsu Provincial Science and Technology Program Project (SBK2024043134) and National Key Research and Development Program of China (2023YFD1401000).

## PhytoAlert-EU: A practical tool allowing for monitoring of virulence and protection of R genes

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### Abstract

*Phytophthora infestans* remains one of the most destructive and difficult-to-control pathogens in potato production. Current management relies heavily on frequent fungicide applications, yet the pathogen has developed resistance to several active ingredients, including metalaxyl, fluazinam, and CAA- and OSBPi-based fungicides. At the same time, EU regulations and sustainability goals are reducing the availability of effective modes of action, meaning farmers will have fewer options to control late blight in the near future. More durable control strategies build on the strategies of Integrated Crop Management (ICM), which combines a range of sanitary measures, more resistant cultivars, decision support, monitoring, and—only as a final step—preventive spraying. ICM can reduce fungicide use by more than 50%, but still requires effective resistance genes and active ingredients. To support sustainable resistance deployment and raise awareness, the PhytoAlert app was developed as a farmer-driven, real-time late blight notification system. Users report infections at postcode level, generating a colour-coded map showing local infection pressure. Alerts can be filtered by Plantum resistance group, ensuring growers receive only relevant warnings. This enables timely adjustments in scouting intensity and crop protection strategies to protect R genes. Since its public release in 2025, adoption among Dutch potato growers has grown steadily. PhytoAlert shows how accessible digital tools can strengthen ICM by improving situational awareness and supporting sustainable potato production.

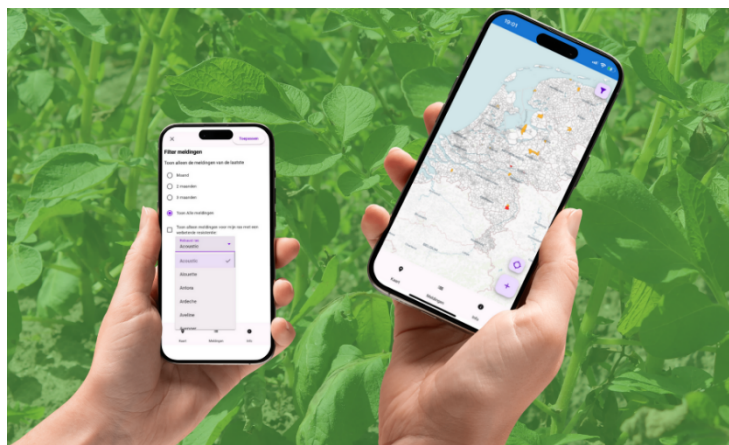


Figure 1. PhytoAlert app dashboard (source: [bionext.nl](https://bionext.nl)).

**Keywords:** *Phytophthora infestans*, resistance genes, Integrated Crop Management (ICM).

**Acknowledgements:** The PhytoAlert App was initiated by organic growers (Bionext) and was further developed at request of the Phytophthora Taskforce (initiated by BO Akkerbouw) by Wageningen University & Research, with funding from the ministry of Landbouw, Visserij, Voedselzekerheid en Natuur (LNVN), Europees Herstel Fonds, and Topsector Agri & Food.

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