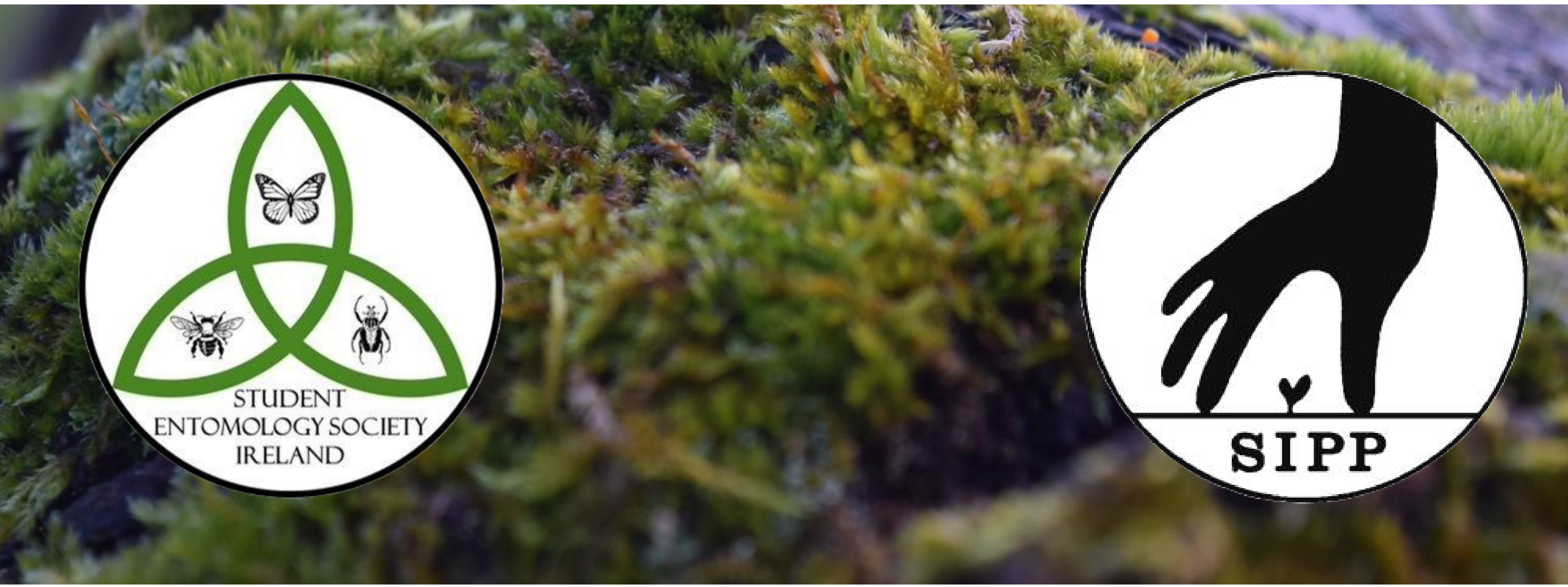
2025 Annual Scientific Conference

Society of Irish Plant Pathologists
Student Entomology Society Ireland

DAFM Backweston, Youngs Cross,
Celbridge, Co.Kildare

24th October 2025



Sponsorship

An Roinn Talmhaíochta,
Bia agus Mara
Department of Agriculture,
Food and the Marine

The organisers would like to thank the Department of Agriculture, Food and The Marine for hosting the conference.

Topics

Ash Dieback
Phytophthora
Fungicide
Genomics
Viruses
Diagnostics
Microbiomes
Forestry
Sequencing
Entomology
BYDV

Participating institutions

*affiliations from the presenting authors

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Agriculture and Food Development Authority

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Universidad Politécnica de Madrid

Heriot Watt University

PennState

Harper Adams University

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Timetable

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11:00	Jack Perry	Use of tolerant varieties to manage BYDV in Ireland
11:15	Ultan O'Donnell	Firmly Rooted: Using host trees to predict new pest invasions
11:30	Conor Copeland	Novel markers confer resistance to *Septoria tritici* blotch in a population of European winter wheat varieties
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13:50	Antoine Pichon	Distribution, impact and monitoring of *Bruchus rufimanus* in Irish faba bean crop
14:05	Wilson Acosta Morel	Survey of the phyllosphere fungal community within Irish forest
14:20	Ricardo J. G. Pimenta	Investigation of viruses infecting common ash (*Fraxinus excelsior*) in Ireland
14:35	Anne Parle	Pushing the boundaries of in-field plant pathogen detection: Applying CRISPR-Cas technology for point-of-need resistant strain testing of *Phytophthora infestans*
14:50		Coffee break & posters
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16:00	Marta Niedzicka	The survey of plant viruses across crops and viral reservoirs in Ireland
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SIPP x EntoSoc Annual Conference 2024

In 2024, the Society of Irish Plant Pathology (SIPP) committee began planning its annual scientific conference on the back of learnings from previous scientific conferences, including the Louise Cooke Memorial Meeting. The conference aimed to empowering early career researchers in plant pathology-themed areas and to strengthen SIPP's connections with other societies. The SIPP committee decided to team up with Student Entomology Society Ireland (EntoSoc), a relatively new society, to showcase early career research in entomology, plant pathology and related areas of plant science. The conference was held in Teagasc Oak Park and featured talks from multiple institutions and topics.

Attendees at the 2024 SIPP x EntoSoc Conference

Society Background

Society of Irish Plant Pathologists

Founded in 1968, our society includes members from across the Island of Ireland, all working in various plant pathology disciplines. The society is dedicated to actively promoting the science of plant pathology among students and professionals.

Student Entomology Society Ireland

Founded in 2021, the objective of our society was to act as a network for Irish entomological research and to bring together like-minded people, to facilitate resource sharing and collaboration. To date, our member list has grown to include academics, students from all levels, and general enthusiasts. Our seminar series has hosted international guest speakers, and we've organised a number of in-person events, in collaboration with societies like SIPP and the Royal Entomological Society. Our society is dedicated to advancing the study of insects and connecting all who are fascinated by them.

Oral Presentations

Welcome Keynote Address

Louise Byrne

Department of Agriculture, Food and the Marine

Louise Byrne is the Deputy Chief Inspector in the Department of Agriculture, Food and the Marine and the Chief Plant Health Officer for Ireland. She has responsibility for food and feed safety, plant health and crop policy.

Louise studied Agricultural Science (specialising in Animal Science) in University College Dublin and she also holds a Bachelor of Arts Degree in Law. Louise has worked for the Department of Agriculture, Food and the Marine since 1998 primarily in the area of official controls along the agri food and feed chain. She headed up Brexit and International Trade Division coordinating the Departments response to and preparation for Brexit before being appointed to her current role in 2022.

Fungicide timings for *Ramularia* Leaf Spot in Barley

Edwina Nolan, Angela Feechan, Neil Havis, Henry Creissen, Steven Kildea

Heriot-Watt University & Teagasc

Ramularia leaf spot (RLS), caused by the fungus *Ramularia collo-cygni*, is a major threat to barley production globally. The disease typically develops post-anthesis and, if left untreated, can significantly reduce yield and quality. Fungicides are essential for RLS control, but fungicide resistance development and the withdrawal of key active ingredients due to regulatory changes have increased challenges. This project investigated effective fungicide strategies for RLS control. A systematic review of existing literature on RLS management in barley was conducted, but due to insufficient data (e.g., lack of confidence intervals and standard errors), a meta-analysis could not be performed. From the data extracted it is clear a knowledge gap exists and highlights the need for further studies to refine RLS management strategies. Field trials were conducted at two Irish sites under varying disease pressures. Treatments with varied spray timings and frequencies were visually assessed for RLS severity, and the Area Under the Disease Progress Curve (AUDPC) was calculated from three winter barley assessments. Analysis of disease severity and yield data will evaluate fungicide performance and define optimal spray timings. Additionally, flag leaf and grain samples were collected for fungicide resistance monitoring and sensitivity testing, aiming to prolong the efficacy of current, invaluable chemistries. These findings will help develop more sustainable management practices for RLS.

Development of phyllosphere suppressive communities towards *Xanthomonas euvesicatoria pv perforans* and their potential applications a biological control against bacterial spot of tomato

Constanza Bartolomeo Koninckx, Sara Hermann, Beth Gugino, Kevin Loren Hockett

Pennsylvania State University & Department of Agriculture, Food and the Marine

Tomatoes suffer from up to 66% yield losses due to bacterial spot. Greenhouse and high tunnel grown tomatoes are usually planted in high densities, creating ideal conditions for the rapid spread of bacterial spot. To combat this disease, farmers rely on frequent copper-based bactericide applications, leading to the emergence and spread of copper-resistant bacteria. The phyllosphere contains a diverse community of microorganisms that play a defensive role in pathogen invasion. Recent work suggests that this community could be harnessed to create a versatile biocontrol that could be effective against copper-sensitive and copper-resistant bacteria. In this study, phyllosphere communities were selected for suppression of bacterial spot through host-mediated indirect selection (passaging) with the objective of employing an augmentative biological control strategy. It was hypothesized that the phyllosphere community would functionally contain multiple modes of action, limiting the pathogen's ability to evade biological control, enhancing suppression. The study found that plants treated with suppressive communities displayed a significant decrease in disease severity compared to pathogen-only and copper treatments. This study provides the foundation for using phyllosphere suppressive communities in plant disease management and offers new information on bacterial spot management strategies.

Use of tolerant varieties to manage BYDV in Ireland

Jack Perry, Stephen Byrne, Louise McNamara, Joe Roberts and Tom Pope

Teagasc & Harper Adams University

Aphids reduce grain yield and quality in cereal crops via direct feeding and vectoring viruses. The most economically important aphid vectored virus in cereals is barley yellow dwarf virus (BYDV), which can cause up to 80% yield losses. Managing aphids is becoming increasingly challenging due to (i) reduced insecticide availability, (ii) insecticide resistance, (ii) lack of robust thresholds and (iv) climate change. Navigating these challenges requires robust alternative management approaches to reduce the risk of BYDV in Irish cereals. Breeding cultivars of cereals, which have genes for resistance/tolerance to BYDV is an environmentally conscious, efficient and affordable alternative management approach. Cultivars of winter barley with tolerance are increasingly being sown by Irish farmers. We carried out a three year in-field trial at two sites, growing plots of tolerant varieties both with and without an insecticide application. Across the three years, 13 tolerant varieties were assessed. During the growing season every plot was assessed for aphids at growth stage 31, BYDV symptoms at growth stage 47 and yield was recorded post-harvest. Our results show, when left without an insecticide application tolerant varieties suffer a reduced yield loss compared to susceptible varieties.

Firmly Rooted: Using host trees to predict new pest invasions.

Ultan O'Donnell, Conor Francis McGee, Andy Bourke, Jon M Yearsley

Department of Agriculture, Food and the Marine & University College Dublin

Sustainable forestry management and the ecosystem services that forestry provides is at increasing risk from the invasion of non-native forest pests. Identifying which invasive species pose the greatest risk of establishment on the island of Ireland would help us provide an evidence base to streamline risk assessment and appropriately allocate detection and management resources. However, there is often not enough location data to describe the niche where these pests occur currently, limiting our ability to quantify risk and prioritise potential pests. To address this, we developed and tested a novel quantitative approach using host tree location data in lieu of pest data to develop 131 Species Distribution Models (SDMs) to describe the potential niche of each pest, ranking their relative risk of establishment. This method was applied to oak and pine forestry pests in the EPPO global database to identify their suitability to Ireland under current and future climate conditions, and was validated using independent pest data. Our findings show that Ireland’s climate is suitable for many forestry pests, and that our methodology of modelling host habitat niches is effective at ranking the relative risk of pests, identifying opportunities for use where pest data is incomplete.

Novel markers confer resistance to *Septoria tritici* blotch in a population of European winter wheat varieties

Conor Copeland, Julio Isidro y Sánchez, Humberto Fannelli, Fiona Doohan

Universidad Politécnica de Madrid & University College Dublin

Septoria tritici blotch (STB) is a major disease of wheat in Northern European conditions, which has seen success in marker-associated breeding to confer resistance. In order to add to the library of resistance sources, a panel of 151 European winter wheat varieties was screened for STB tolerance. A wide range of STB severity was observed, with Southern European varieties particularly susceptible. A Genome-Wide Association Study (GWAS) was performed, and three novel markers were identified as being associated with STB resistance: IWB5774 on chromosome 2D, and IWB72742 and IWB11406 on chromosome 1B. These markers all lie within annotated genes, with IWB5774 being found in the coding region of TraesCS2D03G0669200, an uncharacterized protein similar to TaBx3D, which is involved in benzoxazinoid synthesis (Nomura et al., 2008). IWB72742 is in the 3' UTR of WD40 repeat-containing protein WDR91, an effector which associates with Rab7 (Ma et al., 2024). IWB11406 is in the 3'UTR of NAP1, a nucleosome assembly protein linked with disease resistance in *Arabidopsis* (Feng et al., 2023). All marker-associated genes are in families which are associated with fungal pathogen resistance in plants, making them prime candidates for further research into their potential to confer resistance to STB.

Clonal Variation in Fitness and Barley Yellow Dwarf Virus Transmission Efficiency of *Metopolophium dirhodum* on Winter Barley

Md Munir Mostafiz, Daniel J. Leybourne, Stephen Byrne, and Louise McNamara

Teagasc & Liverpool University

Metopolophium dirhodum, the rose-grain aphid, is a major pest of cereals in Europe, causing yield loss both through feeding and transmission of Barley yellow dwarf virus (BYDV). Differences in biological performance among aphid species and clones can strongly influence pest pressure and virus spread, yet these factors remain poorly understood for *M. dirhodum*, particularly in comparison with the English grain aphid (*Sitobion avenae*). In this study, three geographically distinct clones of *M. dirhodum* (MD-Irish, MD-York, MD-Norfolk) were assessed under controlled conditions for survival, development time, fecundity, longevity, and reproductive period. The Irish clone of *M. dirhodum* exhibited significantly greater adult longevity, fecundity, and reproductive duration compared to *S. avenae*, resulting in a higher intrinsic rate of increase ($r_m = 0.288$) and greater potential for rapid population growth. Virus transmission assays revealed that M. *dirhodum* was an efficient vector of BYDV-MAV (68.3%) but showed very low efficiency for BYDV-PAS (5%). The results demonstrate that demographic variation underpins fitness differences among aphids, while transmission efficiency is virus strain-specific, with the MD-Irish clone emerging as a key vector of BYDV-MAV. These findings strengthen our understanding of aphid pest risk and virus epidemiology, informing predictive models and region-specific integrated pest management strategies.

Detection and analysis of the first Asian Hornet nests in Ireland

Aidan O'Hanlon

National Museum of Ireland – Natural History

The Asian Hornet *Vespa velutina* was accidentally introduced to France in 2004, and has since spread to many other countries across continental Europe. The hornet is a predator of other insects and is listed as a regulated invasive species of union concern. It was first recorded in Ireland in 2021when an individual was found in Dublin. Chaired by the NPWS with input from the NBDC, NMI and DAFM, the Asian Hornet Management Group (AHMG) followed-up on a second Irish record from Cork in August 2025. The AHMG quickly confirmed the presence of the species in Cork, and NPWS rangers triangulated the nest location soon after. Separately, a second nest in Cobh was also tracked down and controlled. Both nests have been dissected to study colony demographics and specimens have been prepared for genetic analysis. Results from the nest dissections show that the Cork and Cobh colonies were mature, containing ca 12,000 and 2,000 individuals respectively. Both nests were controlled before they produced males or future queens and there is no evidence that any other nests went undetected in the area. It is believed that both nests are unrelated, and that their occurrence within the same county is coincidental, since both are within a kilometre of busy ports. Genetic analysis will determine whether the nests were related and inform monitoring strategies for Spring 2026.

Distribution, impact and monitoring of *Bruchus rufimanus* in Irish faba bean crop

Antoine Pichon, Louise McNamara, Eamon Nolan, Sheila Alves

Teagasc & SETU

The Broad Bean Bruchid Beetle (*Bruchus rufimanus*) is a pest of faba bean across Europe, following a univoltine life cycle. Adults colonise fields during flowering and lay eggs on green pods. Larvae develop inside seeds, causing severe damage that significantly reduces grain quality. In Ireland, this pest was first recorded in 2003 in County Clare, far from faba bean production. The first detection on crops dates on 2016. Since then, populations have expanded and become established nationwide. To assess its distribution and impact, we collaborated during three years with Irish farmers who deployed traps in their fields. After harvest, seeds were collected and analysed for larval damage. Preliminary observations show that damage levels vary between years, and *B. rufimanus* populations are now present across all surveyed regions. Final analyses, including quantification of infestation levels and assessment of natural enemies such as larval parasitoids, are ongoing. Comprehensive results and implications for integrated pest management in Irish faba bean production will be presented.

Survey of the phyllosphere fungal community within Irish forest

Wilson Acosta Morel, Flavio Storino, Richard O'Hanlon, Jonathan Yearsley

UCD & DAFM

One of our objectives in the AdaptForRes project is to create an inventory of fungal pathogens and endophytes in Irish forests. For this end we carried out two surveys in which we conducted culturomics (i.e. isolates and DNA sequenced) from leaves of 3 different types of forest trees (Oak, Pine, Spruce) in 8 different locations (Kindlestown Wood, Ballymoyle Hill, Townley Hall, Tibradden/Cruagh, Glendalough, Devil's Glen, Djouce Wood and Roddenagh Wood). Each location had all three hosts sampled. DNA of the isolated fungi was extracted and ITS PCR was performed and sequenced. The sequences were later used for the identification of endophyte fungi present in Irish forests. Preliminary results provide us with a view of the diversity of fungi within Irish forests in which there seems to be more commonality between fungi in the same host tree regardless of location. Analysis to identify the potential pathogens present in the fungal community will be presented.

Investigation of viruses infecting common ash (*Fraxinus excelsior*) in Ireland

Ricardo J. G. Pimenta, Marta Niedzicka, Stephen Byrne, Dheeraj S. Rathore

Teagasc, Forestry Development Department; Teagasc, Crop Science Department, Oak Park Research Centre, Carlow

Teagasc

Common ash (*Fraxinus excelsior*) is the second most widespread native broadleaf tree in Ireland, where it holds major ecological, economic, and cultural importance. However, this species is under severe threat from ash dieback caused by *Hymenoscyphus fraxineus*. Viruses can both exacerbate host stress and provide opportunities for biocontrol, but their diversity in F. excelsior remains poorly characterised. A survey of the viral diversity in Irish ash was conducted on 28 trees from gene banks, field trials, and glasshouses, including symptomatic and asymptomatic individuals. Leaf RNA was extracted, rRNA-depleted, and sequenced on an Illumina platform, producing >22,000 reads/sample. Data were processed through a virus discovery pipeline including quality control, host-genome filtering, taxonomic classification, genome assembly, and homology searches. Two viruses previously described in ash in continental Europe were identified and had complete genomes assembled: ash shoestring-associated virus (ASaV) and privet leaf blotch-associated virus. Reads similar to Nepovirus sequences were also detected in two symptomatic trees, indicating a potentially novel virus. RT-PCR and RT-LAMP assays were designed, confirming the original detections and revealing the presence of ASaV and the new virus in additional symptomatic trees from across Ireland. Current work is focused on transmission trials to evaluate interactions with H. fraxineus.

Pushing the boundaries of in-field plant pathogen detection: Applying CRISPR-Cas technology for point-of-need resistant strain testing of Phytophthora infestans

Anne Parle, Weili Guo, Ciara McDermott, Temi Akinbola, Stephen Kildea, David O'Connor

Dublin City University & Teagasc

DNA-based detection methodologies are increasingly being applied across the spectrum of diagnostics including plant pathogen monitoring. While PCR and DNA sequencing-based methods are a robust approach, these are more suited to central laboratory testing due to their associated energy and cost requirements. More recent advances in isothermal techniques have forged a path for developing in-field testing kits. Among these, Loop-Mediated Isothermal Amplification (LAMP) or Recombinase Polymerase Amplification (RPA) have been a popular approach with some limitations. Inspired by advances in clinical diagnostics, we coupled RPA with CRISPR-Cas technology for the detection of various target species with a view to developing on-site testing solutions. RPA-CRISPR-Cas requires a temperature of just 37°C and offers the most superior specificity of all currently available isothermal methods. We have successfully developed an RPA-CRISPR-Cas assay that can exclusively detect late potato blight (*Phytophthora infestans*) using either fluorescence or lateral flow detection (akin to Covid19 antigen type test) formats. We have advanced our testing capability further, through the development of a lateral flow test that can exclusively detect a resistant strain of *Phytophthora infestans*. These DNA based tests can be used on any sample type, including infected potato leaves or a bioaerosol derived environmental DNA sample.

Insights into the spread of *Phytophthora ramorum* in Ireland.

Richard O'Hanlon

Department of Agriculture, Food and the Marine

Phytophthora ramorum is a fungus-like pathogen of a wide range of shrubs and trees. It is a regulated organism, and was first found in Ireland in 2002. This study examines the population genetics of more than 120 isolates of the pathogen spanning 20 years in Ireland and Northern Ireland. The analysis helps us to understand how the pathogen spread across Ireland, and puts the Irish population in the wider European context.

Reporting on the lure efficiency and sample quality thresholds in tortrix moth surveillance of Irish forests

Ryan Weir, Weir Joanna Kirbas, Ciara Isaac, Peter Williams, Archie Murchie, Florentine Spaans.

AFBI & Queens University Belfast

Several micromoth species belonging to the family Tortricidae are listed as Union Quarantine Pests (UQP) under EU plant health regulations and require surveys to confirm the absence of these hosts in EU territories. A general approach can be taken by using light traps or a more targeted approach by using lure-baited traps. The UQPs relevant to forest health include species of genera *Acleris*, and *Choristoneura*. Several native species of these genera are also present in Ireland. While targeted pheromone lures are available for some of the regulated species, it is expected that these will also attract other closely related species. These could therefore be used as positive controls to determine trapping effectiveness. Here we present the early findings from tortrix moth surveillance in Northern Ireland with a focus on sample collection timing and its impact on sample quality as well as an assessment on the efficacy of targeted lures. Our study suggests that lures containing 11-tetradecenyl acetate are more effective for catching native tortrix moths than a standard light trap in terms species richness and abundance and surveying effort. We further determined that a sample collection timeline of two weeks generated samples of acceptable quality in 80% of instances.

Decoding the grain microbiome for safer oats

Natarajan Subramani, Subramani Natarajan, Israel Ikoyi, Amal Khal, Farhana Affroze, Chanemouga Soundharam Arunachalam, Tancredi Caruso, Fiona Doohan

University College Dublin & University College Cork

Fusarium langsethiae infection in oats is a major food safety concern because both the infection and the associated accumulation of T-2 and HT-2 mycotoxins typically remain asymptomatic. As a result, contamination often goes unnoticed until harvest, highlighting the urgent need for new approaches to understand and manage this hidden risk. We hypothesised that this cryptic pathogenesis is linked to shifts in the oat grain microbiome that either promote or suppress toxin accumulation. To test this, we profiled bacterial and fungal communities from 87 oat cultivars with contrasting toxin levels (<20–573 µg/kg) using 16S rRNA and ITS2 amplicon sequencing. Pathogen inoculation significantly increased bacterial richness and diversity, while fungal diversity remained relatively stable. Community composition analyses revealed measurable shifts in bacterial assemblages, with certain genera enriched under infection and others depleted, including putatively protective taxa. Fungal communities showed more targeted responses, marked by enrichment of Fusarium alongside the loss of beneficial groups. Our findings demonstrate that asymptomatic *F. langsethiae* infection actively restructures the oat grain microbiome, leading to bacterial dysbiosis linked with mycotoxin accumulation. This is the first characterization of the oat grain microbiome under *F. langsethiae* challenge, highlighting microbial signatures that may serve as biomarkers and targets for microbiome-based strategies to improve oat safety.

The survey of plant viruses across crops and viral reservoirs in Ireland

Marta Niedzicka, Louise McNamara, Stephen Byrne

Teagasc

Plant viruses represent a substantial threat to global agriculture. Although understanding viral diversity is essential for optimising disease management strategies, there is a gap of knowledge available regarding viral diversity across Europe, with no surveys conducted thus far in Ireland. The HealthyPlants project addresses this gap by establishing a baseline of plant viruses present present in various crops and wild plant communities, thereby providing valuable insights when assessing phytosanitary risk of potential or emerging threats. In this project, we employed high-throughput sequencing (HTS) to conduct an untargeted survey of viruses, assessing their diversity not only in commercial crops but also in potential viral reservoirs. This survey facilitates creation of the first national database of plant viral sequences in Ireland. Here, we present three case studies highlighting findings from the survey efforts: I) identification of plant viruses present in Irish legumes, II) the utilisation of local viral strains to develop new targeted detection methods, and III) the potential role of pastures and arable margins as reservoirs for important cereal viruses.

Poster Presentations

Assessing the impact of *Phytophthora ramorum* to hybrid larch trees in Ireland

Laura Guillardin, Niall Farrelly

Teagasc

Japanese larch and European larch species have largely been affected by *Phytophthora ramorum* since its appearance in Ireland. However, there is a scarcity of studies looking at the level of tolerance or susceptibility of the hybrid larch towards this disease. Other studies have suggested that European larch may be more resistant to the pathogen, however, hybrid larch varieties produced in seed orchards may contain higher proportions of Japanese larch than European larch. Therefore, we aim to investigate the genetic makeup of the hybrids planted in three trial sites in Ireland that include trees from different sources. These sources include various geographic regions and are either pure European, pure Japanese or hybrid larch. Our hypothesis is that hybrids with maternal European genotypes may show higher levels of tolerance. To look into this, we will use molecular markers to identify the species and to define which type of hybrids exist in the trial sites. To confirm the presence of the fungus-like oomycete in the sites, we will place water containers and will use the *P. ramorum* LAMP detection kit. Finally, aerial images will be used to analyse the crown symptoms to assess the individual and species level of infection.

Exploring Root-Associated Microbes to Combat *Phytophthora alni*-Induced Alder Dieback

Emma Fuller, Kieran Germaine, Dheeraj Singh Rathore

Teagasc & SETU Carlow

Common alder (*Alnus glutinosa*) plays a vital role in wetland ecosystems by promoting biodiversity through nitrogen fixation and enriching soils via symbiosis with nitrogen-fixing bacteria. However, the emergence and spread of dieback disease caused by *Phytophthora alni* has led to declines in alder populations, posing an ecological threat. Gaining a deeper understanding of the rhizosphere—the dynamic zone where tree roots interact with soil microorganisms—is a crucial step toward developing sustainable strategies for disease management. This study explores the microbial communities associated with alder roots and their surrounding rhizosphere, with a focus on identifying bacterial and fungal taxa that may enhance resistance *to Phytophthora alni*. A total of 193 culturable microorganisms were isolated and screened through dual culture assays to evaluate their antagonistic activity against *P. alni*. This screening enabled the selection of promising biocontrol candidates for potential use in disease suppression and enhancement of alder resilience. Among the isolates, 24 bacterial strains—primarily from the genera *Pseudomonas* and *Bacillus*—exhibited strong in vitro inhibition of *P. aln*i growth. Additionally, 8 fungal isolates, notably from the genus Trichoderma, demonstrated significant antagonistic effects. Inhibition levels ranged from 36% to 83% across microbial candidates. These results highlight the potential of specific root-associated microbes as biocontrol agents against *P. alni*. These findings provide a foundation for developing microbe-based strategies to support forest health and ecological restoration. By identifying taxa demonstrating antagonistic activity, the study advances our understanding of root–microbe interactions and highlights the critical role of rhizosphere research in addressing emerging threats to tree health

Analysing the microbiome of ash trees affected by dieback in Northern Ireland

Eugene Carmichael, Neil Warnock, Rhonda Swan, Kirsty McLaughlin

Agri-Food & Biosciences Institute

Ash dieback, caused by the fungus *Hymenoscyphus fraxineus*, has devastated native populations of ash trees across Europe since first appearing over 30 years ago. Recently, Next Generation Sequencing (NGS) has enabled in-depth analysis of the microbiome of ash trees, allowing identification of the microflora therein. We used NGS to analyse the microbiome of ash trees across NI which have been affected to varying degrees by ash dieback to determine differences in populations according to health status.

The evolution of fungicide resistance in Irish *Zymoseptoria tritici* populations

Tapiwa Nyakauru, Fiona Hutton, Stephen Byrne and Steven Kildea

Teagasc

Septoria tritici blotch, caused by the fungal pathogen *Zymoseptoria tritici*, is the most economically damaging disease of winter wheat across northern and western Europe. Management strategies depend largely on fungicides, particularly demethylation inhibitors (azoles), quinone outside inhibitors (QoIs), and succinate dehydrogenase inhibitors (SDHIs). Resistance to these fungicides has been reported in field populations of Z. tritici for over a decade and continues to threaten their effectiveness. In this study, we present an overview of how this resistance has evolved and assess the underlying molecular mechanisms. We assessed the decrease in fungicide sensitivity using in vitro assays and, using molecular techniques, we investigated the alterations in succinate dehydrogenase subunits B, C, and D, as well as inserts in the major facilitator superfamily transporter 1 (MFS1) and the sterol 14α-demethylase gene (CYP51) promoters, and sequence variations in the CYP51 gene. This work shows variations in genes essential for fungicide resistance and provides valuable information to support the development of sustainable strategies for managing septoria tritici blotch.

Investigating Spatio-Temporal Dynamics of Oat Mosaic Virus (OMV) in Irish Tillage Systems

Rabita Zaman, Atikur Rahman, Ewen Mullins, Stephen Bryne, David Fitzpatrick

Teagasc & Maynooth University

Oats are a significant crop in Irish agriculture both economically and rotationally. Oats are at risk, however, from the Oat Mosaic Virus (OMV) that is transmitted by the soil obligate parasite *Polymyxa graminis*. OMV has been shown to reduce yields by 50% and render land infertile for subsequent cultivation. Despite its impact on crops, the epidemiology of OMV in Ireland is little understood. This research aims to fill this knowledge gap with the assessment of spatio-temporal dynamics of OMV in Irish tillage crops. The research aims for three principal objectives: (1) development of a molecular diagnostic test for the diagnosis of P. graminis and OMV, (2) mapping the spatial distribution of OMV over principal oat-producing regions in Ireland, and (3) establishing the correlation between OMV load and yield loss. Field surveys, molecular diagnostics, and disease severity ratings will inform potential control measures and breeding for resistant oat cultivars. Eventually, the outcomes of this research will inform the development of effective management practices for OMV, so that the Irish oats industry continues to be sustainable and the risks associated with the virus are minimized.

Spruce seedling dormancy: key adaptive trait for future climate.

Romane Guernalec, Tomás Byrne, Niall Farrelly , Conor O'Reilly, Brian Tobin

Teagasc & University College Dublin

Irish forestry relies heavily on Sitka spruce, a North American species that thrives here due to similar oceanic climates. But rapid climate change may affect its growth and establishment. Understanding its capacity to adapt will guide future provenance choice, and more southern provenances may better match Ireland’s projected conditions. Bud flushing is a key adaptive trait in temperate trees, triggered by accumulated cold (chilling) to break dormancy and resume spring growth. This study examined phenological responses of three Sitka spruce provenances to varying chilling durations. Controlled environments assessed dormancy levels after chilling. Terminal bud flushing was the main response variable, with additional traits—height, needle chlorophyll content, primordia count and growth cessation—measured throughout the season. Reduced chilling delayed flushing in all provenances. Although treatment and interaction effects were significant, provenance differences appeared only under short chilling, indicating that the timing of chilling and subsequent warming relative to dormancy depth may heavily factor all provenances growth cycles. Southern provenances typically grow longer and yield more, while Northern ones stop earlier, yet this study suggests Northern trees may cope better with minimal chilling. These findings matter for seedling establishment and early growth under climate change.

Ash sawfly (*Tomostethus nigritus)* in Ireland

Florentine Spaans, Weir, R., J. Kirbas, S. Clawson, C. Hall, A. Murchie

AFBI

Ash sawfly (*Tomstethus nigritus F*.) is typically a sporadic pest of European ash (*Fraxinus excelsior* L.) It is a defoliator of ash in the larval stage, with the potential to cause significant damage. It is found across Europe, including Great Britain (GB), and in some areas of Europe it has completely defoliated established stands of ash. However, in GB the damage has been limited to urban environments. Ash sawfly was first recorded on the island of Ireland in Belfast, Northern Ireland, in 2016. In the Belfast area, there has been consistent defoliation of ash trees in parkland, hedgerows and riparian habitats, with the sawfly gradually extending its range, with in some cases evidence of inadvertent carriage on motor vehicles. In 2021, ash sawfly was found in counties Kildare and Dublin in the Republic of Ireland. The consistent defoliation of ash trees each year is not typical of ash sawfly outbreaks elsewhere, which normally subside after a few years. This work assesses the spread of ash sawfly around Belfast, the phenology of the pest and the impact of annual ash sawfly defoliation on ash tree growth. It also investigates the interaction of ash sawfly with ash dieback (*Hymenoscyphus fraxineus*).

Identifying and Conserving Dutch Elm Disease-Resistant Elms in Ireland

Karuna Shrestha, Oliver Gailing, Dheeraj Singh Rathore

Teagasc & University of Göttingen

Elms (*Ulmus spp*.) are ecologically, economically, and culturally important broadleaf trees in Europe. Once abundant across hedgerows, woodlands, and urban landscapes, elm populations experienced catastrophic decline following the spread of Dutch elm Disease (DED), caused by the fungal pathogens *Ophiostoma ulmi* and *O. novo ulmi*. The disease is transmitted primarily by elm bark beetle (*Scolytus spp*.), which vector spores between the trees. Symptoms typically appear in mid-summer and include leaf yellowing and wilting, crown defoliation and eventual tree death. Variation in resistance to DED has been observed within and between elm species, underscoring the need to identify and conserve naturally resistant individuals. This study aims to locate, collect and selectively propagate surviving elms across Ireland to establish a gene-bank. To-date, a gene bank comprising 41 putative 'resistant' elms has been established, alongside the collection of an additional 65 genotypes from the Irish landscape, with further sampling planned to expand the collection. Regular monitoring and screening for resistance are ongoing to validate field performance. These efforts provide a foundation for the long-term conservation, propagation, and potential reintroduction of elms into Irish landscape.

Pathogen Mechanisms to Tolerant Ash: Molecular Insights into Ash Dieback Disease

Abhishek Singh, Fiona Doohan, Richard O'Hanlon, Stephen Byrne, Dheeraj Singh Rathore

Teagasc, University College Dublin & Department of Agriculture, Food and the Marine

Hymenoscyphus fraxineus (formerly *H. pseudoalbidus*), an ascomycete fungal pathogen, is responsible for Ash Dieback Disease (ADB), which has caused extensive decline and mortality of common ash (*Fraxinus excelsior*) across Europe, leading to major ecological and economic losses. Effective mitigation strategies require a deeper understanding of pathogen virulence and host defence mechanisms.

As part of AshPath work package under the AshforFuture project, this study aims to:

I. Assess the virulence variability among *H. fraxineus* isolates collected from different geographical regions.

II. Investigate pathogen population structure using molecular approaches.

III. Explore host-pathogen interactions with omics-based tools (metabolomics, proteomics, or transcriptomics) to understand infection dynamics.

To date, a virulence screening experiment involving ten *H. fraxineus* isolates from different locations within Ireland has been conducted using direct stem inoculations on ash saplings. Significant differences in lesion development were observed three months post-inoculation, with one isolate strain (C221/13) from Northern Ireland displaying hypervirulent characteristics based on lesion length. These preliminary results provide a foundation for selecting candidate isolates for subsequent genomic and other omics-based analyses.

This work will deepen our understanding of pathogenicity mechanisms and disease progression in Ireland. Ultimately, it will inform breeding of tolerant ash genotypes and contribute to wider European conservation strategies for ash.

NATSEED – Developing Seed Sourcing Strategies for Native Species

Saoirse O'Neill, Patrick Langan, Colin Kelleher, Dheeraj S. Rathore

Teagasc

The current targets of the Irish government to increase broadleaf forestry cover brings about an urgent need for suitable seed sources. NATSEED is a one-year DAFM-funded project developed to identify gaps in supply of forest reproductive material (FRM) and explore sustainable solutions. Drawing on the knowledge of species biology, geographical distribution and genetic diversity, the project will develop practical seed sourcing strategies aligned with national forestry targets. Its focus is on high-priority species such as alder, downy birch, silver birch, sessile oak, pedunculate oak and Scots pine, with hazel and holly as medium to low priority.

The project takes a multi-pronged approach including an examination of the effect of long-term storage on seed viability and a GIS analysis to inform seed sourcing in Ireland. The seed sourcing strategies will give specific guidelines for each species to facilitate sourcing and collecting of viable seed from suitable locations and suitable material. The outcomes will support seed suppliers and nurseries in managing mast-year surpluses and help ensure a reliable FRM supply for sustainable native broadleaf planting initiatives.

Evaluating *Betula pendula* Growth from UK Seed Sources under Irish Environmental Conditions

Robert Pim, Oliver Sheridan, Tomás Byrne, Junliang Zou, Nick McCarthy, Dheeraj Singh Rathore

Teagasc & South East Technological University

Silver birch (*Betula pendula* Roth) is a fast-growing native hardwood tree valued for its ecological and economic contributions in Ireland and Europe. With increasing demand for high-quality hardwood across northern Europe, silver birch improvement programmes have expanded its potential as a timber species. In Ireland, a national improvement programme was initiated to address this demand, drawing primarily on Irish-origin trees but also evaluating supplementary material from the UK to assess clinal adaptation under local conditions.

This study analysed tree height and diameter at breast height (DBH) in a long-term field trial established in 2014, comprising half-siblings from UK seed orchard families planted in randomised blocks alongside commercially sourced controls. Measurements collected over successive years, up to 2025, provide insights into growth dynamics and comparative performance.

Preliminary results indicate that some UK-origin families outperform controls in both height and DBH, while variation at family level highlights potential candidates for integration into the Irish breeding populations. Ongoing analysis will refine these comparisons and guide decisions on the incorporation of UK material into future selection cycles. Ultimately, this research contributes to assessing the suitability of UK-origin silver birch for advancing improved, climate-adapted breeding populations in Ireland.

Molecular Strategies for Identifying and Enhancing Ash Dieback Tolerance

Bharatheeswaran Murugan, Richard G F Visser, Marinus J.M. Smulders, Joukje Buiteveld, Stephen Byrne, Dheeraj Singh Rathore

Teagasc & Wageningen University and Research

Ash dieback (ADB), caused by the invasive fungal pathogen Hymenoscyphus fraxineus, poses a severe threat to common ash (*Fraxineus excelsior*) across Europe, with profound ecological and economic consequences. Although natural tolerance is estimated at around 3%, the Teagasc ash breeding programme is dedicated to identifying, propagating and field-trialling tolerant genotypes to ensure durable disease tolerance. As conventional breeding is a long-term process, biotechnological tools may provide opportunities to accelerate the progress.

Therefore, the LivingAsh project focuses on three main objectives:

Characterize transcriptomic responses of tolerant and susceptible ash genotypes to *H. fraxineus*.

Develop molecular and biochemical markers for screening of large ash populations for dieback disease tolerance

Explore New Genomic Techniques (NGTs) to study gene-function in *F. excelsior*.

Overall, these approaches will deepen scientific understanding of the tolerance mechanisms and provide tools to directly support the ash breeding efforts in Ireland and across Europe.

BirchGen: Developing a Genomic Resource for Downy Birch Breeding and Conservation

Tomás Byrne, Stephen Byrne, Dheeraj Singh Rathore

Teagasc

Downy birch (*Betula pubescens*), a native broadleaf species, has a complex evolutionary history and a allotetraploid genome arising from hybridisation between two progenitor species. Despite its ecological and commercial value, breeding progress in birch has been limited by long generation times and limited genomic resources to-date.

Therefore, the BirchGen project aims to generate the first high-quality reference genome for downy birch to underpin modern breeding, conservation, and research efforts. A superior individual was selected from the Teagasc birch breeding programme based on field performance. Young leaf samples were collected and flash-frozen in liquid nitrogen for DNA extraction. Multiple sequencing approaches were applied to capture genome structure, gene activity, and diversity, producing long and short read genomic data.

The resulting genome will provide insight into the species' evolutionary origins, support conservation of marginal populations, and enable genomic selection in the national birch improvement programme. Ultimately, this resource will help accelerate breeding and improve genomic selection approaches to enhance the role of birch in Irish and European forestry.

Modelling ash tree tolerance to Ash Dieback Disease

Carmen R. E. Watkins, Dheeraj S. Rathore, Silvia Caldararu

Trinity College Dublin & Teagasc

Pathogens, insects, and parasites (PIPs) are natural drivers of forest dynamics, but are becoming more common and devastating in forest ecosystems due to a changing climate and novel, invasive pests. Invasive PIPs are especially destructive as trees may have no evolved resistance or defence mechanisms. Ash dieback disease (*Hymenoscyphus fraxineus*) is a novel fungal pathogen present in Ireland and across Europe that has led to the steep decline of native ash trees, killing up to 85% of trees in some areas. A small percentage of ash trees may be tolerant to ash dieback disease, depending on genetics, environmental conditions, and forest characteristics. Predicting tree tolerance and mortality risk in the face of concurrent stressors is essential for planning and decision making at the local scale. We are developing a process-based model of pathogen impact on tree growth, function, tolerance, and defence to model ash tree tolerance to ash dieback disease in Ireland and test the relative importance of genetics and environmental characteristics in determining disease tolerance. This research will allow us to better understand tree defence and tolerance to PIPs and will provide a tool for local decision makers to forecast tree tolerance and mortality risk.

Developing and validating HTS surveillance methodology for detecting plant nursery pathogens

Michelle E. H. Thompson, Kes Daly, Brian McGuinness, Colin Kelleher, Dónall Flanagan, Adam Ryan, Craig Murphy, Michael Gaffney, Richard O'Hanlon, Trevor Hodkinson

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Plant pathogens have an opportunity to spread before they can be found during nursery inspections. These visual inspections are also time consuming. If we can detect the diseases earlier, this could prevent the spread within a nursery, country, or internationally, and help prevent harm to economies and ecosystems. In this project, we are developing and validating methodology for HTS (high throughput sequencing) of eDNA (environmental DNA; genetic material shed into the environment) for early detection of pathogens. *Phytophthora spp*. (oomycete) will be inoculated into stems of susceptible *Rhododendron* 'Cunningham's White' as a model system in glasshouse experiments. Water will be applied over the leaves, stems, and growth media, and the runoff will be collected repeatedly to assess Phytophthora DNA over time. Water from groups of six plants will be filtered to concentrate DNA. One to three plants within the group will be inoculated while the remaining plants will be healthy to represent realistic dilutions. We will track lesion length and dieback symptoms and confirm infection with real time PCR. We will compare symptom onset and development to results from DNA isolation and HTS over time to assess how early disease can be detected. These results may provide a threshold level of detection. Growth media will be sampled as another source for eDNA. We will test these methods in various systems including *Prunus* and *Viburnum* plants, *Pseudomonas syringae* (bacterial pathogen), and alternative growth media. It is important to test methods in alternative media because the industry is shifting away from peat, and we must determine how this affects pathogen growth, survival, and detection. We will use a combination of Illumina MiSeq, MinION, and PacBio for eDNA sequencing. We are also culturing a variety of *Phytophthora spp*. and will use whole genome sequencing to explore the species present in Ireland. Overall, our aim is to create a roadmap for HTS to advance plant health surveillance, in turn mitigating the spread of disease and informing nursery/farm management decisions.

-end of abstracts-

Organisers

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Special thanks to Virgile Ballandras for all his efforts while also writing up his PhD!

Getting Involved

To join SIPP or EntoSoc please email:

- SIPP Secretary: sippsecretary@gmail.com
- EntoSoc: studententosocireland@gmail.com

Committee positions are available for SIPP so please feel free to contact if interested

Thanks

The organisers would like to thank multiple people for their involvement:

- **Presenters:** Thank you very much for submitting a huge amount of abstracts this year. We tried to accommodate as many presentations as possible and are delighted to see such a vast array of talks and posters.
- **DAFM Staff:** Thank you for helping to organise this conference and enable it to run smoothly.
- **Louise Byrne & Aidan O'Hanlon:** Thank you for delivering keynotes for this conference. We really appreciate your support in helping inspire the next generation.
- **Plant Science Division:** Thank you for hosting a tour of the Seed Testing Labs and the Plant Health Labs.
- **Attendees:** It has been a great opportunity for SIPP and EntoSoc to collaborate over the past two conferences in 2024 and 2025. In 2024 the conference was completely sold out and this year we filled all the talk slots before the deadline. Thank you for your participation and we hope you enjoy the conference.

SIPP x EntoSoc 2025

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