

2026 Annual Scientific Conference

Society of Irish Plant Pathologists
The Irish Entomological Network

Ashtown Food Research Centre,
Ashtown, Dublin 15, Co.Dublin

16th October 2026



Host institution



The organisers would like to thank Teagasc for hosting the conference.

Topics



Participating institutions

*affiliations from the presenting authors



Photography on the cover by:
Top: Maximilian Schughart
Bottom: Evelyn Zuniga

Contents

Host institution 2
Topics 2
Participating institutions 2
Timetable 5
SIPP x IEN Annual Conference 2025 6
Society Background 6
Society of Irish Plant Pathologists 6
The Irish Entomological Network 6
Oral Presentations 7
Sampling methods for eDNA detection of phytopathogens in plant nurseries (Detect-PNP) 7
Developing and validating HTS surveillance methods for plant nursery pathogen detection (Detect-PNP) 7
Role of wood sample incubation in the diagnosis of *Bursaphelenchus xylophilus* 8
Boosting Nutrient Use Efficiency and Seedling Establishment in Wheat and Barley Using *Ascophyllum nodosum* Extracts 8
Two Years of Experimental Caged Field Trials Investigating BYDV-Aphid Interactions - What Have We Learned So Far? 9
Towards control of ash sawfly (*Tomostethus nigritus*) 9
The first report of M918L (super-kdr) and L932F voltage-gated sodium channel mutations in the English grain aphid (*Sitobion avenae*) 10
A sustainable co-formulation for plant health enhancement, based on entomopathogenic nematodes and plant growth-promoting rhizobacteria 10
Organic Matter Characterisation in Growing Media Using Chemometrics and the Aromatic-to-Aliphatic Ratio with Benchtop and Handheld MIR and NIR Spectroscopy 11
The evolution of CYP51 in Irish *Zymoseptoria tritici* populations 11
Oat genotype shapes the grain microbiome response to symptomless *Fusarium langsethiae* infection 12
Low-dose deoxynivalenol triggers minimal but highly genotype- and concentration-specific transcriptional reprogramming in wheat 13
Flash talks 14
Predictive performance of a drone-based multispectral reflectance model as an objective proxy for visual disease scoring in perennial ryegrass 14
From disease screening to defence activation: chitosan as a plant defence elicitor in perennial ryegrass 14
Impact of *Ascophyllum nodosum* and *Ecklonia maxima* based biostimulants on plant fertility, adaptation, and reproduction under heat stress 15
First report of QoI resistance mutation G143A in Irish *Venturia inaequalis* populations 15
Characterizing Ash Tree Physiological Capacity Under Ash Dieback Infection populations 16
Exploring near-infrared spectroscopy to assess Irish ash trees with differing levels of ash dieback severity 16
Comparative assessment of virulence and population genetic diversity in Irish and Slovak *Hymenoscyphus fraxineus* isolates 17
Birch Breeding for Forest Diversification: Growth Traits in Irish Progeny Trials 17

Assessing trap and lure performance in native longhorn beetle surveillance trials across Northern Ireland .. 18
Identifying Primary Aphid Vectors of Potato Virus Y in Irish Potato Crops 18
Investigating the Virucidal Activity of Insect Haemolymph Following Diverse Immune Priming 19
Conservation of candidate survivor elms in Ireland 20
Beyond virulence: How DON and NIV mycotoxins shape wheat head microbiome gene expression 20
Clubroot in Ireland: First insights from whole genome sequencing of *Plasmodiophora brassicae* 21
Transcriptomic profiling of the barley fungal pathogen *Ramularia collo-cygni* reveals virulence-associated secreted enzymes and candidate effector proteins 21
Poster Presentations 22
Teagasc National Insect Monitoring Programme 22
Tracking potato late blight through the air: Integration bioaerosol eDNA with CRISPR-Cas for point-of-need detection 22
AshForFuture: Harnessing natural variation in *Fraxinus excelsior* for ash dieback tolerance in the Irish landscape 23
Establishing a Watercourse Surveillance Network for Detection of Phytophthora spp. in NI Forests: Preliminary Findings 23
Understanding oat responses to the Fusarium mycotoxin T-2 24
Mallow - A Novel Agronomic Crop 24
Resbarley: The race towards enhancing durable resistance to leaf scald disease of barley 25
Harnessing Tree Microbiomes to Enhance Forest Health and Resilience: The ResFor_Micro Project 25
Yellow Legged Hornet: The Most Northerly Reported *Vespa velutina* nest, Belfast, Northern Ireland 26
Sitka spruce seeds germination response to chilling across a latitudinal range 26
Gremmeniella abietina 27
Exploring Resistance and Management Strategies for Clubroot in Oilseed Rape 27
Anoplophora chinensis: an interception 28
ResilientForests – Advancing Tree Improvement Research for Climate-Resilient, Diverse and Productive Forests for Ireland 30
Optimising Fungicide Control in Barley: Monitoring of SDHI Resistance in *Ramularia collo-cygni* 28
Genomic prediction of ash dieback severity and budburst in Fraxinus excelsior in Ireland 28
From Microbiome to Candidate Biocontrol Agents: Exploring Alder-Associated Microorganisms with Antagonistic Activity against *Phytophthora* spp. 30
No title ..... **Error! Bookmark not defined.**
Multi-level phenotyping of tar spot disease severity in sycamore maple (*Acer pseudoplatanus)* 32
Organisers 33
Getting Involved 33
Thanks 33

Timetable

Time	Speaker	Title
09:00		Registration and coffee
10:00	**Steven Kildea**	**Welcome**
10:05	**Micheál Rooney**	**Ireland's Plant Health and Biosecurity Strategy 2026–2030**
10:20	Kes Daly	Sampling methods for eDNA detection of phytopathogens in plant nurseries (Detect-PNP)
10:35	Michelle Thompson	Developing and validating HTS surveillance methods for plant nursery pathogen detection (Detect-PNP)
10:50	Anusha Pulavarty	Role of wood sample incubation in the diagnosis of *Bursaphelenchus xylophilus*
11:05	Elomofe Ikuyinminu	Boosting Nutrient Use Efficiency and Seedling Establishment in Wheat and Barley Using Ascophyllum nodosum Extracts
11:20	Ella Mulkerrins	Predictive performance of a drone-based multispectral reflectance model as an objective proxy for visual disease scoring in perennial ryegrass
11:25	Musfirah Binte Mansoor	From disease screening to defence activation: chitosan as a plant defence elicitor in perennial ryegrass
11:30	Juan Francisco Sánchez López	Impact of *Ascophyllum nodosum* and *Ecklonia maxima* based biostimulants on plant fertility, adaptation, and reproduction under heat stress
11:35	Jane Ritchie	First report of QoI resistance mutation G143A in Irish *Venturia inaequalis* populations.
11:40	Bailey Parkhouse	Characterizing Ash Tree Physiological Capacity Under Ash Dieback Infection
11:45	Bharatheeswaran Murugan	Exploring near-infrared spectroscopy to assess Irish ash trees with differing levels of ash dieback severity
11:50	Abhishek Singh	Comparative assessment of virulence and population genetic diversity in Irish and Slovak *Hymenoscyphus fraxineus* isolates
11:55	Robert Pim	Birch Breeding for Forest Diversification: Growth Traits in Irish Progeny Trials
12:00		Lunch
12:30		Poster session
13:00	**Virgile Ballandras**	**Irish Entomological Network**
13:10	Maximilian Schughart	Two Years of Experimental Caged Field Trials Investigating BYDV-Aphid Interactions - What Have We Learned So Far?
13:25	Florentine Spaans	Towards control of ash sawfly (*Tomostethus nigritus*)
13:40	Virgile Ballandras	The first report of M918L (super-kdr) and L932F voltage-gated sodium channel mutations in the English grain aphid (*Sitobion avenae*)
13:55	Islam Ahmed Abdelalim Darwish	A sustainable co-formulation for plant health enhancement, based on entomopathogenic nematodes and plant growth-promoting rhizobacteria
14:10	Ryan T Weir	Assessing trap and lure performance in native longhorn beetle surveillance trials across Northern Ireland
14:15	Mathijs Dejong	Identifying Primary Aphid Vectors of Potato Virus Y in Irish Potato Crops
14:20	Esmeralda Herrero	Investigating the Virucidal Activity of Insect Haemolymph Following Diverse Immune Priming
14:25	Karuna Shrestha	Conservation of candidate survivor elms in Ireland
14:30		Coffee break & posters
15:00	Thulani De Silva	Organic Matter Characterisation in Growing Media Using Chemometrics and the Aromatic-to-Aliphatic Ratio with Benchtop and Handheld MIR and NIR Spectroscopy
15:15	Tapiwa Nyakauru	The evolution of CYP51 in Irish *Zymoseptoria tritici* populations
15:30	Natarajan Subramani	Oat genotype shapes the grain microbiome response to symptomless *Fusarium langsethiae* infection
15:45	Minely Cerón Bustamante	Low-dose deoxynivalenol triggers minimal but highly genotype- and concentration-specific transcriptional reprogramming in wheat
16:00	Sai Sushma Boggarapu	Beyond virulence: How DON and NIV mycotoxins shape wheat head microbiome gene expression
16:05	Marta Niedzicka	Clubroot in Ireland: First insights from whole genome sequencing of Plasmodiophora brassicae
16:10	Enrico Jugadora	Transcriptomic profiling of the barley fungal pathogen *Ramularia collo-cygni* reveals virulence-associated secreted enzymes and candidate effector proteins
16:15		Conference Close

SIPP x IEN Annual Conference 2025

In 2025 The Society of Irish Plant Pathologists and Irish Entomology Network organised a joint conference host by The Department of Agriculture Food and Marine. SIPP invited Louise Byrne, the Chief Plant Health Officer for Ireland to speak about the department's efforts on plant health and Biosecurity. IEN invited Aidian O'Hanlon from the National Museum of Ireland to discuss the recent outbreak of Asian Hornet.



Attendees at the 2025 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.

The Irish Entomological Network

It all started with the creation of the Student Entomological Society of Ireland. 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 late 2025 the society scaled up to a new dimension with two joint conferences, with SIPP and with the Royal Entomological. At this stage, discussions started regarding the official status of the society, it became obvious that the main audience was not the students anymore but any actor in insect science in Ireland and neighbour European countries. It was then decided to focus on the networking goals. The Student Entomological Society of Ireland was then rebranded into the Irish Entomological Network (IEN).

Oral Presentations

Sampling methods for eDNA detection of phytopathogens in plant nurseries (Detect-PNP)

Kes Daly[1], Prof. Trevor Hodkinson[1], Adam Ryan[1], Craig Murphy[1], Michelle Thompson[2], Michael Gaffney[2], Richard O'Hanlon[3]

[1]Trinity College Dublin, [2]Teagasc, [3]DAFM

Phytopathogens are a huge threat to natural and agricultural ecosystems, and ornamental plant trade is a major entry route for these diseases. Current detection methods are based on visual inspection which is insufficient for several reasons. The use of environmental DNA (eDNA) based detection methods for these phytopathogens is gaining increasing interest. However, much work is needed for eDNA based methods to be widely applicable. Sampling methods are an important yet frequently overlooked aspect of using these methods, and there is much to consider when selecting the appropriate sampling method for a given situation. Sampling matrices (water, air, growing media, plant material) and methods have been systematically reviewed to gain a greater understanding of their strengths and weaknesses, for example, which matrix is most appropriate to detect certain phytopathogens, cost, and ease of use. Experiments are also being run to compare various methods of water sampling for eDNA detection using different volumes (200-300mL, 750mL, 5L), sampling tools (syringe, bottles, knapsack sprayer), and storage methods. The results obtained in these trials will allow for the methods to be assessed in terms of their ease of use, cost, and effectiveness at detecting taxa. Based on these results, the optimal method can be chosen and finetuned further in real nursery settings. This work will contribute to the development of eDNA based methods for the detection of phytopathogens in commercial plant nurseries in the near future.

Developing and validating HTS surveillance methods for plant nursery pathogen detection (Detect-PNP)

Michelle E. H. Thompson[1], Kes Daly[2], Brian McGuinness[1], Adam P. Ryan[2], Craig Murphy[2], Dónall Flanagan[1], Colin Kelleher[3], Michael T. Gaffney[1], Richard O'Hanlon[4], Trevor R. Hodkinson[2]

[1]Teagasc, Horticulture Development Department, Ireland, [2]Trinity College Dublin, Botany, School of Natural Sciences, Ireland, [3]National Botanic Gardens of Ireland, [4]Department of Agriculture, Food and the Marine, Ireland

The threats of invasive plant diseases are increasing due to globalisation and climate change. Internationally-traded plants can harbour asymptomatic pathogens, adding to biosecurity challenges. We are developing and validating environmental DNA (eDNA) high throughput sequencing (HTS) methods to detect plant pathogens, with a focus on runoff water. This could prevent damage to ecosystems and economies. To test these methods, our first glasshouse experiment utilized *Phytophthora* (oomycete) in susceptible rhododendrons, followed by *Pseudomonas syringae* (bacteria) in laurel. We designed and implemented SOPs for pathology experiments with waterborne regulated non-quarantine pathogens; this methodology can guide future pathology experiments. 100% of plants inoculated with Phytophthora produced lesions that grew over time and tested positive with qPCR. Water flow-through samples were repeatedly collected over seven months, and a range of samples including growing media, roots, stems, and leaves were also collected to assess *Phytophthora* DNA. Nested PCR for genus-level detection revealed positive results at multiple time points. Species-level metabarcoding results will be compared to symptom development over time, with the aim of determining a threshold level of detection. These methods will be tested in multiple systems, including alternative growing media to observe how peat-free systems may impact pathogen growth and detection. In addition, culturing and whole genome sequencing of additional Phytophthora species in Ireland will contribute to the database of oomycete genomes. This work develops methodologies to assess future use of HTS in horticulture, which may strengthen future plant health surveillance strategies, improve nursery management, and mitigate the spread of plant diseases.

Role of wood sample incubation in the diagnosis of *Bursaphelenchus xylophilus*

Pulavarty Anusha[1], Inácio Maria[2], Amoriello Sara[1], Hoppe Björn[3], Calin Monica[4], van Bruggen Anne Sophie[5], Torrini Giulia[6], Širca Saša[7]

[1]Department of Agriculture Food and the Marine, Ireland, [2]National Institute for Agricultural and Veterinarian Research, Portugal, [3]Federal Ministry of Food and Agriculture, Germany, [4]National Phytosanitary Authority, Romania, [5]Netherlands Food and Consumer Products Safety Authority, the Netherlands, [6]CREA – Centro di Ricerca Difesa e Certificazione, Firenze, [7]Ministry of Agriculture Forestry and Food, Slovenia

The pinewood nematode, *Bursaphelenchus xylophilus*, is presumed to have originated from North America and been transported to Asia during the early twentieth century via contaminated timber. Within Europe, its current presence is restricted to Portugal, Spain, and France. To mitigate the risk of additional introductions and restrict further dissemination, it is imperative to implement surveillance protocols in pine forest ecosystems and conduct examinations of imported wood, bark, and wood packaging materials. Standardized diagnostic methodologies established by EPPO (PM 7/4 and PM 7/119) incorporate an incubation stage within the analytical framework. This stage requires subjecting wood samples to controlled conditions at approximately 25°C for a minimum of 14 days to facilitate the proliferation of potential nematode populations, thereby enhancing detection probability. Nevertheless, the extended duration of this stage represents a substantial obstacle, as the material must remain under official control throughout the analytical process. Within the framework of the EUPHRESCO initiative designated "BxDetect," multiple National Reference Laboratories examined the significance of incubation in facilitating the identification of *B. xylophilus,* with the objective of evaluating its influence on diagnostic results. Each contributing laboratory obtained a collection of samples exhibiting varying infestation intensities and subjected them to two distinct protocols: analysis without incubation and analysis following a fourteen-day incubation period at 25°C. The investigation examined the consequences of incubation duration and infestation intensity on the successful identification of *B. xylophilus* across multiple extraction intervals.

Boosting Nutrient Use Efficiency and Seedling Establishment in Wheat and Barley Using *Ascophyllum nodosum* Extracts

Elomofe Ikuyinminu[1], Oscar Goñi[1,2], Łukasz Łangowski[1], Shane O'Connell[1,2]

[1]Brandon Bioscience, Sycamore Court, Clash, Tralee, Co. Kerry, Ireland, [2]Plant Biostimulant Group, Centre for Applied Bioscience Research, Munster Technological University, Kerry, Tralee, Co. Kerry, Ireland

Seedling emergence and early establishment are critical but highly vulnerable to abiotic stress and nutrient limitation. While biostimulants can enhance crop resilience, their impact on micronutrient dynamics during early development is poorly understood. This study evaluates micronutrient uptake and remobilisation in winter barley and wheat during early seedling growth.

First, three commercial Ascophyllum nodosum extracts (ANE A, B, and C) were compared to determine if compositional differences triggered distinct physiological responses in wheat. The extracts showed clear functional divergence: ANE A and C significantly increased biomass, but ANE A primarily enhanced root growth and uniquely increased several micronutrients.

Consequently, ANE A was selected for a detailed mechanistic evaluation via ICP-MS. Across both cereal crops, ANE A significantly increased root biomass by 12–26% over controls. It induced distinct shifts in the accumulation and partitioning of macronutrients (K, P), secondary nutrients (Ca, Mg), and micronutrients (B, Mn, Cu, Fe, Mo, Zn). Nutrient use efficiency metrics confirmed enhanced uptake and translocation, demonstrating that ANE A actively mobilises micronutrients. Ultimately, this study shows how ANE A reprograms early nutrient allocation under resource-limited conditions, supporting its use in sustainable cereal production.

Two Years of Experimental Caged Field Trials Investigating BYDV-Aphid Interactions - What Have We Learned So Far?

Maximilian Schughart, Louise McNamara, Stephen Byrne, Munir Mostafiz, Gerry Nolan

Crop Science Department, Teagasc, Oak Park, Carlow R93 XE12, Ireland

Barley yellow dwarf virus (BYDV) comprises an economically important group of aphid-transmitted viruses affecting cereal production worldwide. Disease development and the resulting impact on yield are influenced by several factors, including aphid abundance, vector species, virus-vector compatibility and the timing of infection. However, the relative importance of different aphid-virus combinations and infection timings in determining disease development and yield loss in barley remains poorly understood.

Over three growing seasons, a series of large-scale caged field trials is being conducted in winter and spring barley to investigate the effects of aphid-virus combinations and infection timings on BYDV development and crop performance. This study presents findings from the first two years of the field programme. Each trial comprised of 112 plots (winter barley) or 96 plots (spring barley), which were inoculated at different growth stages using a range of virus-vector combinations. Individual plots were caged and inoculated with virus-carrying aphids, allowing disease development and yield effects to be assessed under field conditions while controlling the timing and source of virus inoculation.

Data from the first two years have now been analysed, providing insights into the effects of virus-vector combinations and infection timing on BYDV development and yield in both winter and spring barley. These findings contribute to a better understanding of the factors driving BYDV-associated yield loss and the relative risk associated with different infection scenarios. A third year of field experiments is planned, which will further investigate these relationships and strengthen the evidence base for assessing BYDV risk in barley production.

Towards control of ash sawfly (*Tomostethus nigritus*)

Spaans, Florentine[1], Weir, R.[1], Rathore, D.[2], Lennon, S.[1], Isaac, C.[1], Kirbas, J.[1], McClure, A.[1], Leybourne, D.[1], Murchie, A.[1]

[1]Agri-Food & Biosciences Institute, Belfast, Northern Ireland, BT9 5PX, [2]Teagasc, Ashtown, Scribblestown, Dublin, D15 DY05, Ireland

Ash sawfly (*Tomstethus nigritus* F.) is a defoliating pest of ash (*Fraxinus* spp) native to Europe with sporadic outbreaks having been reported from various countries, particularly in urban areas and river valleys. It was not recorded on the island of Ireland prior to 2016, when it was identified as being present in an urban estate in Belfast, Northern Ireland. Since then, there has been consistent, severe defoliation of ash trees in parkland, hedgerows and riparian habitats in the Belfast area, 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 and it has continued to spread around the island. The consistent defoliation of ash trees each year is not typical of ash sawfly outbreaks elsewhere, which normally subside after a few years. Trees with both ash dieback and ash sawfly are particularly severely impacted. The continued spread of the pest around Belfast is presented alongside initial explorations of possible control methods. Preliminary data regarding ash strains from the Teagasc breeding programme that are potentially tolerant of both ash dieback and ash sawfly are also included.

The first report of M918L (super-kdr) and L932F voltage-gated sodium channel mutations in the English grain aphid (*Sitobion avenae*)

Virgile Ballandras, Stephen Byrne, Louise Mc Namara

Teagasc

The English grain aphid, *Sitobion avenae* (Fabricius, 1794), is the main vector of Barley Yellow Dwarf Viruses (BYDV) in Ireland. BYDV, and consequently its aphid vectors, cause significant economic losses in cereal production. Aphid populations are therefore routinely monitored and controlled to prevent major BYDV outbreaks.
In modern agricultural systems, aphids are managed primarily with insecticides, particularly pyrethroids, following the ban on neonicotinoids in Europe. Their extensive use has selected naturally occurring mutations that confer insecticide resistance. In 2011, knockdown resistance (kdr) was detected for the first time in English grain aphids sampled in the United Kingdom. Aphids carrying the L1014F mutation were able to survive pyrethroid doses that were lethal to non-mutant individuals. Since then, this mutation has been detected in populations across Europe and intensively monitored to inform crop-protection strategies.
However, L1014F is not the only mutation associated with pyrethroid resistance. Other mutations in the same gene have been shown to confer even higher levels of resistance, but these loci have received limited attention in S. avenae. Using a newly developed high-throughput sequencing assay, we screened a large collection of aphids for additional resistance-associated mutations. We report the first detection in wild S. avenae individuals from Ireland of M918L, also known as the super-kdr mutation, and L932F. We discuss the potential implications of these findings for integrated pest management (IPM) and the future monitoring of pyrethroid resistance in Irish cereal aphid populations.

A sustainable co-formulation for plant health enhancement, based on entomopathogenic nematodes and plant growth-promoting rhizobacteria

Islam Ahmed Abdelalim Darwish[1], Daniel P. Martins[2], David Ryan, Thomais[1] Kakouli-Duarte[1]

[1]Molecular Ecology and Nematode Research Group, enviroCORE, Department of Applied Science, South East Technological University, Kilkenny Road Campus, R93 V960 Carlow, Ireland, [2]School of Computer Science and Electronic Engineering, University of Essex, Colchester CO4 3SQ, UK

Combining entomopathogenic nematodes (EPN) and plant growth–promoting rhizobacteria (PGPR) in a single delivery approach has strong potential for efficacy and reliability towards plant health, particularly when the two organisms are compatible and ideally work together. A calcium alginate bead formulation has been developed to co-encapsulate the EPN *Steinernema feltiae* (SB 12[1]) and the PGPR *Pseudomonas ogarae* F113 gfp for pest management and to enhance plant health. The results revealed that nematodes and rhizobacteria can coexist within a single formulation while maintaining their functions following storage at 4°C for up to three months. In greenhouse experiments, cabbage plants showed signs of stress and visible root damage after infestation with the cabbage root fly (*Delia radicum*). Following bead treatment, the nematode caused the highest mortality, and the damaged root system began to re-establish with the development of new root hairs. Additionally, significant increases in root and shoot length were observed in the bead treatment, compared to treatment using nematodes only. Currently, a molecular communication framework for modelling the behaviour dynamics of the co-encapsulated organisms is being developed for better performance across different environments.

Organic Matter Characterisation in Growing Media Using Chemometrics and the Aromatic-to-Aliphatic Ratio with Benchtop and Handheld MIR and NIR Spectroscopy

Thulani De Silva[1,2], Felipe Bachion de Santana[3], Karen Daly[3], Michael Stock[2], Michael Gaffney[1], Eoghan Corbett[1]

[1]Horticulture Development Department, Teagasc, Ashtown Food Research Centre, Ashtown, Dublin 15, Ireland, [2]Department of Geology, Trinity College Dublin, Dublin, Ireland [3]Environment, Soils and Land Use (ESLU) Department, Teagasc, Environment Research Centre, Johnstown Castle, Co. Wexford, Ireland

The transition from peat-based to sustainable plant growing media requires rapid, non-destructive analytical tools to characterise alternative substrates. This study evaluated five FTIR spectroscopic approaches; Bruker benchtop MIR and NIR, Agilent handheld MIR, and NeoSpectra and Innospectra handheld NIR for predicting organic matter (OM%) in growing media, alongside three data fusion strategies combining the two portable NIR instruments. Forty-one samples were prepared as binary mixtures of peat, coir, composted bark or wood fibre with horticultural perlite in 10% mass-based increments, spanning 1.3-99.5% OM determined by loss on ignition. Preprocessing was selected from seven algorithms using a common calibration/validation partition, followed by PLS regression with seven-fold cross-validation. Bruker benchtop MIR achieved the highest accuracy (RMSEP = 1.14 OM%, RPIQval = 27.44), with variable importance in projection analysis identifying lignin, carbonyl, polysaccharide and silica bands as dominant predictors. NeoSpectra (RMSEP = 2.56 OM%) performed similarly to Agilent handheld MIR (2.61 OM%) and outperformed all three fusion strategies (4.38-5.19 OM%), indicating that combining a spectrally weaker portable instrument with a stronger instrument can reduce rather than improve prediction. A baseline-corrected aromatic-to-aliphatic ratio differentiated the four organic materials. Leave-one-material-out validation, in which each material was excluded from calibration, increased errors to 5.2-27.9 OM%, with Agilent handheld MIR transferring best (5.18 OM%). These results demonstrate that within-set prediction accuracy and transferability to unseen substrates are distinct properties. Nevertheless, a single low-cost portable NIR spectrometer can provide robust OM% quantification, supporting the transition towards sustainable substrate formulations.

The evolution of CYP51 in Irish *Zymoseptoria tritici* populations

Tapiwa Nyakauru, Fiona Hutton, Steven Kildea

Teagasc Department of Crop Science, Oak Park, Carlow, Ireland

Septoria tritici blotch, caused by *Zymoseptoria tritici*, is a major constraint to winter wheat production in Ireland, with disease management relying heavily on fungicides. Management strategies depend largely on fungicides such as demethylation inhibitors. Resistance to these fungicides due to mutations has been reported in field populations of *Z. tritici* for over a decade and continues to threaten their effectiveness. While resistance-associated mutations are well documented, the long-term temporal evolution of complete CYP51 mutation combinations within Irish populations remains poorly understood. Here, we characterised CYP51 sequence variation in *Z. tritici* isolates collected across Ireland between 2005 and 2024. Full-length CYP51 amplicons were sequenced using nanopore technology, and haplotypes were defined from concatenated nonsynonymous mutations. Across the study period, 22 distinct nonsynonymous mutations and 75 CYP51 haplotypes were identified. Mean mutation burden per haplotype increased from approximately 2.8 to 7.0. Haplotype richness increased from six in 2005 to a maximum of 22 in 2010 before declining to seven by 2024, while Shannon diversity peaked at 2.84 in 2017 and declined to 1.69 by 2024. Pairwise association analysis revealed strong positive co-occurrence among ΔY459/G460, S188N, A379G and N513K, with several mutations showing negative associations. Over 14% of isolates carried haplotypes not previously reported. These findings demonstrate that CYP51 diversity in Ireland is dynamic, with increasing mutation accumulation and declining haplotype diversity, consistent with ongoing fungal pressure selection. Surveillance of complete CYP51 haplotypes is essential to provide the information needed to inform integrated disease management.

Oat genotype shapes the grain microbiome response to symptomless *Fusarium langsethiae* infection

Natarajan Subramani[1], Israel Ikoyi[1,2], Amal Kahla[1], Farhana Afroze[1], Julio Isidro-Sánchez[3], Tancredi Caruso[1], Fiona Doohan[1]

[1]School of Biology and Environmental Science, Earth Institute, University College Dublin, Dublin, Ireland, [2]School of Biological, Earth and Environmental Sciences, Sustainability Institute, University College Cork, Cork, Ireland, [3]Centro de Biotecnología y Genómica de Plantas (CBGP, UPM-INIA), Universidad Politécnica de Madrid (UPM) - Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Campus de Montegancedo-UPM, 28223 Pozuelo de Alarcón, Madrid, Spain

Plant–pathogen interactions occur within complex microbial communities, yet how host genetic variation shapes these communities during infection remains poorly understood. This may be particularly important for symptomless pathosystems, where interactions among the host, pathogen and resident microbiota could influence disease outcomes and contribute to their longer-term ecological and evolutionary dynamics. *Fusarium langsethiae* represents an unusual cereal pathogen, colonising oat panicles with few or no visible symptoms while contaminating grain with the potent T-2 and HT-2 mycotoxins. We investigated bacterial and fungal communities associated with a diverse panel of oat genotypes grown under controlled glasshouse conditions, comparing uninoculated plants with plants inoculated with *F. langsethiae*. Grain-associated communities were characterised using 16S rRNA and ITS amplicon sequencing. Microbial diversity and community composition were examined in relation to pathogen treatment, host genotype and T-2/HT-2 accumulation. We further investigated host genetic control of microbial taxa using heritability estimates and microbiome genome-wide association analysis. *F. langsethiae* inoculation reshaped the grain microbiome, with responses varying among oat genotypes. Several bacterial and fungal taxa were associated with variation in mycotoxin accumulation, while a subset of microbial features showed evidence of host genetic control. Genome-wide association analysis identified host genomic regions associated with variation in specific microbial taxa, revealing candidate genes with potential roles in host–microbe interactions. These findings highlight the grain microbiome as a genetically influenced component of the oat–*F. langsethiae* interaction and provide new insight into the ecological and evolutionary complexity of symptomless, toxin-producing plant–pathogen interactions.

Low-dose deoxynivalenol triggers minimal but highly genotype- and concentration-specific transcriptional reprogramming in wheat

Minely Cerón Bustamante, Fiona Doohan

University College Dublin

Deoxynivalenol (DON), a mycotoxin and a phytotoxic virulence factor for *Fusarium graminearum*, the main causal agent of Fusarium head blight (FHB), is typically studied at high, acutely toxic concentrations, leaving the transcriptional impact of the low DON levels encountered during early infection poorly characterised. We used RNA-sequencing to compare the wheat transcriptional response to low (0.2 and 10 ppm) DON concentrations in two contrasting genotypes, the FHB-resistant CM82036 and the susceptible Remus, at 24 and 48 hours post-exposure, with a high-dose (1000 ppm) treatment included for reference. At 0.2 ppm, the transcriptional response was minimal, with the large majority of treatment-specific genes failing to reach statistical significance ($Q \leq 0.05$) in either genotype. A clear threshold effect emerged at 10 ppm, where a substantially higher proportion of treatment-specific genes were statistically significant, particularly in Remus (up to 83%). This low-dose response, however, was almost entirely genotype-specific: only one of 45 significant treatment-gained genes at 10 ppm/24h was shared between cultivars, and gene sets responding to 0.2 ppm and 10 ppm within the same genotype showed comparably little overlap. Functional annotation of the low-dose gene sets revealed suppression of grain-defense proteins (puroindolines, glutenins, amylase/trypsin inhibitors, defensins) at 0.2 ppm in CM82036, and induction of detoxification- and kinase-signalling-associated genes at 10 ppm, with genotype-specific sub-family usage. These results show that even sub-lethal, field-relevant DON concentrations trigger discrete, dose- and genotype-restricted transcriptional programmes in wheat, rather than a scaled-down version of the high-dose response, with implications for early resistance signalling and biomarker discovery in FHB.

Flash talks

Predictive performance of a drone-based multispectral reflectance model as an objective proxy for visual disease scoring in perennial ryegrass

Ella Mulkerrins[1,2], Michael O'Donovan[1], Jack McDonnell[2], Joseph P. Lynch[2], Sarah Walsh[1]

[1]Teagasc, Animal and Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork, Ireland, [2]Dundalk Institute of Technology, Co. Louth, Ireland

Visual scoring of disease severity of perennial ryegrass (*Lolium perenne* L; PRG) in grassland trials is labour intensive and subject to observer bias. Remote sensing offers an objective, high-throughput alternative for monitoring canopy health under field conditions with the use of multispectral indices. This study aimed to validate drone derived multispectral data as a reliable proxy to detect disease in PRG.
Drone imagery from field plots exhibiting natural fungal disease pressure were captured using a DJI Mavic 3M multispectral sensor. Canopy reflectance metrics (Normalised Difference Vegetation Index (NDVI), Green Normalised Difference Vegetation Index (GNDVI), and Normalised Difference Vegetation Index Red-Edge (NDVIre)) were correlated with visually observed disease scores from two independent observers (calculated as % of the plot infected x % of the leaf infected). A Random Forest model (1000 trees) was trained to evaluate predictive accuracy and feature importance.
The Random Forest model demonstrated a basis of predictive capability for visual disease score (R2 = 0.648, Root Means Square Error (RMSE) = 8.52, Mean Absolute Error (MAE) = 5.72). Variable importance metrics indicated that NDVI (% Increase in Mean Square Error (%IncMSE) = 37.03) and NDVIre (%IncMSE = 32.79) were the primary drivers tracking visual canopy damage, outperforming GNDVI (%IncMSE = 29.2)
Multispectral drone imagery effectively captures fungal disease severity in PRG. Both NDVI and NDVIre have the potential to serve as spectral proxies, enabling fast, and objective canopy health scoring for identifying the impact of plant pathogens.

From disease screening to defence activation: chitosan as a plant defence elicitor in perennial ryegrass

Musfirah Binte Mansoor, Fiona Doohan

University College Dublin

Perennial ryegrass (*Lolium perenne*) underpins temperate grassland production, but fungal and oomycete diseases threaten its productivity and persistence. Sustainable disease management strategies are therefore needed to reduce reliance on conventional fungicides. This study evaluated the potential of chitosan (CHT) to control diseases in perennial ryegrass. Six diseases: leaf blast (*Pyricularia oryzae*), leaf spot (*Bipolaris sorokiniana*), powdery mildew (*Blumeria graminis*), take-all patch (*Gaeumannomyces graminis*), brown patch (*Rhizoctonia solani*), and root rot (*Pythium irregulare*), were screened across three varieties: AberWolf, AberChoice, and AstonVision. Based on disease development, AberChoice was identified as the susceptible host, with leaf blast, take-all patch, and root rot prioritised for further testing. Chitosan was evaluated at 0, 500, 750, and 1000 ppm, initially using combined seed and foliar application, followed by comparisons of seed, foliar, and combined delivery methods. Disease suppression varied with pathogen and application method, with CHT at 1000 ppm showing strong potential against all three selected diseases. These findings support chitosan as a promising, sustainable disease management option for perennial ryegrass. Future transcriptomic analysis will examine the defence-related pathways underlying chitosan-mediated protection.

Impact of *Ascophyllum nodosum* and *Ecklonia maxima* based biostimulants on plant fertility, adaptation, and reproduction under heat stress

Juan Francisco Sánchez López[2], Elomofe Ikuyinminu[2], Oscar Goñi[1,2], Łukasz Łangowski[2], Shane O'Connell[1,2]

[1]Plant Biostimulant Group, Shannon Applied Biotechnology Centre, Munster Technological University, Kerry, Tralee, Co. Kerry, Ireland, [2]Brandon Bioscience, Tralee, Co. Kerry, Ireland

As the global population increases, securing food production has become a major challenge worldwide. Climate change and heatwaves compromise crop production by damaging the reproductive phase of plants, particularly female gametophyte development.
While plant biostimulants offer a sustainable mitigation strategy, their specific mechanisms of action are not always properly understood. In this study, we evaluated and compared the efficacy of two commercial seaweed extracts, produced using *Ascophyllum nodosum* (ANE) and *Ecklonia maxima* (EME), in enhancing heat stress tolerance in chilli pepper plants exposed to severe heatwaves for 15 days during the flowering stage.
Our findings showed that ANE application outperformed EME treatment by significantly reducing leaf oxidative stress while upregulating key genes that regulate the heat shock response in plants, such as HSFA2 or HSP101. In main stems, ANE stimulated a 35% increase in the number of xylem vessel elements and a 60% increase in the abundance of ray parenchyma, improving water transport and secondary starch storage under high temperatures. During the reproductive phase, ANE protected pollen and ovule development, resulting in a 25% increase in marketable yield compared to untreated or EME-treated plants. This biostimulant represents a robust solution for mitigating heat stress and securing crop productivity.

First report of QoI resistance mutation G143A in Irish *Venturia inaequalis* populations

Jane Ritchie

Teagasc, UCD

Apple scab, caused by the fungus *Venturia inaequalis* (Cooke) Winter, presents a significant disease challenge to Irish apple producers. Disease management relies heavily on fungicide applications, including the quinone outside inhibitor (QoI) fungicides. A point mutation in the mitochondrial cytochrome b gene, leading to the mutation G143A confers high levels of resistance to QoI fungicides in *V. inaequalis*. Leaf samples were collected from five orchards in 2025 and analysed using a PCRbased CAPS assay to investigate if this mutation is present in Irish V. inaequalis populations. The mutation was detected in all conventionally managed orchards sampled, but absent in the organically managed orchard. Differences in frequencies of the mutation was observed amongst the four orchards where it was present and warrant further investigations as to the reasons for these differences.

Characterizing Ash Tree Physiological Capacity Under Ash Dieback Infection populations

Bailey Parkhouse[1,2], Christos Chondrogiannis [2], Carmen Watkins[2], Jie Huang[1,2], Ricardo J. G. Pimenta[1], Silvia Caldararu [2], Dheeraj S. Rathore[1]

[1]Teagasc, Forestry Development Department, Oak Park Research Centre, Carlow, R93 XE12, Ireland, [2]Trinity College Dublin, School of Natural Sciences, Discipline of Botany, College Green, Dublin 2, D02 PN40, Ireland

Ash dieback, caused by the invasive fungal pathogen *Hymenoscyphus fraxineus*, poses a serious threat to European ash (*Fraxinus excelsior*). Under field conditions, linking pathogen presence to visible symptoms and tree performance remain challenging.
While the pathogen's life cycle has been widely studied, less is known about how leaf function changes as dieback develops. This study uses leaf gas exchange and chlorophyll fluorescence to assess photosynthetic performance in European ash trees across a range of dieback disease severity in Ireland. These measurements help us examine how leaf function relates to visible disease symptoms.
The work aims to improve our understanding of how ash trees respond to dieback and explore whether these measurements could provide useful indicators of disease progression. Further work will quantify pathogen load and incorporate UAV-derived canopy measurements to examine relationships between leaf function, infection and canopy condition.

Exploring near-infrared spectroscopy to assess Irish ash trees with differing levels of ash dieback severity

Bharatheeswaran Murugan[1,2,3], Felipe B. de Santana[4], Ricardo J. G. Pimenta[1], Bailey Parkhouse[1], Donnacdha Williams[5], Richard G. F. Visser[2], Marinus J. M. Smulders[2], Joukje Buiteveld[6], Stephen Byrne[7], Karen Daly[4], Dheeraj S. Rathore[1]

[1]Teagasc, Forestry Development Department, Oak Park Research Centre, Carlow, Ireland, [2]Plant Breeding, Wageningen University & Research, Wageningen, the Netherlands, [3]Graduate School Plant Ecology and Genetic Resources, Wageningen University and Research, Wageningen, the Netherlands, [4]Teagasc, Soils and Land Use Department, Johnstown Castle Research Centre, Wexford, Ireland [5]UCD School of Agriculture and Food Science, University College Dublin, Ireland [6]Centre for Genetic Resources, Wageningen University & Research, Wageningen, the Netherlands [7]Teagasc, Crops Science Department, Oak Park, Carlow, Ireland

Ash dieback, caused by the fungal pathogen *Hymenoscyphus fraxineus*, is a major threat to European ash (*Fraxinus excelsior*). Differences in disease severity among ash trees provide an opportunity to investigate biochemical characteristics associated with their response to the disease. Conventional biochemical analyses provide detailed information on individual compounds but are generally labour-intensive and require destructive sample preparation. Near-infrared spectroscopy (NIRS) offers a rapid, non-destructive approach that captures information related to the chemical composition of plant tissues.
This study investigates whether leaf and bark spectral profiles can distinguish ash trees with differing levels of ash dieback severity. Measurements were taken directly from leaves and bark on 170 living ash trees using a handheld NIRS instrument under field conditions. Spectral data is being processed using appropriate machine learning methods to examine patterns associated with genotype and observed disease severity.
The work will evaluate the potential of NIRS as a complementary tool for biochemical phenotyping of ash. If useful spectral differences are identified, they could help select trees for more detailed biochemical analysis and controlled disease screening.

Comparative assessment of virulence and population genetic diversity in Irish and Slovak *Hymenoscyphus fraxineus* isolates

Abhishek Singh[1,2], Ricardo José Gonzaga Pimenta[1], Fiona Doohan[2], Richard O'Hanlon[3], Stephen Byrne[1], Dheeraj Singh Rathore[1]

[1]Teagasc, Oak Park, [2]University College Dublin, [3]DAFM

Despite the relatively low genetic diversity reported for European populations of *Hymenoscyphus fraxineus*, the pathogen responsible for ash dieback in European ash (*Fraxinus excelsior*), variation in aggressiveness has been observed among isolates. This study aims to examine variation among Irish isolates and compare them with isolates from Slovakia.

Irish isolates were obtained from symptomatic stem material collected across multiple locations in the country. Aggressiveness is being evaluated through artificial stem inoculation of *F. excelsior* seedlings, using lesion length as a quantitative measure. Comparisons among isolates and between geographic origins will examine variation in disease development under the assay conditions.

In parallel, genetic diversity is being investigated using microsatellite (SSR) markers identified from *the H. fraxineus* reference genome, alongside previously published polymorphic SSR loci. Candidate loci were screened for suitable repeat motifs and flanking regions, and primers were designed for subsequent multiplex genotyping. The resulting multilocus profiles will be used to assess genetic diversity and structure among the sampled isolates and explore whether genetic differences are associated with geographic origin or aggressiveness.

By integrating phenotypic virulence assessment with population genetic analysis, these analyses will help characterise variation within the sampled Irish isolates and their similarities and differences with those from Slovakia. They will also allow us to examine whether differences in lesion development are associated with genetic variation detected by the SSR markers.

Birch Breeding for Forest Diversification: Growth Traits in Irish Progeny Trials

Robert Pim[1,2], Tomás Byrne[1], Junliang Zou[3], Nick McCarthy[2], Dheeraj Singh Rathore[4]

[1]Teagasc, Forestry Development Department, Ashtown, Dublin, D15DY05, Ireland, [2]South East Technological University, Cork Road Campus, Waterford, X91K0EK, Ireland, [3]Teagasc, Forestry Development Department, Johnstown Castle, Co. Wexford, Y35TC97, Ireland, [4]Teagasc, Forestry Development Department, Oak Park Research Centre, Carlow R93 XE12, Ireland

Biotic and abiotic disturbances are placing increased pressure on forest ecosystems. Diversifying forests through mixed-species planting offers one approach to reducing these risks. Silver birch (*Betula pendula*) and downy birch (*B. pubescens*) are native, fast-growing species with potential for wider use in Irish forest mixtures. Birch is valued for its ecological contribution and its timber for furniture and plywood. Improving growth performance through breeding could help make birch a more attractive option for forest diversification in Ireland. Two half-sib progeny trials in counties Waterford and Sligo, containing improved Irish silver and downy birch planting material, were assessed periodically up to eight years of age. Height and diameter at breast height were measured to compare growth among families and with controls. Linear mixed models were used to assess family and site differences and estimate genetic parameters. Comparisons with selected controls showed increased growth performance in the improved family progeny.

These findings, alongside estimated breeding values, will help identify promising families for further testing and selection. The work will inform future breeding efforts for silver and downy birch in Ireland and may support the development of improved planting material for wider use in mixed-species forestry.

Assessing trap and lure performance in native longhorn beetle surveillance trials across Northern Ireland

Ryan T Weir, Florentine Spaans, Archie Murchie

AFBI

Early detection of *Anoplophora* sp. and *Monochamus* sp., (vector of pine wood nematode), depends on trapping systems that perform under local conditions. Neither genus occurs in Northern Ireland, so we explored native Cerambycidae as surrogate species in an assessment of trap and lure performance. In four pine stands, cross-vane flight intercept traps were baited with either of two Monochamus lures (GP, MG). In four broadleaf stands, flight intercept traps (suspended ~1 m) and ground traps were baited with an *Anoplophora* lure. No *Anoplophora* sp. or *Monochamus* sp. were detected across the survey. In total over 100 individual native cerambycids were caught across five species: *Rhagium bifasciatum*, *Pogonocherus hispidus*, *Grammoptera ruficornis*, *Rhagium mordax* and the rarely recorded *Asemum striatum*. Some 88% of this catch fell between 25 May and 19 June and the peak flight of each species has been calculated.

Across the trials GP and MG lures showed similar success rates in pine (34 vs 37). However GP proved more successful at catching a range of species (3 vs 1). In broadleaf, flight intercept traps caught all relevant beetles of the family Cerambycidae; ground traps caught none (0 of 41 collections). Against controls lured traps out preformed non-lured controls in every instance.

It is presented then that lured flight intercept traps successfully capture native longhorns and are the better broadleaf design, with little preference shown between lure formulation in conifers. Future trials will be assessing lower stratum trapping vs canopy trapping and the introduction of brightly coloured traps as an alternative to lures.

Identifying Primary Aphid Vectors of Potato Virus Y in Irish Potato Crops

Mathijs Dejong[1,2], Louise McNamara[1], Denis Griffin[1], Rene van der Vlugt[2]

[1]Teagasc, [2]Wageningen University

Potato Virus Y (PVY) is an RNA virus that can infect many crop species, among them potatoes. When a potato plant is infected, there is yield loss, potentially paired with decreased tuber quality, both particularly severe when early infection occurs. PVY is transmitted non-persistently by aphids. Worldwide, more than 60 aphid species have been found to be able to vector the virus. In Ireland, it is unclear which species serve as the primary PVY vectors. This research focuses on identifying aphid species in potato fields. In 2025 and 2026, a nationwide survey was conducted in collaboration with potato growers across eight counties in Ireland. Alate aphids were collected on a weekly basis throughout the growing season using yellow water pan traps raised just above canopy height. More than 20,000 aphids were collected, of which more than 6,000 were identified to genus level. Insect samples collected in the first five weeks after crop emergence consisted of aphids belonging to 48 genera. The genera found to be most abundant were Aphis, Myzus, Brevicoryne, Cavariella, Metopolophium, and Rhopalosiphum, in that order. Future research will focus on species identification, virus transmission efficiency and insecticide resistance, as well as integrated pest management strategies.

Investigating the Virucidal Activity of Insect Haemolymph Following Diverse Immune Priming

Esmeralda Herrero, Michael Huynh

SETU Carlow

Insects possess sophisticated innate immune systems that can be enhanced through immune priming, yet the extent to which priming influences virucidal activity remains poorly understood. This study aims to determine whether immune stimulation can induce virucidal factors within insect haemolymph capable of inactivating viral particles. As an initial proof-of-concept, a bacteriophage-based screening platform has been developed and optimised using the mealworm beetle, *Tenebrio molitor*, and bacteriophage T4.

To date, methodologies for insect immune priming, haemolymph collection, processing, and phage infectivity assays have been successfully established and standardised. Preliminary investigations examined immune priming through abiotic stressors, including heat exposure and mechanical shaking, applied individually and in combination, as well as biotic challenge with the entomopathogenic nematode *Steinernema feltiae*. Haemolymph collected from treated insects was assessed for its ability to reduce T4 bacteriophage infectivity. Under the conditions tested, none of the immune priming treatments thus far resulted in detectable virucidal activity against T4. These findings may indicate that the selected priming stimuli do not induce broad-spectrum virucidal factors effective against T4, or alternatively that T4 is a relatively resistant viral model for detecting such effects.

Ongoing work will expand the study to include additional viral surrogates, namely bacteriophages Φ6 and MS2. Given its lipid envelope, Φ6 is hypothesised to be more susceptible to insect-derived antimicrobial and antiviral effectors than the non-enveloped T4 and MS2 phages. Future experiments will also employ the lesser wax moth, *Achroia grisella*, alongside *T. molitor*, and will also investigate bacterial immune priming through *Escherichia coli* injection. Together, these studies aim to determine whether immune priming can enhance virucidal activity in insect haemolymph and establish a robust platform for investigating insect antiviral defences.

Conservation of candidate survivor elms in Ireland

Karuna Shrestha[1,2], Antonia Alessandra Lemos Dos Santos[3], Oliver Gailing[2], Ricardo Pimenta[1], Dheeraj Singh Rathore[1]

[1]Teagasc, Forestry Development Department, Oak Park Research Centre, Carlow, R93 XE12, Ireland, [2]Forest Genetics and Forest Tree Breeding, Büsgenweg-Institute, Georg-August University of Göttingen, Büsgenweg 2, 37077, Göttingen, Germany, [3]Department of Mathematics and Statistics, Maynooth University, W23 XY3X Maynooth, Ireland

Elms (*Ulmus* spp.) are important broadleaf trees in Europe, valued for their ecological, economic and cultural contributions. Once widespread across the Irish landscape, they have suffered severe declines following Dutch elm disease (DED). Caused by the fungal pathogens *Ophiostoma ulmi* and *O. novo-ulmi*, the disease is primarily transmitted by elm bark beetles (*Scolytus* spp.). Young elms continue to regenerate from root suckers and seedlings, although they may become infected as they grow. Identifying and conserving surviving mature trees could provide material for future assessment and breeding.

We used a citizen science approach to locate candidate elms across Ireland and collected stem cuttings from selected mature trees to evaluate rooting success. Between February 2024 and July 2026, public outreach generated 117 reports. Propagation trials included 75 donor trees and 2,171 cuttings collected in early summer, summer and winter of 2025 and treated with three concentrations of indole-3-butyric acid.

Rooting success was low, at 7.1%, with rooted cuttings obtained from only 28 donor trees. These results highlight the difficulty of propagating mature elms from cuttings, while providing material for conservation and further assessment. Molecular identification continued monitoring and controlled DED screening are planned to assess the selected trees and their potential use in future breeding.

Beyond virulence: How DON and NIV mycotoxins shape wheat head microbiome gene expression

Sai Sushma Boggarapu, Fiona Doohan

School of Biology and Environmental Sciences, University College Dublin, Dublin, Ireland

Fusarium head blight (FHB) is a major disease of wheat causing significant yield losses and contaminating grains with deoxynivalenol (DON) and nivalenol (NIV), mycotoxins of serious concern for food safety and animal feed. While DON and NIV are established virulence factors facilitating pathogen spread and disease progression, recent evidence suggests that trichothecenes function not only as pathogenicity determinants but also as ecological molecules capable of mediating interactions between Fusarium and surrounding microbial communities. The wheat head microbiome plays a critical role in plant health and disease dynamics, yet how different mycotoxins and their chemotypes shape the wheat head microbiome during FHB infection remains unexplored. We hypothesize that DON and NIV toxins, produced by distinct chemotypes (*Fusarium graminearum* and *F. poae*), exert distinct selective pressure on the resident microbial communities, differentially reshaping their composition and function. Using microbiome profiling and metatranscriptomics, we will determine how mycotoxins restructure microbial communities and gene expression during early FHB infection. This research will reveal the relation between mycotoxin production and microbiome function, potentially identifying microbiome-based biomarkers for disease resistance and informing new management strategies.

Clubroot in Ireland: First insights from whole genome sequencing of *Plasmodiophora brassicae*

Marta Niedzicka[1], Ewen Mullins[1], Emmanuelle Graciet[2]

[1]Crop Science Department, Teagasc, Oak Park, Carlow, [2]Department of Biology, Maynooth University, Maynooth

Clubroot is a devastating disease of Brassica crops, occurring worldwide and causing significant economic losses. The disease is caused by the soil-borne protist *Plasmodiophora brassicae*. Resting spores infect the roots of susceptible Brassica plants, causing characteristic galls that disrupt water and nutrient uptake. These spores can persist in soil for up to 20 years, making it very difficult to control once established. The genetic diversity of P. brassicae, including the presence of multiple genotypes within a single root, suggests a capacity for rapid adaptation and the breakdown of host resistance, further complicating disease management. Recent reports of increasing clubroot incidence in Ireland highlight the need for a robust integrated pest management (IPM) approach.

In this project, we initiated surveillance of clubroot in Irish soils and conducted the first assessment of the pathogen's genetic diversity in Ireland. As part of the preliminary study, six samples collected from six fields in south-eastern Ireland were sequenced using high-throughput sequencing with Oxford Nanopore long reads. P. brassicae genomes were assembled, providing the first local genome assemblies of this pathogen. These assemblies represent a valuable resource for future research and enable an initial assessment of the pathogen's genetic diversity in Ireland. Preliminary phylogenetic analysis indicates that the Irish assemblies form a distinct cluster from the publicly available genomes.

Transcriptomic profiling of the barley fungal pathogen *Ramularia collo-cygni* reveals virulence-associated secreted enzymes and candidate effector proteins

Enrico Jugadora[1], Angela Feechan[2], Sujit Jung Karki[1]

[1]University College Dublin, [2]Heriot-Watt University

Ramularia collo-cygni (Rcc), the causal agent of Ramularia leaf spot (RLS), poses a major threat to barley production, with yield losses reported to reach 70%. The chlorothalonil ban, increasing restrictions on fungicide use, and the absence of effective genetic resistance highlight the need for alternative control strategies. Here, we investigated the effector repertoire of Rcc to identify virulence-associated candidates during barley infection. We phenotypically screened 20 Rcc isolates on the susceptible barley cultivar RGT Planet. Disease development was quantified using combined area under disease progression stairs (AUDPS) and ImageJ-based lesion analysis, confirming Rcc02 as the most aggressive and Rcc06 as the least aggressive isolates. Dual host-pathogen RNA-seq at 2, 4, 6, 10, and 14 dpi identified 7,562 differentially expressed genes in Rcc02, of which 581 were significantly more highly expressed than in Rcc06. SignalP-6.0 and EffectorP-3.0 predicted 55 secreted effector proteins, which were further refineD to 18 high-confidence candidates showing peak expression during infection. Further analysis revealed seven distinct phase-specific co-expression clusters, abundant proteases and redox-related enzymes, and candidate effectors associated with both biotrophic and necrotrophic stages of Rcc infection. The identification and characterisation of these fungal effectors would help in the development of RLS-resistant barley varieties.

Poster Presentations

Teagasc National Insect Monitoring Programme

Gerard Nolan, Louise Mc Namara, Stephen Byrne

Teagasc, Crop Science Department, Oak Park, Carlow, R93XE12

Long-term, standardised monitoring of insect populations is critical to understanding pest dynamics and informing sustainable crop protection strategies. Building on internationally recognised models, Teagasc established the National Insect Monitoring Programme to track cereal aphids and other airborne pests across Ireland. At the core of the nationwide network, a series of high-altitude 12.2m suction towers, provide continuous, comparable data on aphid flight activity and species composition.

Each year, the programme aims to process approximately 1,200 suction tower samples, requiring daily collections, insect sorting, and cereal aphid identification—representing a significant national dataset. These samples are collated in a central database, while samples are securely archived following best practice biobanking protocols to support future molecular analyses. The resulting datasets underpin ongoing research in integrated pest management (IPM), virology, resistance monitoring and long-term trends, with potential to provide early warnings of pest and viral pressure to growers.

Tracking potato late blight through the air: Integration bioaerosol eDNA with CRISPR-Cas for point-of-need detection

Weili Guo[1*], Yongda Li[1*], Stephen Kildea[2], David O'Connor[3*], and Anne Parle-McDermott[1*]

[1]School of Biotechnology; Dublin City University, Ireland, [2]Teagasc, Crops Research Centre, Oak Park, Carlow, R93 XE12, Ireland, [3]School of Chemical Sciences; Dublin City University, Ireland, *DCU Life Sciences Institute

The genomic complexity of bioaerosols allows airborne eDNA to serve as an effective tool for biodiversity assessment, predictive public health surveillance, and agricultural pathogen monitoring. European potato crop yields are persistently threatened by late blight, caused by the oomycete pathogen Phytophthora infestans. Timely detection of Phytophthora infestans species and its aggressive strains (e.g., EU43), particularly through airborne spores using bioaerosol eDNA, is critical for tracking pathogen movement and implementing targeted interventions. Traditional PCR-based molecular detection require laboratory infrastructure and are unsuitable for point-of-need Phytophthora infestans monitoring. Recent advances in eDNA sampling coupled with CRISPR-Cas detection system provides transformative opportunities for rapid and accurate blight monitoring at the point of need.

In the AGSENSE project, we first established an isothermal RPA/CRISPR-Cas12a assay for species-level detection of Phytophthora infestans in both bioaerosol eDNA and leaf genomic DNA. Bioaerosol samples were captured using a multi-vial cyclone sampler, followed by eDNA isolation. Utilizing the collateral cleavage activity of Cas12a, the assay achieved sub-femtomolar sensitivity at a constant 37°C. Beyond species-level detection, a strain-specific RPA-CRISPR-Cas9 assay was developed to enable the discrimination of nucleotide-level mutation, including the differentiation of homozygous and heterozygous variants. Time-course optimisation revealed a rapid assay reaction time, with clear differentiation between mutant and wild-type sequences on lateral flow strips after only five minutes of incubation. The assay has been applied for detection blight strains from both bioaerosol eDNA and infected leaf genomic DNA.

AshForFuture: Harnessing natural variation in *Fraxinus excelsior* for ash dieback tolerance in the Irish landscape

William O'Neill[1], Rodrigo Olave[1], Dheeraj Rathore[2], Oliver Sheridan[3], Eugene Hendrick[3], Gerry Douglas[3]

[1]Agri-Food and Biosciences Institute, Newforge Lane, Belfast, BT9 5PX Northern Ireland, UK, [2]Teagasc, Oak Park Research Centre, Carlow, R93 XE12, Ireland, [3]Forest Genetic Resources Trust, Dublin 6W XA38, Ireland

AshForFuture, a collaboration between Teagasc, AFBI, UCD and FGRT, aims to identify ash trees displaying potential tolerance to ash dieback, propagate selected genotypes, and establish a living gene bank to support conservation and breeding. Initial grafting material has been collected from 18 candidate trees: 17 from County Kilkenny and one from County Mayo. Kilkenny candidates were selected from a 6.3 ha, 30-year-old, ash-dominated stand comprising 95–100% ash. Trees were assessed in September 2025 and selected using a ≥90% crown fullness threshold, with apparently healthy trees representing ~0.3–0.5% of the assessed population.
Subsequent assessment of crown scions in April 2026 identified visible ash dieback symptoms on scions from 11 candidate trees, while no symptoms were detected on scions from six trees, reinforcing the need for replicated grafting and phenotypic validation. Collected scions were grafted onto ash rootstocks under glasshouse conditions.
Throughout 2026, the AshForFuture project will expand field surveys across Northern Ireland, assessing 45 infected ash stands. Field selection will be based on crown transparency, shoot dieback, dead branchlets, crown vitality and basal stem/root-collar condition. Standardised scoring and permanent tree identifiers will allow selected candidates to be re-visited, compared across sites and linked to future phenotypic and genetic data.
The gene bank will preserve candidate genotypes as a living resource for replication, genetic screening, controlled crossing, seed orchard development and future field trials, supporting evidence-based breeding and conservation of *F. excelsior*.

Establishing a Watercourse Surveillance Network for Detection of Phytophthora spp. in NI Forests: Preliminary Findings

Catherine McGuckin, David Craig, Mark Wilson

Agri-Food and Biosciences Institute

Phytophthora species pose a significant threat to forest health and require effective surveillance for early detection. This study established a watercourse surveillance network across twelve forest sites in Northern Ireland and evaluated water baiting as a monitoring approach. Bait bags were deployed at three-week intervals and recovered for pathogen isolation and molecular identification.
To date, six sites have yielded positive detections, with four Phytophthora species identified: *P. ramorum* EU2, *P. pseudosyringae*, *P. lacustris* and *P. gonapodyides*. A total of 39 positive detections have been recorded, with clear variation in species composition between sites. Preliminary findings demonstrate the value of watercourse baiting as a practical tool for forest health surveillance and early pathogen detection.

Understanding oat responses to the Fusarium mycotoxin T-2

Kanipriya Ravichandran, Fiona Doohan

School of Biology and Environment Science, Earth Institute, University College Dublin, Belfield, Dublin, Ireland

T-2 and HT-2 mycotoxins are important food and feed safety concerns in oats and are mainly associated with *Fusarium langsethiae*, which can infect oat panicles without producing obvious disease symptoms. Although T-2 toxin is well recognised as a contaminant of cereal grains, its role in the plant–fungus interaction and how plants respond directly to the toxin remain poorly understood. Understanding the response of oat to T-2 toxin may therefore provide insight into the role of toxin production during Fusarium–host interactions. Here, oat seedlings were used as a model to investigate the morphological effects of T-2 toxin and associated molecular responses. Three-day-old seedlings of oat cv. Husky were vacuum-infiltrated with 1, 5 or 10 ppm T-2 toxin, alongside water and solvent controls, and maintained under controlled conditions for six days. Root systems were scanned and analysed using RhizoVision Explorer. Twelve seedlings per treatment were assessed in each of three independent trials. Root traits included total root length, root tips, branch points, network area, root diameter, perimeter, surface area and volume. T-2 toxin affected root development, with total root length decreasing with increasing toxin concentration and the greatest reduction observed at 10 ppm. Changes were also observed in root branching, network area, surface area and volume, with similar patterns across the three trials. These results show that T-2 toxin directly alters root development in oat. Transcriptomic analysis is underway to investigate the molecular responses associated with T-2 exposure and the observed changes in root development.

Mallow - A Novel Agronomic Crop

Patrick Herron[1,2], Lisa Black[2], Brian Green[1], Paul Cottney[2]

[1]Queens University Belfast, School of Biological Sciences, [2]Agri-Food and Biosciences Institute

Medicinal plants is a fast-growing global industry with more than 50% of all new drugs being directly derived from modified products of medicinal plants or the active constituents of the plant itself (Wang et al, 2020). Paired with concerns of the impact of climate change on global food security and increased focus on a need for one health has resulted in a growing demand for novel and historic medicinal crops to be evaluated as potential mitigation strategies, to reduce the use of environmentally harmful chemicals in livestock production.

Common Mallow (Malva Sylvestris L.) is a novel agronomic crop with high immunomodulatory content. Its use as a medicinal crop dates to ancient Rome and is still used in traditional remedies and recipes (Mousavi et al, 2021). The plant is known to have antioxidant, anti-microbial, antibacterial, anti-inflammatory, anti-ulcerogenic, anti-cancer and therapeutic properties (Delfine et al, 2017). It contains bioactive polysaccharides which can improve immune response in livestock and therefore has potential to be used in animal feeds to reduce reliance on prophylactic antibiotic use.

Although the health benefits from different bioactives originating in M. sylvestris are identified (Azab, 2017) there is currently no guidance on how to reliably cultivate it as a commercial crop. The proceeding research will identify the optimal agronomic techniques to produce M. Sylvestris for maximal yield and bioactive returns. 2 years of trials have been conducted, identifying optimal seeding rates, sowing and harvest dates, fertilizer and weed management regimes, ensilement capability and DUS variety trials.

The findings of which research will create a comprehensive agronomic toolkit to inform and guide on the most cost effective, efficient and reliable method to cultivate M. Sylvestris for commercial purposes to maximise bioactive yield. This will offer growers a new lucrative crop that will also assist in accomplishing climate and environmental targets.

Resbarley: The race towards enhancing durable resistance to leaf scald disease of barley

Éabha Gilroy[1, 2], Emmanuelle Graciet[1], Ewen Mullins[2]

[1]Maynooth University, Maynooth, Ireland, [2]Teagasc crops research, Oak Park, Carlow, Ireland

Barley dominates the Irish tillage sector, yet farmers remain overly reliant on the use of fungicides to maintain yield and quality. Leaf scald, caused by the fungal pathogen Rhynchosporium commune is a particular threat to barley, resulting in yield losses of up to 40% in susceptible cultivars. There are currently no varieties on the recommended list with adequate levels of resistance to support pesticide use reduction against leaf scald. In response, this project aims to (i) identify candidate susceptibility genes (s-genes) involved in the infection process of leaf scald and (ii) validate their role via gene editing, with the purpose of supporting future breeding efforts to combat leaf scald. Silencing or complete knockout of s-genes has the potential to deliver barley lines with durable resistance to disease as demonstrated in mlo mutants resistant to powdery mildew (Kusch & Panstruga, 2017). Temporal analysis of data from RNA sequencing previously carried out by inoculating a susceptible cultivar with R. commune identified 54 differentially expressed genes that have orthologues corresponding to known s-genes in other species. From this, 16 genes were shortlisted based on proposed functionality in the literature relative to the investigated host-pathosystem. From this list, 5 genes were selected for validation via CRISPR-CAS9 editing / virus induced gene silencing (VIGs) to create novel barley lines with s-gene mediated resistance. The edited cultivars will then be tested for agronomic fitness and resistance to other diseases.

Harnessing Tree Microbiomes to Enhance Forest Health and Resilience: The ResFor_Micro Project

Nadya Doyle[1], Kieran Germaine[1], Dheeraj Rathore[2]

[1]South East Technological University (SETU), Carlow, Ireland, [2]Teagasc, Oak Park, Carlow, Ireland

Forests in Irelands are facing challenges from climate change, disease outbreaks and demands for sustainable wood production. The ResilientForests project aims to develop new research tools and capacity to support forest resilience in Ireland. As part of this project, ResFor_Micro will investigate microbial communities associated with key tree species and their potential role in improving tree health and resilience.

Microorganisms living within the rhizosphere, rhizoplane, and endosphere can influence forest resilience, not just tree genetics and environmental conditions. These microorganisms can influence nutrient acquisition, tree development, stress resilience, and defense against pathogens. However, these interactions remain relatively underexplored in Irish forestry systems.

Previous research on the common alder (Alnus glutionosa) microbiome has highlighted potentially beneficial microorganisms and their possible use as biological control agents against alder disease. However, further work is required to understand which microorganisms are associated with healthier or disease-tolerant trees and whether their beneficial effects can be demonstrated experimentally.

ResFor_Micro will build on this research by characterizing microbial communities associated with Sitka spruce, Scots pine, Douglas fir, Alder, Birch, Sweet chestnut and Ash across sites and contrasting health status. Bacterial and fungal communities will be investigated using culture-independent and culture-dependent approaches. Potentially beneficial microorganisms will be isolated and screened for antagonistic activity against important tree pathogens. Promising isolates will then be investigated for their potential development of bio-inocula aimed at improving tree establishment and resilience. The project will also contribute to the development of a microbial biobank for future forestry and biosecurity applications.

Yellow Legged Hornet: The Most Northerly Reported *Vespa velutina* nest, Belfast, Northern Ireland

Florentine Spaans, Joanna Kirbas, Ciara Isaac, Andrew McClure, Peter Williams, Archie Murchie

Agri-Food & Biosciences Institute, Belfast, Northern Ireland, BT9 5PX

The yellow-legged or Asian hornet (*Vespa velutina*) is an invasive species that was introduced into France for the first time in 2004 and is rapidly spreading across the rest of Europe since then. Densities can be high, with 5-6 nests per km2 present in Jersey. The first hornet nest was discovered in the UK in 2016 and by 2025, despite removing all known nests every year, 163 nests were found in 2025. The hornets are voracious predators of other insects, also attacking bees and damaging crops. The first Asian hornet nests on the island of Ireland were found in Cork in 2025, followed by a nest in Dundonald, Belfast in October the same year. This poster presents details of the nest structure of the Dundonald nest, which had advanced to the early reproductive phase at the time it was taken down. Males, female workers and gynes were found in the nest at various stages of development. The size of the nest as well as the size of individuals within the nest were smaller than average when compared to reports in the literature. The nest remains the most northernly find of a *Vespa velutina* nest in Europe and the world.

Sitka spruce seeds germination response to chilling across a latitudinal range

Romane Guernalec[1,2], Tomás Byrne[1], Conor O'Reilly[2], Brian Tobin[2]

[1]Teagasc, Ashtown, Co. Dublin, D15 DY05, [2]University College Dublin, School of Agriculture and Food Science, Belfield, Dublin 4

Sitka spruce, a species originally native from North America, quickly became a key established species in the Irish forestry sector due to similar wet and mild maritime climate than the native range.
Dormancy is a key adaptive trait in tree seeds, protecting it from unfavourable conditions – and is lifted by accumulated cold (chilling) followed by warmth, allowing spring growth through germination and radicle expansion. But rapid climate change may affect its germination and subsequent establishment in forests where regeneration happens naturally, as the winter and spring temperatures are rising. Understanding its capacity to adapt will guide future provenance choice.
We examined the germination responses from native seeds ranging from 54°N (Skeena, BC) to 45°N (Oregon, WA) at 15 and 20°C after chilling treatments including 0, 2, 6, 10 and 15 days. Mean germination time was calculated from seed counts over 45 days and was the main response variable.
Chilling up to 6 days reduced the time to germinate significantly for all provenances, at both temperatures. After 6 days, germination time plateau, suggesting longer chilling start degrading the seeds and is not effective. Control seeds germinated as well, showing expression of conditional dormancy, i.e. the ability to germinate without chilling in temperature above 10°C only. Overall, the seeds expressed both a shallow and conditional dormancy, and faster germination at 20°C than 15°C. Latitudinal differences were expressed as well, with the northern seedlots germinating quicker.

Gremmeniella abietina

David Craig, Catherine McGuckin, Mark Wilson

AFBI

Gremmeniella abietina also known as Brunchorista disease (Europe) or Scleroderis canker (America) is a fungal pathogen commonly found associated with Pinus spp (pine) but has also been known to infect Abies, (fir) Picea (spruce) and Larix (larch).
Shoot blight caused by *Gremmeniella abietina* was first recorded as part of an EEC led survey in Northern Ireland in 2010 at Koram Wood, then in subsequent years in Aghyaran, Altmore, Ballyboley, Ballycastle, Banagher, Big Dog, Carrickholten, Castlewellan, Clabby, Clare, Cleggan, Coolavely, Creggan, Crocknagrally, Fardross, Favor Royal, Moneyglass, Moyola, Slieve Donard, Slieve Gullion, Slieveanorra, Springwell and Tollymore.
Pine stands were extensively surveyed and samples taken where appropriate. Initially all samples collected were scanned under a low power binocular microscope. Sub-samples were taken and examined under higher magnification in an attempt to authenticate the infection. After the preliminary microscopic examination of the complete sample, subsamples were sent to be processed by the AFBI PPMB Lab. DNAs were extracted and amplified using a two-step nested PCR technique to confirm the presence of *Gremmeniella abietina*.

Exploring Resistance and Management Strategies for Clubroot in Oilseed Rape

Reshma Akter Tonu

Maynooth University

Oilseed rape (OSR; *Brassica napus*) is an important break crop in cereal rotations and has both economic and environmental benefits for Irish tillage farming. It provides a source of high-protein animal feed and oil, supports pollinators, and can reduce nitrogen losses by taking up residual soil nitrogen. However, the increasing incidence of clubroot, caused by the soil-borne protist *Plasmodiophora brassicae*, presents a significant threat to the sustainable expansion of OSR production in Ireland. The long-term persistence of *P. brassicae* resting spores in soil and the potential contribution of Brassica-containing cover crops further complicate disease management. This project aims to develop an integrated, evidence-based approach to detect, understand and manage clubroot in Irish OSR production. A robust molecular assay will be developed and validated for the detection and quantification of *P. brassicae* resting spores in soil, with pathogen concentrations investigated in relation to field disease severity and cropping history. In addition, a diverse collection of commercial OSR varieties will also be screened under controlled conditions to identify differences in resistance and provide material for investigating genetic factors associated with clubroot resistance.
By integrating soil-based pathogen detection, pathogen characterisation, field observations and varietal resistance, this research will contribute to a practical decision-support framework for clubroot management. The outcomes will support informed variety selection and improved agronomic practices, helping to safeguard and sustainably expand OSR production within Irish tillage systems.

Anoplophora chinensis: an interception

Shane Kirk

Department of Agriculture, Food and the Marine

Anoplophora chinensis was recently found in Ireland. A single specimen was intercepted in a consignment of coats. This is the first finding of this pest, an EU Priority Pest, on the island of Ireland. The pest was identified by the Plant Science Division of DAFM and confirmed by the EU Reference Laboratory for Insects and Mites.

Optimising Fungicide Control in Barley: Monitoring of SDHI Resistance in *Ramularia collo-cygni*

Edwina Nolan[1,2], Angela Feechan[2], Neil Havis[3], Henry Creissen[4], Steven Kildea[1]

[1] Teagasc, Crops Science Department, Oak Park, Carlow, [2]Heriot-Watt University, Edinburgh, UK, [3]Scotland's Rural College, Edinburgh, UK, [4]University of the Highlands and Islands, Orkney, UK

The continued development of fungicide resistance in key fungal pathogens poses a growing threat to the productivity of Irish barley crops. *Ramularia collo-cygni* is one key fungal pathogen of barley that causes Ramularia leaf spot (RLS), a disease that can significantly reduce grain yield and quality. RLS control has relied on fungicide application (mainly multisite, DMI and SDHI fungicides). However, fungicide control efficacy has declined as *R.collo-cygni* has developed resistance to fungicides that previously provided good disease control including QoI, DMI and SDHI fungicide classes. In the absence of reliable and effective non-fungicidal control measures, effective fungicide resistance management and optimised fungicide application are required to prolong the efficacy of important crop protection chemistries.
In response to these challenges, field trials were conducted at two locations of differing disease pressures to optimise fungicide application and monitor fungicide resistance. Fungicide programmes with varying spray timings and frequencies were assessed for RLS severity and yield. Across 2023–2025 field trials, GS45–49 emerged as a key application timing for RLS control, although an additional application may be required. Post fungicide application, infected leaf samples were collected and were screened for SDHC gene alterations known to confer SDHI resistance in *R. collo-cygni* using Illumina-based amplicon sequencing. A total of 22 haplotypes were identified. Further analysis will examine mutation prevalence based on location, fungicide application timing and year. These findings will inform fungicide programmes aimed at mitigating resistance while maintaining RLS control, protecting yield and grain quality.

Genomic prediction of ash dieback severity and budburst in Fraxinus excelsior in Ireland

Ricardo J. G. Pimenta[1], Jie Huang[1], Stephen Byrne[2], Joanna Meger[3], Dheeraj Singh Rathore[1]

[1]Teagasc, Forestry Development Department, Oak Park Research Centre, Carlow, Ireland, [2]Teagasc, Crops Science Department, Oak Park Research Centre, Carlow, Ireland, [3]Department of Genetics, Faculty of Biological Sciences, Kazimierz Wielki University, Bydgoszcz, Poland

Ash dieback (ADB) disease, caused by the invasive fungal pathogen *Hymenoscyphus fraxineus*, is placing severe pressure on European populations of common ash (*Fraxinus excelsior*), with up to 90% of trees succumbing to the disease following infection. However, a small proportion of ash trees show a low severity of ADB, which has been shown to be heritable. Additionally, earlier spring budburst may also provide a mechanism for reducing disease severity by limiting the exposure of young leaves to *H. fraxineus* spores. The selection and breeding of ash trees with reduced severity of ADB can be supported and accelerated by genome-wide association studies (GWAS) and genomic prediction (GP). Here, we analysed a diverse F. excelsior population established at two sites in Ireland. ADB severity was assessed twice annually for four years, while budburst was scored weekly for three

years during spring. The population was whole-genome sequenced, and single nucleotide variants (SNVs) were called and used for GWAS and GP of ADB severity and budburst progression. Using the full dataset of over 7 million markers resulted in moderate to low prediction accuracies for ADB severity and budburst. In contrast, reduced marker sets based on top-ranking SNVs from GWAS substantially increased prediction accuracy for both traits. Following validation, these reduced marker datasets could be applied to support the selection of trees with earlier budburst and reduced ADB severity.

ResilientForests – Advancing Tree Improvement Research for Climate-Resilient, Diverse and Productive Forests for Ireland

Emma Fuller[1], Dheeraj Singh Rathore[1], Tomás Byrne[1], John Casey[1], Brian Clifford[2], Derek Gibson[1], Brian Tobin[3], Charles Harper[3], Jon Yearsley[3], Niall Farrelly[1], Sameer Mehra[4], Kieran Germaine[5], Dermot O'Leary[6], John Kavanagh[7] and Finbarr Curran[8]

[1]Teagasc, Forestry Development Department, Ireland, [2]Department of Agriculture, Food and the Marine, Forest Sector Development Division, Ireland, [3]University College Dublin, Ireland, [4]Technological University Dublin, School of Architecture, Building and Environment, Ireland, [5]South East Technological University, enviroCORE Research Laboratory, Ireland, [6]Coillte, Ireland, [7]None So Hardy (Forestry) Ltd., Ireland, [8]Irish Distillers Limited, Ireland

Ireland's forests are facing increased pressures from climate change, extreme weather, pests and diseases, alongside the need to deliver biodiversity, carbon storage and high-quality timber. Funded by the Department of Agriculture, Food and the Marine (DAFM), ResilientForests is a multidisciplinary project developing science-based approaches to protect and strengthen the diversity, health and productivity of Irish forests. The project integrates tree breeding, forest genetic resources, field evaluation, ecological modelling of forest biodiversity, wood quality assessments and microbiome research to inform the selection and deployment of planting material.

Research will develop species-specific breeding plans, evaluate existing trials, seed orchards and mixed-species stands, and combine phenotypic and genomic approaches to support tree improvement. By evaluating a broad genetic base, the project will explore how tree improvement can respond to dynamic climatic conditions while improving resilience to climate-related risks. Multi-trait wood characterisation will examine relationships between timber properties and genetic information. Forest biodiversity surveys and existing datasets will identify factors associated with promoting biodiversity in forest stands. Microbiome research will evaluate beneficial microorganisms for their potential to improve tree health, suppress forest pathogens and support seedling establishment.

The ResilientForests project aims to generate knowledge, genetic and microbial resources, and decision-support tools for Irish forestry. The project will support the development of forest reproductive material (FRM) resources, forest diversification and the evaluation of nature-based approaches to tree health. Through stakeholder engagement and knowledge transfer, the findings will inform forestry practice and contribute to the long-term development of more climate-resilient, diverse and productive forests in Ireland.

From Microbiome to Candidate Biocontrol Agents: Exploring Alder-Associated Microorganisms with Antagonistic Activity against *Phytophthora* spp.

Dheeraj Singh Rathore[1], Emma Fuller[1,2], Kieran Germaine[2], Dhrati V. Patangia[3], Kieran Kilcawley[3]

[1]Teagasc, Forestry Development Department, Oak Park, Carlow, Ireland, [2]South East Technological University, Kilkenny Road, Carlow, Ireland, [3]Teagasc Food Research Centre, Moorepark, Fermoy, Cork, Ireland

Common alder (*Alnus glutinosa*) is an ecologically important riparian tree species threatened by alder dieback associated with Phytophthora spp. This research characterised the alder-associated microbiome and investigated naturally occurring microorganisms as potential biological control agents.
Bacterial and fungal amplicon sequencing was used to characterise microbiome structure across plant and soil compartments, four seasons and two contrasting sites. Distinct microbial communities occurred among compartments, alongside recurrent core taxa and seasonal patterns of persistence.
A total of 257 bacterial and fungal isolates were screened against *P.* × *alni* and *P. uniformis* using dual-culture assays. Twenty-four isolates exhibiting ≥40% inhibition against at least one pathogen were selected for further characterisation. From these, two alder root isolates, *Bacillus mycoides* CR36B and *Trichoderma koningii* CR113, were taken forward for detailed investigation, inhibiting *P.* × *alni* by 73% and 74%, respectively, and *P. uniformis* by 73% and 68% in dual culture. Both isolates also exhibited volatile-mediated antagonistic activity, while genome analyses identified predicted biosynthetic potential associated with secondary metabolite production. In alder bark inoculation assays, both isolates significantly reduced lesion development caused by *P.* × *alni* relative to the pathogen-only treatment (adjusted $p < 0.05$), whereas comparable suppression was not observed against *P. uniformis*.
Retrospective comparison with the amplicon datasets showed that Bacillus and Trichoderma were recurrent components of the belowground alder microbiome and both met the study definition of root-core taxa. However, marker-sequence comparisons did not establish that the cultured isolates corresponded to the same strains detected by amplicon sequencing.
Together, these findings integrate microbiome ecology with culture-based screening and experimental antagonism, identifying alder-associated microorganisms that warrant further evaluation as candidate biological control agents for alder dieback.

Optimising the detection of insect wing beat signatures using high-frequency micro-Doppler radar

James Driessen2, Pieter Barnard1, Maryam Norouzi1, Ian Donohue2

1 CONNECT Centre, Trinity College Dublin, Dublin, Ireland, 2 School of Natural Sciences, Trinity College Dublin, Dublin, Ireland

In order to effectively conserve insect species, it is vital that insect populations are efficiently monitored over long periods and large areas. Recent advances in high-frequency Doppler radar systems enable the development of a cost-effective and practical micro-Doppler radar to detect and monitor insects based on their micro-Doppler wing beat frequencies. This offers the potential of an automated insect monitoring system that can be deployed at scale. This study measures the radar signatures of the micro-Doppler wing beats of honeybees (*Apis mellifera*) over distance and optimises the signal analysis process in order to establish the potential detection range of a micro-Doppler radar system for insect detection. It finds that the micro-Doppler radar system has a detection range of up to 113 centimetres when the parameters of the signal analysis are adjusted to analyse only large segments of flight data at the peak insect flight signal frequencies. This indicates the importance of wing beat signal quality in the data analysis stage and suggests that analysis should focus on the micro-Doppler wing beat frequencies of target insects. These findings represent a step towards a practical solution for the deployment of a large-scale pollinator monitoring network and the efficient conservation of pollinating insects.

Multi-level phenotyping of tar spot disease severity in sycamore maple (*Acer pseudoplatanus)*

Donnacdha Williams[1,2], Ricardo J. G. Pimenta[2], Bailey Parkhouse[2], Jie Huang[2], Tomás Byrne[2], Derek Gibson[2], Miguel Nemezio-Gorriz[3], Dheeraj Singh Rathore2

[1]University College Dublin, School of Agriculture and Food Science, Dublin, Ireland, [2]Teagasc, Forestry Development Department, [3]Grupo Tragsa, Madrid, Spain

Sycamore maple (Acer pseudoplatanus) is an introduced broadleaf tree in Ireland, valued for its growth, timber quality and wildlife habitat. It may complement other broadleaf species facing pest and disease pressures. Tar spot, caused by the fungus Rhytisma acerinum, produces dark lesions on sycamore leaves. Variation in disease severity offers an opportunity to investigate differences among genotypes and compare disease assessment methods.

In 2016, a sycamore seed orchard comprising of 571 trees representing 155 Irish and British plus trees was established in County Wicklow. In August 2020, trees were assessed visually for the percentage of the crown affected by tar spot. In September 2026, five symptomatic leaves from each of 175 trees were collected and scanned to quantify the percentage of leaf area covered by lesions. The orchard was also surveyed using drone imagery.

Analyses will examine variation in disease severity and compare crown assessments, leaf measurements and drone imagery for phenotyping. Leaf measurements describe severity on symptomatic foliage rather than overall crown infection. Existing genotyping-by-sequencing data provide scope to explore genetic contributions to this variation. The study aims to inform sycamore disease assessment and future breeding research, with repeated assessments needed to establish consistent differences among genotypes.

-end of abstracts-

Organisers

Dr Marta Niedzicka (SIPP)

Dr Virgile Ballandras (IEN)

Mr Andy Bourke (SIPP)

Dr Anna Tiley (SIPP)

Dr Marta Niedzicka (SIPP)

Dr Emma Fuller (SIPP)

Dr Aisling Moffat (IEN)

Dr Dheeraj S. Rathore (SIPP)

Getting Involved

To join SIPP or IEN please email:

- SIPP Secretary: sippsecretary@gmail.com
- IEN: the.irish.entomological.network@gmail.com

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, flash talks and posters.
- **Attendees:** It has been a great opportunity for SIPP and IEN to collaborate over the past two conferences in 2024 and 2025, and to continue this collaboration in 2026. Thank you for your participation and we hope you enjoy the conference.

SIPP x IEN 2026

-End-