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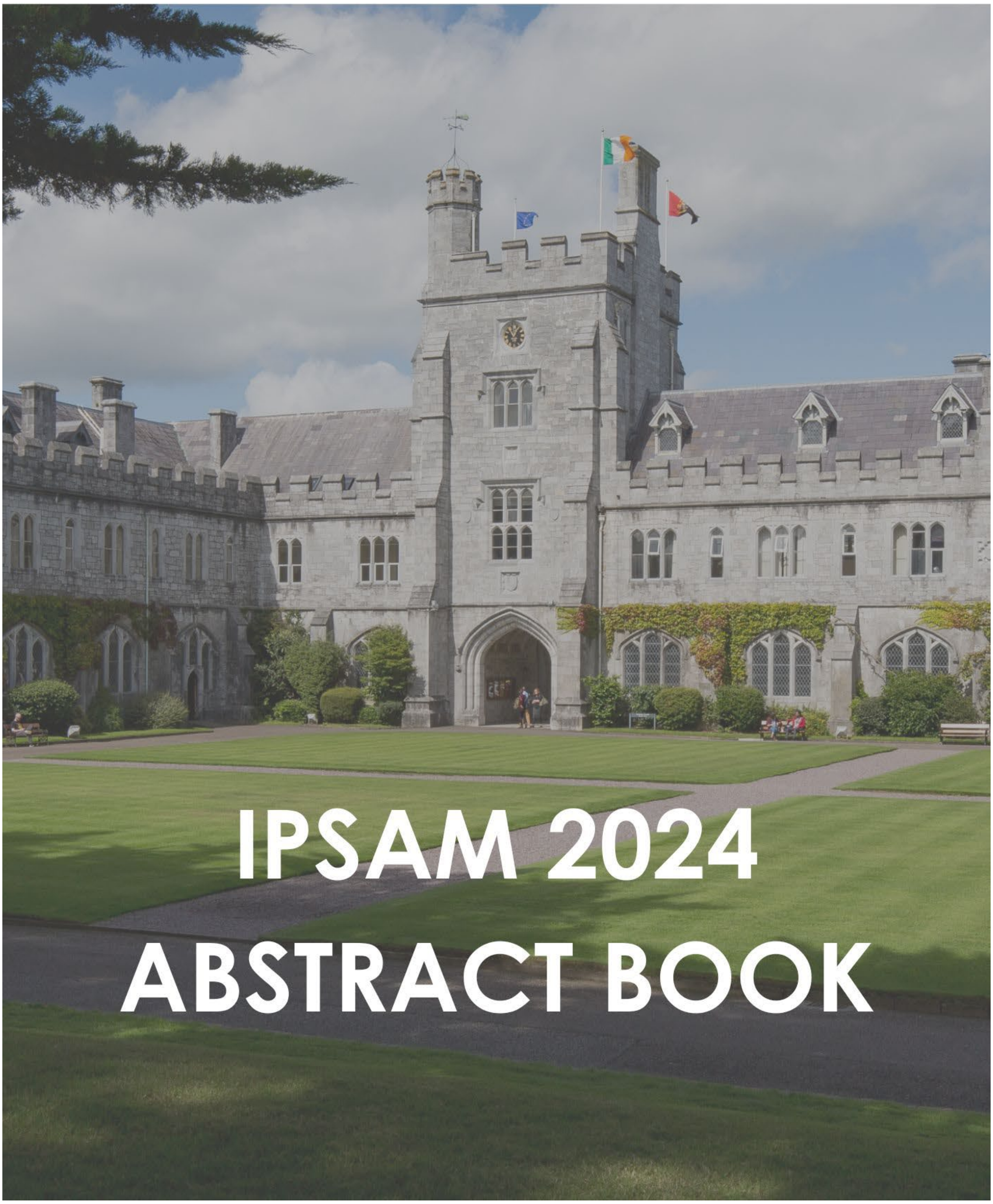

IPSAM 2024 ABSTRACT BOOK

The Irish Plant Scientists Association (IPSAM)

IPSAM (formerly Irish Botanists Meeting (IBM)) was founded in the 1970s and has been going strong ever since, with breaks mainly for Foot and Mouth (2001) and during the recent pandemic (2020 to 2022). IPSAM provides a platform particularly for early-stage researchers to showcase work, and to facilitate the building of networks across the island of Ireland. Plant Science research in Ireland today is cutting edge, vibrant and diverse, a remarkable feat given the lack of public investment in basic research in Ireland. Compared to many other parts of Europe, Ireland has the lowest public investment as a percent of GDP. As a collective, maybe IPSAM members could consider lobbying for a greater share of public investment for core Plant Science research activities given the level of grand challenges we face on a global scale?

IPSAM 2024 has an excellent schedule of talks and posters which will be presented over two days beginning with the Keynote by Dr Richard O Hanlon from DAFM who will speak on Plant Health and Diagnostics. There will be plenty of opportunity during the two days to network, interact with delegates and to participate in Mas Arte Mas Acción**.** We encourage you to enjoy our internationally accredited arboretum which sits on 42 acres and boasts

> 2, 500 trees. UCC is a Green Campus, recently becoming the first University in the world to secure five green flags. The university places a great emphasis on sustainability practices including the reduction/elimination of single use plastics where practicable.

We are delighted to welcome you to the UCC campus for IPSAM 2024 (jointly organised by UCC & MTU) and we hope you have a wonderful conference from a professional and social perspective. We would like to thank all our sponsors for their generous support of IPSAM.

From the UCC IPSAM Organising team

Barbara (Chair), Astrid, Joe, Rossana, Eoin, Deirdre, Israel, James, and Callum

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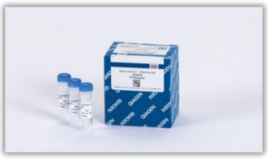

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Programme

IPSAM Programme 2024

Monday 17th June 2024	
09.00 to 10.00	**Registration & putting up of Posters (Boole 5 & 6) (Tea & Coffee available)** **Boole Basement – UCC Main Campus**
10.00 to 10.05	Opening & Welcome to IPSAM 2024 – Dr Barbara Doyle Prestwich, Head of Plant Science & IPSAM Conference Chair
10.05 to 10.10	Professor Astrid Wingler – Head of School of BEES
10.10 to 10.15	Introduction from **Mas Arte Mas Acción**
Session I: Plant Stress I – Boole 1 **Chair: Prof Astrid Wingler**	
10.15 to 10.45	**Keynote:** *Plant health diagnostics and science in Ireland* Dr Richard O Hanlon, DAFM
10.50 to 11.05	*The Dark Side of Salt Stress: Shining a Light on Organ Specific Stress Responses During Skotomorphogenesis* Ms Elizabeth van Veen, Wageningen University & Research
11.05 to 11.20	*Improved Strawberry Resistance and shelf-life through Genome Editing* Dr Raghu Ram Badmi, University College Cork

11.20 to 11.35	*Comparison of droplet digital PCR and quantitative PCR assays for the detection of Fusarium head blight pathogens in oats.* Dr Subramani Natarajan, University College Dublin
11.35 to 11.50	*Identifying novel sources of Septoria* tritici *blotch resistance and susceptibility in wheat using transcriptomic techniques* Mr Conor Copeland, University College Dublin
11.50 to 12.05	Flash Presentations (5 minutes per presenter) *Seaweed cell wall-derived carbohydrates as a bio elicitor in barley against Ramularia Leaf Spot (caused by the fungi* Ramularia collo-cygni*)*; Ms Wendy Delpont, University of Galway *The activity of an* Ascophyllum nodosum *extract enhances thermotolerance in chili peppers*; Dr Juan Francisco Sanchéz-López, Brandon Bioscience *The* Zymoseptoria tritici *effector Zt-11 contributes to aggressiveness in wheat*; Dr Sujit Jung Karki, University College Dublin
12.05 to 2pm	**Group Photo (Steps near Boole Library – follow the instructions from organisers) and Lunch.** **(Poster Viewing or Mas Arte Mas Acción)**
Session II: Plant Stress II – Boole 1 **Chair: Dr Israel Ikoyi**	
14.00 to 14.15	*Advancements in Ash Breeding for Sustainable Forestry: Insights from the Teagasc Research* Dr Dheeraj Singh Rathore, Teagasc
14.15 to 14.30	*Barley's Hidden Protectors: Unravelling the functional attributes and biocontrol potential of fungal endophytes*

	combatting Ramularia collo-cygni (RCC) Dr Seema Dharni, University College Dublin
14.30 to 14.45	*White acacia* (Faidherbia albida) *water-use in an agroforestry parkland in Senegal* Dr Mame Sarr, Maynooth University
14.45 to 15.05	Flash Presentations (5 mins per presenter) *Adapting our forests for climate change - why genetic diversity matters*; Dr Laura Guillardin, Teagasc *Microbial Diversity in Vascular Plant-Dominated Tropical Peatlands – abiotic and biotic environmental drivers of diversity*; Ms Leanne O'Donoghue, University College Cork *Towards enhancing resilience in black alder by identifying potential bio-agents from the core microbiome against* Phytophthora alni*; the causal agent for alder dieback*; Ms Emma Fuller, South East Technological University *AVENA: Understanding cold adaptability traits in oats* (Avena sativa L.)*, a future food / feed crop for East Africa / Ethiopia*; Dr Elena Grosu, Teagasc
15.05 to 15.45	**Tea & Coffee (Poster Viewing or Mas Arte Mas Acción)**
Session III: Evolution & Development – Boole 1 **Chair: Dr James Richardson**	
15.45 to 16.00	*Are we on the cusp of the first mass extinction of plants in Earth history – Leaf traits hold the answer* Mr Harrison O’Rourke, University of Galway
16.00 to 16.15	*Large scale genotyping of North American spruces for the understanding of evolutionary patterns and climate resilience*

	Dr Tomas Byrne, Teagasc
16.15 to 16.30	*Evolutionary Emergence and Conservation of PWWP DOMAIN INTERACTOR OF PLOYMCOMBS (PWO) in Land Plants* Mr Saqlain Haider, University of Galway
16.30 to 16.45	*Evaluating how Perennial Ryegrass responds to a warming climate* Mr Gary Strain, Queen’s University Belfast
16.45 to 17.00	*Enhancing productivity and resilience through understanding genetic diversity in hemp* Ms Nina Trubanova, University College Dublin
17.00 to 17.05	**Flash Presentation** *Phenotypic and Genetic Engineering of Hemp* (Cannabis sativa L.) Ms Grace Lynch, University College Cork
17.10 to 18.00	**General Assembly of IPSAM (All welcome) ; Boole 1**
18.00 - 8 pm	**Evening Reception (Networking and/or Mas Arte Mas Acción)** **Aula Maxima UCC**
	Tuesday 18th June 2024
Session IV: Plant Diversity – Boole 1 **Chair: Mr Joe Croke**	

09.00 to 09.15	*Changes in plant diversity and composition of semi-natural grasslands between the 2007/2012 Irish Semi-natural Grassland Survey and today* Mr Oliver Lynch Milner, University of Galway
09.15 to 09.30	*Seeds for Survival: Establishing the National Seed Bank at the National Botanic Gardens* Dr Darren Reidy, National Botanic Gardens of Ireland
09.30 to 09.45	*Status of herbicide resistance in difficult-to-control grass weeds in Ireland* Dr Vijaya Bhaskar Alwarnaidu Vijayarajan, Teagasc
09.45 to 09.55	Flash Presentation (5 mins per presenter) *Investigating the functional strategies underlying the 'weediness' of grass weeds*; Mr Callum Myers, University College Cork *DigiHerb: A transnational Herbarium Digitisation Project*; Dr Wuu Kuang Soh, National Botanic Gardens of Ireland
09.55 to 10.30	**Tea & Coffee (Poster Viewing or Mas Arte Mas Acción)**
Session V: Applied Plant Science – Boole 1 **Chair: Dr Eoin Lettice**	
10.30 to 10.45	Mucoromycotina 'fine root endophyte' fungi – exploration of their rhizospheric bacteria Dr Grace Hoysted, Maynooth University
10.45 to 11.00	*Developments in high spatial resolution analysis of the rhizosphere using Diffusive Gradients in Thin-Films (DGT)* Dr Paul Williams, Queen's University Belfast

11.00 to 11.15	*Multi-species grasslands improve belowground soil ecological health* Dr Israel Ikoyi, University College Cork
11.15 to 11.30	*Unlocking the Potential of Seaweed Extracts: A Sustainable Solution for Plant Disease Management in a Warming World* Ms Sofia Tretiak, University of Galway
11.30 to 12.05	**Flash Presentations (5 mins per presenter)** *Relationship between community functional traits, biodiversity and ecosystem processes in semi-natural grasslands*; Mr Eoin Halpin, University College Cork *Investigating the Role of Fungicides, Micronutrients and* Zymoseptoria tritici *in Determining Wheat Phyllosphere Microbiome*; Ms Rabisa Zia, Teagasc / University of Galway *Mitigating the risks of Mycotoxin production in Cereal Grain*; Ms Naoise Mc Kenna, The Agri-Food & Biosciences Institute *Exploring the Selection Efficiency of* Alnus glutinosa *Trees using Combined Conventional and Genomics-Assisted methods: Insights from the Irish Gene-Bank and Half-Sibling Progeny Trial*; Jie Huang, Teagasc *A study on the natural variation in the nutritional composition of 100 oat samples;* Nefeli Lampoglou, Teagasc *Cultivation of high-protein plant biomass using an agri-food wastewater for a circular economy;* Miss Jingrou Chen, University College Cork *Elder (*Sambucus nigra*) flowers help find badgers'* Meles meles *setts and help tuberculosis management*, Dr Eoin Lettice, University College Cork
12.05 to 1pm	**Lunch (Poster Viewing or Mas Arte Mas Acción)**

Session VI: Science Communication and Policy – Boole 1

Chair: Dr Rossana Henriques

13.00 to 13.15	*Regulation of New Genomic Techniques in Europe - Implications for Irish Agriculture* Dr Barbara Doyle Prestwich, University College Cork
13.15 to 13.30	*Establishing a baseline of plant blindness in Ireland* Dr Karen Bacon, University of Galway
13.30 to 13.45	*The role of tree collections in tackling plant blindness* Dr Eoin Lettice, University College Cork
13.45 to 13.50	**Flash Presentation** *How to select appropriate indicators, for a multiple performance evaluation, assessing system innovations for on-farm experiments?*; Dr Niamh Power, Munster Technological University
14.00 to 14.30 pm	**Closing ceremony and prize giving** **Dr Barbara Doyle Prestwich**

Abstracts

Plant health diagnostics and science in Ireland

Dr RICHARD O HANLON1

[1]DAFM

The Department of Agriculture, Food and the Marine Ireland is the government body with responsibility for leading on the protection of Irelands plant health. Ireland is generally understood to have one of the highest plant health statuses in Europe, and the country lacks many of the plant pests and pathogens present elsewhere in Europe. Legislation exists that provides important protections for plants, including laying down that surveys must take place, that plants must be free from pests, and that testing must be done to confirm pest absence. Testing of plant commodities is vital to provide evidence that a commodity is safe from a plant health point of view. The plant health laboratories team in DAFM carry out testing and provide technical advice across all of the plant health disciplines. This presentation will provide an update from the lab team over the last number of years, discussing some of the trends and challenges involved. Staff with technical expertise, international networking, and consideration of lab quality assurance are all vital to providing robust plant health science to safeguard Irelands plant health.

The Dark Side of Salt Stress: Shining a Light on Organ Specific Stress Responses During Skotomorphogenesis

Miss. Elizabeth Van Veen[1], Miss Tirza van den Dikkenberg[1], Dr. René Boesten[2], Miss Cornelia Rommens[1], Dr. Scott Hayes[1], Prof. Christa Testerink[1], Dr. Charlotte Gommers[1]

[1]Laboratory of Plant Physiology, Wageningen University & Research,
[2]Laboratory of Genetics, Wageningen University & Research

Seedling establishment is highly sensitive to environmental conditions, with light being a principal cue. When establishing in the dark, a seedling enters skotomorphogenesis. This developmental programme is characterized by rapid elongation of the hypocotyl, and tight folding of the cotyledons into a hook at the shoot apex, which upon light exposure open and become photosynthetic. To date few studies have investigated how abiotic stress affects early seedling development. Here, we address this by documenting the impact of salinity on Arabidopsis skotomorphogenesis. Salinity impaired apical hook formation and maintenance, and this response appeared to be under non-Na+ specific, monovalent ionic regulation. Contrastingly, hypocotyl elongation was reduced under both salinity and iso-osmotic controls. These physiological changes associated with an inability to emerge from a physical sand layer, but hastening of de-etiolation upon light exposure. Through RNA-sequencing of cotyledons, apical hooks, and hypocotyls, we show little overlap in stress induced gene expression between organs. Moreover, within the apical hook we observed altered spatial distribution of the E3 ubiquitin ligase CONSTITUTIVE PHOTOMORPHOGENESIS 1. Finally,

using natural variation we identify a novel role for the Methylerythritol Phosphate pathway in regulating apical hook twisting. Together, our findings shed light on stress responses during early seedling development.

Improved Strawberry Resistance and shelf-life through Genome Editing

Dr Raghu Ram Badmi[1], Dr Barbara Doyle Prestwich[1]

[1]School of Biological Earth and Environmental Sciences, University College Cork

Global production of fruit and vegetables is increasingly threatened by pests and diseases. Currently, pesticides are heavily used for crop protection that have direct biocidal activity, leading to concerns about their environmental and health hazards of pesticide residues in food products. Excessive use of these chemicals has lead to the evolution of pesticide-resistant pathogen strains as in the case of grey mould fungus in strawberry production. Accordingly, there is an urgent need to understand how plants respond to the spreading disease. In this project, strawberries were infected with grey mould causing Botrytis cinerea fungus and the samples were harvested every 3 hours until 36 hours after infection. RNA-sequencing of the samples was performed to study changes in gene expressions and to perform Weighted Gene Co-expression Network Analysis (WGCNA) to identify the 'hub genes' central to strawberry-Botrytis interactions. The identified hub genes can be used as targets for genome editing to develop grey mould disease resistant strawberries. A highly efficient CRISPR-Cas12 genome editing system is established in the group which can be used for genome editing in strawberry. In addition to developing improved strawberry variety, the results of this project have the potential to be translated to other important crop species.

Comparison of droplet digital PCR and quantitative PCR assays for the detection of Fusarium head blight pathogens in oats

Dr Subramani Natarajan[1], Dr Diana Bucur[2], Dr Steven Kildea[2], Prof Fiona Doohan[1]

[1]University College Dublin, [2]Teagasc

Fusarium head blight (FHB) poses significant threats to oat cultivation, often affecting grains without visible symptoms and necessitating advanced detection methods. Droplet digital PCR (dPCR) technology, which replaces qPCR for quantifying nucleic acid targets, directly measures copy numbers and offers greater measurement accuracy by eliminating the need for external standard curves. We adapted existing qPCR assays to the dPCR platform for quantifying trichothecene-producing Fusarium species, including F. langsethiae, F. poae, and F. sporotrichoides, optimizing annealing temperatures and primer/probe concentrations. Our results show that dPCR assays maintain excellent linearity (R2=0.99) across various DNA dilutions and exhibit specificity comparable to qPCR. dPCR demonstrated higher sensitivity and robustness, particularly in detecting low concentrations of target DNA, compared to qPCR. Furthermore, dPCR proved less susceptible to interference from the presence of plant DNA in the samples, enhancing its reliability for accurate quantification of pathogens causing FHB in oats. Field tests on 20 pre-harvest oat grain samples confirmed dPCR's practical applicability, with a strong positive correlation to qPCR estimates. Our study highlights the potential of dPCR as a sensitive and reliable alternative to qPCR for the detection of these Fusarium species in oat grains.

Identifying novel sources of Septoria tritici blotch resistance and susceptibility in wheat using transcriptomic techniques

Mr. Conor Copeland[1], Dr Danilo Sarti[2], Dr Daniel Bellieny-Rabelo[3], Professor Fiona Doohan[1]

[1]Earth Institute, University College Dublin, [2]Hamilton Institute, Maynooth University, [3]Innovative Genomics Institute, University of California

Septoria tritici blotch (STB) is a major fungal pathogen of wheat which is particularly damaging in Northern European conditions. Several resistance genes and quantitative trait loci have been identified, but more are needed to ensure disease resistance to a broad spectrum of STB strains in future varieties and climate conditions. A phenotypic screen of 200 varieties of winter bread wheat from around Europe was used to evaluate varietal resistance to STB. RNA was extracted from wheat cultivars at two timepoints post-fungal inoculation, and a differential expression analysis for 80 of the varieties, relating disease phenotype and transcriptome was performed using DESeq2. Genes including MADS-Box transcription factor TaAGL33 were shown to be upregulated in the most resistant versus the most susceptible varieties. A transcriptome-wide association study (TWAS) was performed using transcriptome, phenotypic and genomic data for 130 of the 200 varieties, leading to the identification of 14 genes which are positively correlated with the STB response, including JAZ transcription factor TaJAZ8-D. The results of this study can inform future breeding strategies, as well as helping to better understand the mechanisms of wheat defence to STB infection, particularly at the early stages.

Seaweed cell wall-derived carbohydrates as a bio elicitor in barley against Ramularia Leaf Spot (caused by the fungi Ramularia collo-cygni)

Miss. Wendy Delpont[1], Dr Zoe A. Popper[1]

[1]University of Galway

Ramularia collo-cygni, the causative agent of Ramularia Leaf Spot (RLS) infects barley (Hordeum vulgare). The results of this infection are ~30% loss in yield and decreased grain quality. Barley, is a cereal grain mainly used for animal fodder, beer production and human consumption. In 2022, around 47 million hectares of barley were cultivated worldwide, with

production reaching almost 155 million tonnes. Europe is the lead producer producing 33.7% of the global production.

Climate change impacts, in combination with recent legislation, have led to increased incidence of many plant pathogens. In the case of RLS there remain no effective biopesticides available. Therefore, there is significant demand for effective environmentally friendly, sustainable measures for its control.
Plant-derived polysaccharides have been reported to stimulate the plant immune system. We investigated the bioactive potential of different seaweed polysaccharides, extracted from a range of different seaweeds, to protect plants against RLS.
To study their elicitation effects, the different seaweed extracts were sprayed on three-week- old barley plants, two days prior to inoculating them with fungi. The effect of the extracts, on the plant and the fungi was monitored and characterized by the quantification of several molecules involved in the plant defence.

The activity of an Ascophyllum nodosum extract enhances thermotolerance in chilli peppers

Dr Juan Francisco Sánchez López[1], Dr Elomofe Ikuyinminu[1], Dr Lukasz Langowski[1], Dr Oscar Goñi[1,2], Dr Shane O'Connell[1,2]

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

Progressing climate change has negative impact on crop production worldwide. High temperatures affect gamete development, fertilization, and fruit development, reducing yield and threatening the production of many crops worldwide.

Ascophyllum nodosum, a brown algae, has been utilized in farming for centuries. Over the last 20 years, Ascophyllum nodosum extracts (ANE) were reported promoting plant growth and tolerance under stresses conditions. Martello, an ANE biostimulant manufactured in Ireland, was previously shown to improve yield in drought and heat stresses .

In our recent work, we conducted a comparative performance analysis of Martello and a commercial Ecklonia maxima extract in long-term heat stress mitigation in flowering chilli pepper plants (cv. Lingua do fuoco). Flowering plants were treated with biostimulants, exposed to stress conditions for two weeks and subsequently moved to optimal conditions for recovery. Martello application enhanced thermotolerance of chilli peppers and improved the recovery of plants more effectively than the Ecklonia extract. Pollen viability and pollen count were also improved when plants were treated with Martello and exposed to stress. Interestingly, only Martello treated plants showed yield increase. Analysis of other stress markers indicate that Martello has a stronger protective activity comparing to compositionally different Ecklonia extracts.

The Zymoseptoria tritici effector Zt-11 contributes to aggressiveness in wheat

Dr Sujit Jung Karki[1], Dr Angela Feechan[1,2]

[1]School of Agriculture and Food Science, University College Dublin, [2]Institute for Life and Earth Sciences, School of Energy, Geosciences, Infrastructure and Society, Heriot-Watt University

Zymoseptoria tritici is an ascomycete fungus and the causal agent of Septoria tritici leaf blotch (STB) in wheat. Z. tritici secretes an array of effector proteins that are likely to facilitate host infection, colonisation and pycnidia production. In this study we demonstrate a role for Zt-11 as a Z. tritici effector during disease progression. Zt-11 is upregulated during the transition of the pathogen from the biotrophic to necrotrophic phase of wheat infection. Deletion of Zt-11 delayed disease development in wheat, reducing the number and size of pycnidia, as well as the number of macropycnidiospores produced by Z. tritici. This delayed disease development by the ΔZt-11 mutants
was accompanied by a lower induction of PR genes in wheat, when compared to infection with wildtype Z. tritici. Overall, these data suggest that Zt-11 plays a role in Z. tritici aggressiveness and STB disease progression possibly via a salicylic acid associated pathway.

Advancements in Ash Breeding for Sustainable Forestry: Insights from the Teagasc Research

Dr Dheeraj Singh Rathore[1], Ms Jie Huang[1], Ms Karuna Shrestha[1]

[1]Teagasc

Ash trees (Fraxinus excelsior) are integral to Ireland's ecosystem, economy, and cultural heritage. However, they are increasingly threatened by ash dieback disease caused by the invasive fungal pathogen; Hymenoscyphus fraxineus. The Teagasc research is focused on breeding ash for dieback disease tolerance to counter this challenge by developing resilient ash trees suitable for future forestation. Previous studies reveal that approximately 1% of the ash population exhibits high tolerance to the pathogen, while up to 10% show moderate tolerance.

In 2015, Teagasc launched an ash-breeding programme aimed to develop tolerant genotypes. Initial trials involved 1000 Irish ash genotypes in Lithuania, followed by further trials in Ireland. Based on preliminary data collected over the last two years, around 15% of the trees are showing higher tolerance to the disease.

Additionally, the AshforFuture project, recently funded by DAFM and DAERA, aims to preserve ash as a species of commercial and biodiversity significance through conducting genetic research, developing markers, disease screening of large ash populations, field assessments, and pathogen analysis. These interdisciplinary efforts underscore Teagasc's commitment to ensuring the survival and sustainability of ash trees in Ireland.

Barley's Hidden Protectors: Unravelling the functional attributes and biocontrol potential of fungal endophytes combatting Ramularia collo-cygni (RCC).

Dr. Seema Dharni[1], Dr Olga Lastovetsky[2], Dr Sujit Jung Karki[1], Junhao Xie[1], Diego Bianchi[3], Dr. Brian Murphy[3], Prof. Trevor Hodkinson[3], Associate Prof. Angela Feechan[1,4]

[1]School of Agriculture and Food Science, University College Dublin, [2]School of Biology & Environmental Science, University College Dublin, [3]Department of Botany, Trinity College Dublin, [4]Institute of Life and Earth Science, School of Energy, Geosciences, Infrastructure and Society, Heriot-Watt University

Barley is the most important cereal crop in Ireland. Ramularia leaf spot (RLS) is one of the major devasting diseases in barley caused by the fungal pathogen Ramularia collo-cygni (RCC). Biocontrol agents have attracted attention as a sustainable alternative to fungicides, offering an eco-friendly option. From 137 fungal endophytic isolates from barley, two (EF2 and EF3) exhibited various functional attributes specifically phosphate solubilization, IAA, siderophore, and hydrolytic enzyme production. Further, EF2 and EF3 showed significant antagonistic effects in vitro by supressing fungal development of RCC in direct confrontation. These finding were later confirmed through microscopic analysis, which showed hyphal distortion of RCC compared to mock. Additionally, the study analysed the cell free culture filtrate of the EF3 which inhibits the growth of RCC in vitro. A metabolomics approach was executed to acquire an understanding of the secondary metabolic profile of EF3 and the antifungal activity. The results indicate that EF3 could be a potential biofertilizer and biocontrol agent in barley.

White acacia (Faidherbia albida) water-use in an agroforestry parkland in Senegal

Dr Mame Sarr, Dr John Devaney

[1]Maynooth University

In dryland areas, water-use is a key metric of productivity and sustainability, particularly in rain fed agricultural systems. Understanding ecosystem water balance is crucial in the context of climate change. White acacia Faidherbia albida is recognized as a promising agroforestry species and is widely used in landscape restoration in Africa. However, little is known about white acacia water uptake. We used sap flow measurement to monitor white acacia seasonal WU in an agroforestry parkland observatory in Senegal. Results revealed a significant WU variability between rainy and dry seasons and leaf phenological phase. Maximal values were observed in December and January with large between-tree variability from 100 to 250 L kgH2O tree-1d-1. WU decreased during the dry season and reached minimal values during the defoliated phase (rainy season, which prevents competition for

water with crops). Annual water consumption in 2019/2020 was estimated on average about 40,000 l/tree, i.e 27 mm according to the density of 6.8 trees ha-1, which represents only 5.3 % of 2019 annual rainfall (513 mm). This study revealed that white acacia water use represents a small fraction of water balance. This increased understanding of species-specific water-use strategies can enhance agroforestry management and landscape restoration in dryland areas.

Adapting our forests for climate change - why genetic diversity matters

Dr Laura Guillardin[1], Dr Niall Farrelly[1]

[1]Teagasc Forestry Development Department

Genetic diversity is the raw material and main mechanism trees have in which to adapt and evolve in response to climate change. Changes in local climate can result in negative consequences for natural forests and planted woodlands, therefore, understanding the genetic composition of the forest is important to developing conservation, restoration and management strategies. By using molecular tools to study trees' DNA, we can estimate how diverse forests are and their potential to tackle environmental challenges. It is possible to increase the genetic diversity of forests by planting trees from target populations that can be added to forests where necessary. The transfer of trees acclimatised to growing in specific climate conditions is becoming a popular method (assisted migration) to enhance other areas' genetic diversity. For example, targeting populations from southerly locations allows foresters to transfer trees adapted to growing in warmer conditions to northerly locations which are warming, thus future-proofing the forest. This knowledge will be a key strategy to support sustainable forest management plans and ensure high levels of genetic diversity are present in our forests which ensure the resilience of forests over the long term.

Microbial Diversity in Vascular Plant-Dominated Tropical Peatlands – abiotic and biotic environmental drivers of diversity

Miss. Leanne O'Donoghue[1]

[1]University College Cork

Peatlands occupy 3% of the global land area but contain ~600 gigatonnes of carbon. While most peatlands are located north of 45°N, the largest concentration of carbon is stored in tropical peatlands. Peatlands store carbon when the additional of organic matter from plants exceeds loss under waterlogged and anoxic conditions. Unlike bryophyte-dominated peatlands common in temperate and boreal regions, tropical peatlands differ in terms of their plant ecology, hydrology, nutrient availability, and climate. As vascular plants are a common feature on many tropical peatlands, where lignin forms an important fraction of the peat, understanding plant and microbial diversity along hydrological gradients can help bridge knowledge gaps in these understudied systems. The overarching goal of the HUMID project is to increase our scientific understanding of the contemporary microbial diversity across different plant ecotones within two tropical peatlands from the South Pacific region (Fiji and Wallis et Futuna) and identify the dominant environmental (biotic and abiotic) controls that drive changes in microbial community structure.

Towards enhancing resilience in black alder by identifying potential bio-agents from the core microbiome against Phytophthora alni; the causal agent for alder dieback

Ms. Emma Fuller[1,2], Kieran Germaine[1], Dheeraj Singh Rathore[2]

[1]South East Technological University, Kilkenny Road, Carlow, [2]Teagasc, Forestry Development Department, Oak Park, Carlow, R96XE12, Ireland

Black Alder (Alnus glutinosa) holds significant ecological importance, especially in wetlands where it enriches biodiversity through its soil nutrient enrichment and colonization capabilities. However, the emergence of the root-rot pathogen, Phytophthora alni, poses a threat to alder populations causing symptoms like crown thinning, bleeding trunk cankers, as well as tree mortality. The disease has been recently detected in Northern Ireland with the potential to spread country-wide. Given its significant value, the decline of alder could result in substantial economic and ecological losses.

Trees exists in close relation with diverse microbial communities (referred as microbiome), which have the ability to influence tree growth and tolerance to a/biotic factors. Previous research shows that specific microbes can positively impact tree development. Understanding these relationships could help protect trees from diseases like alder dieback by inoculating trees with beneficial microbes. Therefore, current research aims to enhance the resilience in alder trees by exploiting potential bio-agents against dieback disease. The key objectives include:

1. Studying the core microbiome of alder trees in Ireland.
2. Isolation of culturable microbes to study antagonistic activity against Phytophthora alni.
3. Evaluation of potential bio-agents to enhance disease tolerance in susceptible alder genotypes.

AVENA: Understanding cold adaptability traits in oats (Avena sativa L.), a future food / feed crop for East Africa / Ethiopia

Dr Elena Grosu[1], Dr Abel Teshome Gari[2], Dr Mesfin Dejene[3], Dr Stephen Byrne[1], Dr Chris Jones[2], Dr Atikur Rahman[1], Dr Susanne Barth[1]

[1]Teagasc Crop Science Department, Crops Environment and Land Use Programme, [2]Feed and Forage Development, International Livestock Research Institute, [3]Feeds and Nutrition Research Program, Ethiopian Institute of Agricultural Research, Holetta Research Center, POBOX 2003

Recent statistics (FAO, 2023) highlight that East Africa is on the verge of a food catastrophe. Agriculture could contribute to solving the food insecurity issue by cultivating high-nutritional crops suitable to the region's highlands. Ethiopia cultivates oat (Avena sativa L.) for human and animal consumption. Nevertheless, during the flowering stage, a period of cold nights (~4°C) impacts grain production limiting oats' usage for human consumption. In this context, the AVENA project aims to identify cold resilient oat varieties and assess what genetic mechanisms contribute to cold tolerance. So far, 169 genotypes were evaluated for their performance to withstand cold stress at three locations in Ethiopia. A Min-Max normalisation and score ranking on parameters linked to biomass production identified high and low performing genotypes. Moreover, genotyping by sequencing identified over 55,000 SNPs and a Bitwise Distance dendrogram grouped the 169 genotypes into two main clusters. The next steps include identifying molecular mechanisms that contribute to cold resilience (4°C night) through transcriptomic analysis of two top performers (5450 and 1513), one standard variety (1506), and a low performer (1842) over 21 days during flowering. The identified traits could be targeted to breed cold resilient lines, contributing to the self-sustainability of Eastern Africa.

Are we on the cusp of the first mass extinction of plants in Earth history – Leaf traits hold the answer.

Mr. Harrison O'rourke[1,2], Dr Karen Bacon[1], Dr Eimear Nic Lughadha[2]

[1]University Of Galway, [2]Royal Botanic Gardens, Kew

It is widely believed that a sixth mass extinction event is imminent; however, this may be the first time that plants, particularly angiosperms, experience a mass extinction event. It is thought that plants do not experience mass extinction on the same scale as animals, due to the lack of evidence across plant mass extinction boundaries. However, plant groups at greatest risk of extinction may not be preserved in the fossil record, thereby biasing our view of plant extinction. By improving our understanding of plant preservation in the fossil record and how leaf traits may be associated with preservation potential and extinction risk, we can ascertain whether we are witnessing the beginning of a unique mass extinction in the plant kingdom. This outcome can be achieved by studying; the correlation between leaf traits and extinction risk in modern floras; the preservation potential of leaf traits in the fossil record; and comparing leaf traits seen in modern floras with those preserved in the

fossil record. We have assessed 3,745 specimens from Spitsbergen for leaf trait preservation and taphonomic completeness; assessed the impact of decay on leaf traits in decomposition experiments and related leaf traits to extinction risk in modern floras.

Large scale genotyping of North American spruces for the understanding of evolutionary patterns and climate resilience

Dr Tomas Byrne[1], Dr Stephen Byrne[2], Dr Niall Farrelly[4], Dr Colin Kelleher[5], Prof Trevor Hodkinson[3], Dr Susanne Barth[2]

[1]Teagasc Forestry Development Department, [2]Teagasc Crop Science Department, [3]Trinity College Dublin, School of Botany, [4]Teagasc Forestry Development Department, [5]National Botanic Gardens

Spruce has a large commercial importance in Europe and high conservation value in North America. Picea sitchensis (Sitka spruce) is native to the Pacific North West where it stretches from Coastal Alaska to Costal California. It shares this location with other spruces where it can hybridise freely in some areas. The unique range that it occupies allows for a wide range of adaptations to its environment. In this study, Genotyping-by-sequencing (GBS) was used to characterise a population of Sitka spruce collected from the native range and grown in the same environment. This unique provenance trial allowed the expression of traits.
A large amount of genetic data was obtained and processed showing interesting evolutionary patterns. Post glacial recolonization was traced from several islands in the Pacific North West. Like most conifers there was a high degree of gene flow between populations but there were markers distinct to each region. The GBS data also allowed for the investigation of traits based off canonical correlation analysis. This data can inform the selection of breeding ranges for Sitka spruce and also be used to identify and conserve unique traits and genotypes.

Evolutionary Emergence and Conservation of PWWP DOMAIN INTERACTOR OF PLOYMCOMBS (PWO) in Land Plants

Mr. Saqlain Haider[1], Dr Ahamed Khan[2,3], Dr Iva Mozgova[3], Dr Sara Farrona[1]

[1]University of Galway, [2]Institute of Biology Freie Universität, [3]Biology Centre of the Czech Academy of Sciences, Institute of Plant Molecular Biology

Epigenetic modifications regulate chromatin structure and subsequently pattern of gene transcription, thus ensure developmental plasticity by acting at an interphase between environment and plant genome. In Arabidopsis, PWWP DOMAIN INTERACTOR OF POLYCOMBS (PWO) (PWO1, PWO2, PWO3) are chromatin associated proteins that recognize histone 3 (H3) and interact with catalytic subunit of POLYCOMB REPRESSIVE COMPLEX 2 (PRC2), which belong to the POLYCOMB GROUP (PcG) proteins. Previously, PWO1 was shown to regulate Arabidopsis flowering time and nucleus morphology. Recently, our lab (and others) has shown that PWOs are part of a large complex of proteins

(PEAT-complex) whereby they play roles in transcriptional de-repression. Phylogenetic analyses show that PWOs emerged during the colonization of land by vascular plants (i.e. Selaginella moellendorffii) while they are absent in lower plants such as bryophytes or algae. Here, I will present my recent work on the developmental role of ancestral Selaginella PWOs (SmPWOa and SmPWOb) in plant development. Strikingly, my data indicate that Arabidopsis SmPWOa/b transgenic lines can partially complement nearly all developmental defects observed in pwo1-1;pwo2-2 double mutants indicating a at least partial conservation of PWOs molecular functions throughout the evolution of land plants.

Evaluating how Perennial Ryegrass responds to a warming climate.

Mr. Gary Strain[1,2], Dr. Gillian Young[3], Dr. Lisa Black[2], Prof. Trevor J. Gilliland[1,2], Dr. Adam Gauley[2]

[1]Queen's University Belfast, [2]Agri Food and Biosciences Institute, [3]Agri Food and Biosciences Institute

Most land use in Ireland is dedicated to the production of perennial ryegrass (Lolium perenne) Crop usability is dictated by heading date, after flowering, ryegrass becomes unpalatable to cattle and undesirable for silage. Using historic data, we show that heading date has been getting gradually earlier as the climate warms. Before heading, plants must go through a period of vernalization to enter reproductive growth. It has been widely accepted that this process takes eight weeks below-10oC, under short day conditions. The vernalization requirement of early, intermediate, and late flowering cultivars were examined across both natural and controlled conditions. Preliminary results show that there is a variance in vernalization requirement, with some cultivars commencing reproductive growth after as short as a four-week vernalization period, while others remained vegetative up to the end of the more widely accepted 8 weeks, splitting cultivars into groups of weak and strong vernalization types. Preliminary RNA-sequencing results have shown key Vernalisation and flowering genes are behaving differently on a varietal basis. As conditions suitable for vernalization are predicted to become shorter due to climate change a greater understanding on the mechanisms underpinning these processes will help grass breeders to create cultivars better equipped for future conditions.

Enhancing productivity and resilience through understanding genetic diversity in hemp

Ms. Nina Trubanova[1], Dr Sachiko Isobe[2], Dr Kenta Shirasawa[2], Dr Akiko Watanabe[2], Mr Georgios Kelesidis[1,3], Dr Rainer Melzer[1], Dr Susanne Schilling[1]

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The high-value multipurpose crop hemp (Cannabis sativa), known for its genetic heterogeneity and variability in phenotypic traits, offers potential for creating productive, sustainable, and resilient agricultural systems. However, its intravarietal variability remains inadequately elucidated.

We employed a population derived from a single plant to extensively explore variability in plant growth, development, and reproductive patterns. Furthermore, we found statistically significant single nucleotide variants and haplotypes associated with traits of interest identified through the innovative implementation of a genome-specific association study (GSAS) framework. The GSAS methodology consolidates a streamlined generation of an S1 population, selection of alleles heterozygous in the parent plant, and the application of a model conducive to the polygenic association of studied traits. The GSAS approach emerges as a pivotal tool for advancing our comprehension of the genetic determination of intravarietal phenotypic variability in hemp. Furthermore, these insights are transferable to other genetically diverse crops, enriching the broader field of crop genetics and breeding.

Findings of prospective GSA studies hold the potential to be harnessed in marker-assisted breeding, yielding new cultivars with enhanced uniformity and improved performance in traits relevant to various applications, ranging from pharmaceuticals to the manufacturing of materials with superb properties, such as hempcrete or bioplastics.

Phenotypic and Genetic Engineering of Hemp (Cannabis sativa L.)

Ms. Grace Lynch[1], Dr. Barbara Doyle Prestwich

[1]University College Cork

Hemp (Cannabis sativa L.) is a versatile, sustainable crop with diverse agro-industrial and therapeutic uses. Phenotypic engineering involves using environmental modifications to induce desirable traits, such as increased biomass or bioactive compound yields. Genetic engineering can achieve this through genome modification. Herein, both approaches were explored. The effects of different spectral compositions of LEDs on the growth of mature hemp were investigated in a glasshouse pot experiment and also on hemp microgreens. In mature Kompolti, light recipes utilising red-to-blue ratios LED1 and LED2 enhanced floral biomass compared to high-pressure sodium lamps by 245% and 417%, respectively. LED2 also increased height, stem diameter, stem biomass, leaf biomass, and leaf thickness. Of the three hemp microgreen varieties tested, LED1 substantially increased leaf area and biomass. FT-Raman spectroscopy was explored to investigate inflorescence leaf phytochemicals. The amenability of Earlina 8FC to Agrobacterium-mediated transformation was confirmed using the β-glucuronidase histochemical assay. The protocol utilised here could provide a worthwhile avenue for developing efficient transformation platforms for hemp. This study suggests that specific LEDs can significantly alter the growth and architecture of the hemp crop, from microgreens to maturity. The substantial yield increases found here could economically benefit farmers in the indoor hemp cultivation industry.

Changes in plant diversity and composition of semi-natural grasslands between the 2007/2012 Irish Semi-natural Grassland Survey and today.

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Semi-natural grasslands have experienced dramatic declines in their area and species diversity since the mid-1900s in the UK and Europe. This study, using the 2007-2012 Irish Semi-Natural Grassland Survey (ISGS), aims to assess whether the plant diversity of Irish semi-natural grasslands has also changed. Twelve sites of three habitat types (GS1 – Dry calcareous & neutral grasslands; GS3 – Dry-humid acid grasslands, and GS4 – Wet grassland) were re-surveyed in 2023. Diversity was defined using diversity indices (e.g. Species Richness, Simpson's Diversity, and Simpson's Evenness) and differences in composition was assessed through ordination. No significant differences were found between the species richness or other diversity measures for the study sites between the ISGS and the 2023 surveys. However, a clear shift in species composition occurred between the two surveys in most sites. This compositional difference was significant when analysed at the plot level but not at site level. Further investigation into the species composition is needed to understand the impact of these compositional alterations better.

Seeds for Survival: Establishing the National Seed Bank at the National Botanic Gardens

Dr Darren Reidy[1]

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In a time of global ecological crisis botanic gardens and herbaria are responding by adapting their collections to also ensure the ex situ conservation of the global flora. Seed banks are an efficient method of ex situ plant conservation, capable of conserving genetic diversity of flora should it be lost in the wild. Establishing the National Seed Bank at the National Botanic Gardens to ensure the long term survival of Ireland's threatened flora has become a key target in the recently published National Biodiversity Action Plan (2023-2030). We developed a seed collection strategy and viable workflow which meets the standards required by the Millennium Seedbank Partnership. Seeds are collected using ENSCONET protocols, are dried at 15°C to 15% relative humidity and frozen at -20°C to maximise their viability over time. To date the seed bank has preserved seeds from over 100 populations of 90 taxa of vascular plant, contributing to the ex situ conservation of populations of a

number of rare & threatened flora in Ireland. The seed bank will serve as a resource for seed based restoration of the most vulnerable of Irish flora into the future.

Status of herbicide resistance in difficult-to-control grass weeds in Ireland

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Wild oats (Avena fatua), black-grass (Alopecurus myosuroides) and Italian ryegrass (Lolium multiflorum) rank among the top-fifteen problem weeds worldwide from a resistance perspective. In Ireland, populations of these species are increasing, aided by our mild damp weather, changes in cropping patterns and farming systems, new weed introductions, and climate change. Growers exclusively rely on limited ACCase/ALS-inhibitor herbicides for control, and their repeated use risks promoting target-site and/or non-target-site resistance. As part of the ECT and EVOLVE grass-weed research projects, resistance (phenotypic/molecular)-testing was conducted on resistance-suspect populations submitted by growers/advisors, or collected through surveys, from 2019-to-2023. The findings indicated:

- 30% (n=142) of A. fatua were ACCase-resistant mostly due to Ile-1781 and/or Asp-2078 mutations.
- 63% (n =46) of A. myosuroides were ACCase- and/or ALS-resistant. ACCase Ile-1781 or ALS Pro-197 and/or Trp-574 mutations dominate.
- 75% (n =36) of L. multiflorum, were ALS-resistant and associated mostly with Pro-197 and/or Trp-574. 60% of these populations were also ACCase-resistant, associated with target-site (Ile-1781 and/or Asp-2078) or metabolism-based non-target-site resistance.

The sector faces a significant threat from multiple-resistant A. myosuroides and L. multiflorum, which were virtually unknown in Irish crops a decade-ago. Continuous monitoring, a zero-tolerance approach and integrated weed management are all crucial.

Investigating the functional strategies underlying the ‘weediness’ of grass weeds

Mr. Callum Myers[1], Prof. Astrid Wingler[1], Dr. Vijaya Bhaskar[2]

[1]UCC, [2]Teagasc

Weeds are, if left unmanaged, the most serious problem faced by farmers around the globe, causing higher crop losses than pests and pathogens. The grass weed Avena fatua (wild common oat) is closely related to Avena sativa (oat) and reduces crop yields of, e.g. wheat and barley, through competition.

Our work intends to characterize the traits that lead to the weediness in A. fatua. Through experiments documenting functional traits and strategies we are comparing populations of A. fatua from around Irish farms, predominantly tillage based.
Early findings indicate minimal differences in traits such as leaf area, dry matter content, and specific leaf area among various populations. Ongoing experiments aim to further investigate traits of A. fatua and elucidate strategies based on the competitive-stress tolerant-ruderal (CSR) system. Moreover, comparisons are being made between A. fatua and species of tillage crops including wheat (Triticum aestivum), barley (Hordeum vulgare), oat, and other significant grass weeds, using data from the TRY database. Initial results suggest that A. fatua exhibits higher specific leaf area than the other species.
Our future research strives to answer questions related to the functional strategies that lead to elevated weediness in A. fatua and its performance under environmental stress.

DigiHerb: A transnational Herbarium Digitisation Project

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Digital herbarium collections are crucial for biodiversity research, benefiting both science and society. However, smaller herbaria struggle to disseminate collection data due to limited resources, as larger herbaria dominate in cataloguing and digitising efforts. An ambitious herbarium digitisation project, named DigiHerb, was approved for funding by the Interreg North-West Europe (NWE) Programme (2024-2025). The project will improve uptake of digitisation technology and capabilities, and access to botanical records in small herbaria by establishing a shared digitisation hub and a unified digital portal. This will facilitate more equitable access to digitisation for regional herbaria and will act as a pilot project for future programmes. The National Botanic Gardens of Ireland is spearheading this initiative in partnership with The State Museum of Natural History Karlsruhe and Ghent University. The project will receive a €478,776 grant over an 18-month period through co-funding from the EU. In Ireland, the project will result in the digitisation and transcription for approximately 100,000 sheets of Irish specimens. Digitised specimens from the three collaborating partners will be made accessible to the public via a shared online platform. This project marks the first instance in the EU where transnational herbarium collections are consolidated under a unified digital portal.

Mucoromycotina ‘fine root endophyte’ fungi – exploration of their rhizospheric bacteria.

Dr Robert Leigh[1], Ms Katie Connolly[2], Mr Luke Daly[2], Dr Sonia Negrao[2], Dr Grace Hoysted[3]

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Fungi have engaged in intimate symbioses with plants for >500 million years and bacterial associations are being increasingly appreciated for shaping phenotypes, function and ecology of plant-fungal interactions in diverse settings. Recently, it was demonstrated that fungal partners of plant roots, known as mycorrhizal fungi, are more diverse than previously thought and include ‘fine root endophytes’ of the Mucoromycotina (MFRE). MFRE usually occur in plants co-colonised by Glomeromycota arbuscular mycorrhizal fungi (AMF). Like AMF, MFRE host symbiotic bacteria and the latest research, using novel monoxenic cultures and wild-collected plants and fungi, has shown MFRE associations also confer nutritional benefits on host plants. However, the role of the soil bacterial community in MFRE colonisation and function remains unexplored. Using novel techniques developed for MFRE fungal isolation and culture, we plan to manipulate MFRE singly and in combination with AMF and their associated bacterial communities to provide evidence of how different fungi communicate and interact in diverse ecosystems. This research will have implications for microbial soil ecology, from controlled to field conditions, especially if diverse bacteria allow fungi to engage in unexpected partnerships and unlock their potential as bioenhancers of globally important crops.

Developments in high spatial resolution analysis of the rhizosphere using Diffusive Gradients in Thin-Films (DGT)

Dr Paul Williams[1]

[1]QUB

Laser ablation (LA) remains one of the most challenging, yet potentially rewarding applications for ICP-based environmental metrology. The attributes of DGT lend themself very well, for imaging and semi-quant/fully quantitative and multi-calibrant approaches via LA-ICP-MS. Thus, there has been a steady development over the past ca. 20 years in all aspects of chemical imaging with DGT and LA, especially for studies in sediment, soils and rhizospheres. This encompasses developments in the DGT configurations for high-resolution ion mapping, in particular the use of new/emerging functionalised mesoporous silica based binding layers. These materials offer new opportunities for not just bulk elemental capture but provide selective measurement opportunities for speciation analysis too. Next, improvements to the latest laser systems, especially, in visualisation and control, not only provide for a smoother/faster operator experience but are enabling access to even higher resolution (sub-100 µm) perspectives. Combined with ICP-QQQ-MS now rapidly becoming the sector standard, with greater mode/set-up options to overcome interferences and improved limits of detection, and exciting new couplings with other systems such as LIBs and LA-REIMS, these platforms are progressing the state-of-the-art. This presentation will explore how these new technical developments can be used to enhance understanding of the soil-root continuum.

Multi-species grasslands improve belowground soil ecological health

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Plant-soil-biota interactions underpin agricultural productivity and modulate essential ecosystem functions. However, in intensively managed grasslands it remains unclear how sward diversity impacts belowground communities driving these processes. We investigated how plant species diversity affected the soil nematode community and associated indices. Nematodes were extracted and identified from 61 experimental field plots in which plant species diversity was systematically manipulated from a pool of six plant species from three functional groups (FGs; grasses, legumes, herbs). Strong effects of plant species identity on the nematode community were observed; interspecific interaction effects did not occur consistently. The six-species plant community had a significantly higher nematode diversity, maturity index (MI), structure index (SI) and proportion of sensitive taxa but a lower enrichment index (EI) than the individual monocultures. The community structure of nematodes in the six-species community was significantly different from that in the monocultures, and was associated with higher biomass yield and total nitrogen in harvested biomass, and lower biomass of weed species. Overall, our results show that multi-species forage sward mixtures can have a positive effect on the soil nematode community and associated indices. This is of practical relevance for farmers and EU policies on soil health and farming for biodiversity benefits.

Unlocking the Potential of Seaweed Extracts: A Sustainable Solution for Plant Disease Management in a Warming World

Miss. Sofiia Tretiak[1], Dr Zoe Popper[1]

[1]University of Galway

Plant disease management presents a challenge to farming since the synthetic chemicals used to combat plant diseases are harmful to humans and the environment. Seaweeds offer a sustainable source of polysaccharides with various beneficial properties, but the lack of research on their efficacy as biostimulants for plant protection limits their agricultural application. We conducted detailed research to test the potential of polysaccharide extracts obtained from the brown seaweed Ascophyllum nodosum to stimulate the immune system of Arabidopsis thaliana. Arabidopsis grown under normal (N) conditions (21°C, 70% humidity, 12/12 light /dark cycle) were sprayed with the extracts and left to grow (control plants) or subjected to either heat stress (H) or inoculated with the fungus Rhizopus stolonifer (F). Several parameters including photosynthetic efficiency, and generation of Reactive Oxygen Species (ROS), one of the early stress signals, were measured over 7 days.

Our study suggests that the seaweed extracts improved the plants' ability to cope with heat stress and could therefore be of potential agricultural or horticultural value in the context of global climate change.

Relationship between community functional traits, biodiversity and ecosystem processes in semi-natural grasslands

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The aim of this research project is to investigate the diversity of functional traits and strategies in Irish semi-natural grassland communities and how these strategies influence greater ecosystem processes such as net primary productivity and yield stability. Grasslands are highly dynamic ecosystems, and their ecosystem services are greatly influenced by environmental perturbations. We hypothesise that functional traits and functional diversity underlie grassland functioning and ecosystem processes. Plant functional traits were analysed using a combination of field collected samples and analysis of database values. The diversity of plant traits and strategies was analysed using both emergent and well-established functional diversity metrics which are then compared against soil measurements as indicators of environmental conditions and ecosystem processes. The results thus far suggest relationships between some functional diversity metrics and carbon content in the soil. For example, relevés with higher soil organic matter had communities with more divergent functional traits (high functional dispersion and Rao's quadratic entropy). These relationships also appear to be stronger than those with species diversity. This puts forth a case for the use of functional diversity in understanding ecosystem processes.

Investigating the Role of Fungicides, Micronutrients and Zymoseptoria tritici in Determining Wheat Phyllosphere Microbiome

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In field trials in 2014-2017 the micronutirents boron and sulphur provided moderate levels of septoria tritici blotch control when applied alone. However, the impact of these micronutrients on wheat microbiome was unknown. In this study, we analysed the

microbiome of wheat-Zymoseptoria tritici pathosystem, following treatment with boron and sulphur, and in combination with an azole/SDHI fungicide. The field trials were conducted at three Irish locations, namely Carlow, Cork and Meath, and fungal and bacterial populations of the upper leaf layer were subsequently sequenced. Our results showed no variation in wheat phyllosphere microbiome following foliar application of boron or sulphur, but highlighted the role of fungicides in deriving the fungal diversity. We did not observe any impacts on the bacterial populations present. Fungal population was undisturbed by Zymoseptoria tritici levels in the samples. However, the data requires a deep understanding of the interactions of bacterial and fungal populations. Exploration of co-occurrence networks will be an ideal strategy to analyse the complex community dynamics of wheat-Zymoseptoria tritici pathosystem.

Mitigating the risks of Mycotoxin production in Cereal Grain

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Mycotoxin contamination of food crops remains a global issue with studies showing 20-25% of samples exceeding the regulatory guideline set by the EU commission and Codex standards. Climate change and agronomic factors influence the severity of Fusarium infection and mycotoxin production in crops, making it imperative to understand the underlying mechanisms to improve food security. This study focuses on the threat posed by mycotoxins, T-2 and HT-2, produced by Fusarium fungi in oat crops (Avena sativa). A combination of analytical methods such as quantitative-PCR and Liquid Chromatography Triple Quadrupole Mass Spectrometry are being deployed for fungal and mycotoxin detection in field and greenhouse inoculation trials to investigate the impact of agricultural chemicals on mycotoxin production. Preliminary results indicate that existing fungicides have little impact on reducing the impact of Fusarium mediated mycotoxins accumulation and may increase their severity. Plant growth regulator application may result in increased mycotoxin levels in cereal grain. RNA sequencing will be used to improve our understanding of genes associated with oat plants’ response to Fusarium infection and mycotoxin contamination. Project outcomes will inform breeding efforts for Fusarium-resistant crops and provide insights into crop management for reduced mycotoxins in Irish grains.

Exploring the Selection Efficiency of Alnus glutinosa Trees using Combined Conventional and Genomics-Assisted methods: Insights from the Irish Gene-Bank and Half-Sibling Progeny Trial

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Studying and understanding the evolution of populations and key economic traits is critical for tree improvement, conservation, and sustainable afforestation. Alder (Alnus glutinosa (L.) Gaertn.) is a native pioneer tree species commonly found throughout Europe and is increasingly threatened by the pathogen Phytophthora. An alder gene-bank consisting of plus trees, selected for stem straightness and overall growth from across Ireland, and a trial comprising of half-sibling progenies from these plus trees, have been established for alder improvement. Genetic diversity of 103 selected alder trees from the gene bank was assessed using 59,677 SNP markers identified using Genotyping-By-Sequencing (GBS). We observed a similar heterozygosity level and little population structure among all assessed populations, indicating the origins of selected trees from highly admixed populations. Moreover, heritability of height and diameter-at-breast-height (DBH) at different years of growth were examined from a half-sib progeny trial. Both height and DBH at early years exhibited higher phenotypic coefficient of variation and broad-sense heritability. The results suggest successful selection of improved alder materials in our gene bank and half-sib progeny trial using conventional and genomics-assisted improvement methods. Furthermore, the breeding cycle for alder could be shortened by utilizing early-year growth data as predictor of overall growth potential.

A STUDY ON THE NATURAL VARIATION IN THE NUTRITIONAL COMPOSITION OF 100 OAT SAMPLES

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Oats are linked to numerous health claims, including lowering of blood cholesterol and postprandial glucose levels. However, in order to meet the daily intake targets,

unrealistically high amounts of oat would need to be consumed daily. While it is known that the nutritional composition of oats can vary widely among the different varieties, this is largely underexplored in the current yield-driven market. The objective of this study was to conduct a nutritional analysis to investigate the extent of the inter-varietal differences. Ninety-eight varieties grown in Ireland under different conditions, along with one commercial and one reference sample, were analysed for moisture, ash, fat, protein, beta-glucan, total starch and fibre. Compositional analyses revealed high variations; specifically, protein (11.3 to 22.9% based on dry matter), fat (2.5 to 10.0% based on dry matter), and beta-glucan (2.8 to 6.7% based on dry matter) contents showed great variability. To put things into perspective, Husky, the most commonly grown oat variety in Ireland, showed average composition. Future work involves studying the release patterns of the main nutritional components using in vitro digestion. Further research on the available oat varieties, along with their agronomical characteristics, can aid in bridging the gap between breeders, producers and consumers.

Cultivation of high-protein plant biomass using an agri-food wastewater for a circular economy

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The water fern, Azolla filiculoides (Azolla), is a small, floating, aquatic plant that can exhibit rapid growth even on wastewater with a high crude-protein content (25-30%). The incorporation of Azolla into a wastewater management scheme could support wastewater valorisation and promote a closed plant-nutrient cycle. Within the laboratory, preliminary investigations were performed to cultivate Azolla on wastewater sourced from a large commercial meat processor. Azolla was grown on various concentrations of wastewater (Control, 5%, 25%, 50%, 100%), three pH levels (pH 5, 6, 7.8), and different treatments (daily pH adjustment vs. adjustment on the initial day only) for seven days. The relative growth rate of Azolla tended to be similarly high across all concentrations, while pH of 5 and 6 displayed similar growth compared to Azolla grown on the unadjusted pH (pH 7.8). The data demonstrated that when 100% of wastewater with pH6 without daily pH adjustment, the highest removal rate of phosphorus and nitrogen reached 91.6% and 26.4%, respectively. These results indicate that abattoir processing wastewater can be a suitable cultivation medium for Azolla. The results of the study underpin the promising development of Azolla phytoremediation and high-protein biomass production in agri-food wastewater treatment.

Elder (Sambucus nigra) flowers help find badgers' Meles meles setts and help tuberculosis management.

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Badgers on intensive cattle farms cause a major problem as bovine tuberculosis spills over to the cattle from badgers. This spill over can occur anywhere but most commonly occurs at the badgers' setts (burrows). Most setts occur in field boundaries making them accessible for cattle which facilitates the spill-over. Culling badgers was a very difficult and unpopular solution. The culling is being replaced by vaccinating the badgers with BCG and/or fencing off the badgers' setts from cattle. This requires the setts to be located. Such setts are one of the most distinct signs of any wild mammal. They can however be missed during surveys as they are often overgrown especially by blackberries (Rubus spp) and elder (Sambucus nigra). Badgers eat both blackberries and elder fruits, and improve germination in the former, and probably the latter, to judge from how frequently elder occurs at the setts. These can be especially obvious when elder flowers in late May to mid-June. Little Island in Waterford has one of the highest densities of badgers anywhere. We identified 2,485 flowering elder at setts and badgers' territorial boundaries on the island. We found they showed strong potential for locating setts, but not territory boundaries.

Regulation of New Genomic Techniques in Europe - Implications for Irish Agriculture

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New Genomic Techniques (NGTs) constitute a suite of tools that allow for more precise modification of plant genomes than was hitherto thought possible. Their regulation in Europe, however, is still a matter of debate, notwithstanding the recent vote of the EU Parliament to relax the rules on regulation. Currently, the EU regulations governing the use of NGTs predates the discovery of many of the techniques involved. It is now timely to re-visit the legislation in Europe and to develop what many call 'proportionate regulation' to allow for the development of crops which are tolerant of, or resistant to, various biotic and abiotic stresses. Many other countries outside of the EU have already done this and are reaping the economic rewards of innovation in this space. This paper will examine the current situation in Europe and other continents, and the implications for the development of climate-resilient crops which can contribute to economic and environmental sustainability alongside food security. This may give farmers the opportunity to lower on-farm inputs whilst simultaneously meeting many of the demands set out under the European Green Deal.

Keywords: New Genomic Techniques (NGTs), Climate-resilient crops,

Establishing a baseline of plant blindness in Ireland

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Plant blindness - the tendency to consign plants to background and not to pay them much attention - is a known phenomenon and impacts on how people in general perceive plants. This further impacts on conservation, teaching and research. However, the baseline of how well people can identify plants is not well developed or studied. We have tested the basic plant identification skills of a selection of students in the UK and Ireland to determine if they can identify a suite of common plants. Preliminary findings have identified that students even in ecologically-focused degree programmes (including Botany, Environmental Science and Physical Geography) can, on average, identify five common wildflowers and commonly mis-identify invasive species. The project aims to develop a robust methodology to assess plant blindness across a wider sample of Irish society including university students, school students and the general public.

The role of tree collections in tackling plant blindness

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Trees are critical to the mitigation of and adaptation to climate change as well as conserving biodiversity and providing a host of benefits to the environment and to humans. Despite this well-known fact, however, plant-blindness – 'the inability to notice plants in one's everyday life' – continues to be prevalent to the degree that the unnecessary destruction of trees and other natural habitats remains a common occurrence. The UCC-based Irish Tree Explorers Network (ITEN) project seeks to combat tree-blindness in particular by engaging diverse audiences with living tree collections (e.g. arboreta, forest parks, urban parks, historic sites, etc.) throughout Ireland. By highlighting the scientific and cultural significance of trees in compelling ways, the project aims to encourage individuals to develop a meaningful connection with and a new appreciation of trees. This paper will present the progress of the ITEN project to date, discussing some of the methods and applications used to engage different audiences. It will also present some of the preliminary survey data, demonstrating the potential for engagement with tree collections to facilitate a greater awareness of trees and the broad range of benefits they offer to both people and planet.

How to select appropriate indicators, for a multiple performance evaluation, assessing system innovations for on-farm experiments?

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Crop production is undergoing transformation with resilience and sustainability becoming increasingly important. Innovations such as reduced fertiliser and pesticide use along with less environmentally damaging inputs with lower energy requirement are just some of the sustainable goals. But do the new innovative methods work better than conventional methods, if so, by how much?

The SIMONE project will use the living lab concept to assess farm system innovations in three areas, integrated weed management, sustainable crop nutrition and crop establishment. This INTERREG funded project involves farmers in several northwest Europe countries.

There are many appropriate indicators for research comparison of new innovative practices with current conventional methods that living labs in the various regions can choose. Choosing optimum indicators to best improve sustainability and resilience across northwest Europe is challenging. SIMONE is a stakeholder lead process, where multi-disciplinary teams examine potential indictors from a stakeholder perspective. In this study, a collaborative on-line platform was used to perform initial brainstorming of potential measurements that could be used under agronomic, ecological, economic, and social headings. This initial brainstorming was collated to give a framework of suitable indicators.

Posters

Analysis of sex determination system in Cannabis sativa

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Cannabis sativa is mainly a dioecious plant, meaning female and male flowers develop on separate individuals. This crop presents high sexual dimorphism. C. sativa has a XY sex determination system: female have two X chromosomes and male plants carry X and Y; but the sexual system of this crop is much more complex, as sex is not only determined genetically, but also by environmental and hormonal factors.

While the developmental processes of male and female Cannabis sativa flowers involves the orchestrated activation of numerous genes, it is conceivable that one or two key genes act as molecular switches. The aim of our research is to understand how genes, phytohormones and environmental conditions interrelate and contribute to sex determination in hemp.

Utilizing transcriptomics analysis, we have pinpointed potential candidate genes on the sex chromosomes apparently associated with both female and male functional development. Among those candidates are transcription factors with homologs know to be involved in reproductive development. We have also developed a PCR-based method to determine sex genotype and establish genotype-phenotype relationships. Our results indicate that sex determination is established very early during Cannabis development and the genetic basis of sex determination is robust across different cultivars.

Comparative crop rhizosphere microbiome function in urban and space agriculture

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Perchlorates are agricultural and industrial contaminants that damage the environment, and as endocrine disruptors, endanger human health. Perchlorates have also been detected on the surface of Mars. As a safe and resilient food source is essential for human health, both on Earth and in Space, developing perchlorate-tolerant crops is an important challenge.

To address this, rhizosphere functions in three crops are being explored: tomato (carbohydrates, pathogen resistance), broad bean (protein, nitrogen fixation), and willow (biorefinery, phytoremediation). Crop development and root morphology (RhizoVision, µCT) will be measured during growth in Lunar and Martian regolith simulants contaminated with perchlorates. Changes in the rhizosphere microbial community and their potential influence on perchlorate fate will be captured with metagenomics.

Initial results indicate that most regolith types can be tolerated by all the three crops, with only minor detrimental impacts on crop development. Assessment of perchlorate fate will reveal either reduction by rhizosphere bacteria, leaching from substrate, and/or accumulation in plant organs. Tracking changes in microbial populations should reveal those taxa underlying compromised rhizosphere function or enabling stress tolerance.

Understanding how regolith and perchlorates affect plant rhizosphere functions will aid in the development of biotechnology solutions for sustainable agriculture on Earth and in Space.

Hemp’s future: Streamlined CRISPR Gene Editing for Innovation

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Hemp (Cannabis sativa) is a vital global crop, renowned for its adaptability, versatility, and rich history. However, unlocking the plant's full genetic potential for targeted breeding and sustainable agriculture requires overcoming the inherent challenges of its heterozygous nature and limited application of genetic techniques. While CRISPR has transformed gene editing in traditional crops, its application in hemp remains underdeveloped. This research aims to establish CRISPR-based genome editing technique suitable for hemp by developing a streamlined transformation process for stable gene editing. Central to this protocol is the establishment of a replicable regeneration process, essential for the successful integration of heritable genetic changes. We use transformation methods targeting hypocotyl explants in combination with RUBY, a synthetic reporting system that visually confirms successful transformations. Our research promises to revolutionize hemp genetics by enhancing desirable characteristics of hemp, broaden the plant's potential, and promote agricultural sustainability and innovation.

LONG NON-CODING CDF1 modulates drought stress responses in Arabidopsis thaliana

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Climate change impacts plant growth and development due to the increase in extreme weather events such as prolonged drought. Therefore, identifying and characterizing molecular regulators of drought stress responses would be critical to maintain food security worldwide. Although most research has focused on protein-coding transcripts, we have recently identified the circadian-regulated long non-coding RNA lncCDF1 that is a natural antisense transcript to the CDF1 (Cycling DOF Factor 1) transcription factor. We had previously observed that the lncCDF1 promoter is activated in lncCDF1promoter::GUS reporter lines subjected to either drought conditions or ABA treatments. Here, we investigated how modulating lncCDF1 levels associated with different responses to drought conditions. We characterized several physiological parameters (e.g., rosette diameter, stomatal density and aperture) of 20 day-old wild type (Col-0) plants, lncCDF1 mutants and lncCDF1-overexpressors (pSUC::lncCDF1 #1.3 and #2.3) subjected to drought conditions for over 8 days. We observed that different levels of lncCDF1 lead to different responses to drought, possibly via mediation of CDF1 transcriptional activity. These findings suggest a role for the non-coding transcriptome in mediating abiotic stress responses and thus expand the available genetic landscape for future breeding of climate resilient crops.

Assessing the role of specific bio-stimulants in regulating Arabidopsis thaliana growth and developmental responses

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Plant growth responses depend on photoperiod (hours of light), water availability and nutrient levels. These cues are then integrated by different signaling pathways of which the Target of Rapamycin (TOR) is one of the most relevant. Therefore, it is possible that specific bio-stimulants affect plant growth and development by modulating their activity. To address this hypothesis, we have characterized specific growth responses (e.g., rosette area, fresh and dry weight, yield) and developmental transitions (e.g., flowering time) of soil-grown Arabidopsis thaliana plants kept under control conditions or treated with bio-stimulants. In parallel, we investigated the accumulation of different components of the TOR pathway, such as its direct target, the 40S ribosomal protein 6 kinase (S6K). Our findings show that bio-stimulant treatments promote early flowering without a detrimental effect on overall rosette areas, which is also shown by comparable accumulation of total S6K protein. However, treated plants also showed an increase in total biomass and yield. These findings suggest that bio-stimulant application could promote specific developmental transitions such as flowering time, a critical agricultural trait with added economic value.

Establishment of an agronomic tool kit to enhance the commercial cultivation of Malva sylvestris plant species for the production of value-added animal feed materials

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The concerns of climate change, global food security and one health has resulted in the necessity to evaluate both novel and historic crops for potential mitigation strategies. Mallow (Malva Sylvestris) is a novel agronomic crop, with high immunomodulatory content and historic medicinal and nutritional benefit. The bioactive it contains can improve immune response of livestock and reduce the requirement for antibiotics. Subsequently this can

assist the livestock sector in reaching antibiotic reduction goals for broader benefits. However, there is no agronomic guidance on the production of mallow to allow large scale production.

Research will be undertaken to establish an agronomic tool kit to enhance the commercial cultivation of Mallow for Northern Ireland to produce value-added animal feed materials. Mallow will be grown in four field trials to identify the ideal variety, sowing rate, sowing date, cutting date, number of cuts, fertiliser and herbicide requirements and optimal crop storage. This will optimise sustainable cultivation whilst also maximising the quantity and quality of bioactive compound found in Mallow. The research will lead to a comprehensive agronomic toolkit to inform and guide on the most cost effective and efficient method to cultivate Mallow for agricultural and commercial purposes.

Detection and characterisation of suspected herbicide-resistant broadleaf weeds

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[1]Teagasc

In Ireland, while herbicide resistance in grass weeds is of major concern, resistance in broadleaf weeds is also increasing. Due to our high proportion of spring crops and reliance on ALS-inhibitor herbicides, control difficulties have been reported in Stellaria media (common chickweed, STEME), Veronica persica (common field-speedwell, VERPE) and Chrysanthemum segetum (corn marigold, CHRSE). In 2023, glasshouse dose-response assays were conducted to confirm resistance to ALS inhibitors on three resistance-suspect populations of STEME and one each of VERPE and CHRSE. Two types of ALS inhibitors, sulfonylurea (metsulfuron + tribenuron or mesosulfuron + iodosulfuron) or triazolopyrimidine (florasulam), were evaluated at the 4-6 true leaf stage. Target-site resistance analysis using pyrosequencing was also conducted to identify the mutation(s) that confer resistance. We found:

- For STEME, heterozygotic mutations (T-G/T-G) for Trp-574 in R1 and R2, and combined heterozygotic Trp-574 and Pro-197 (C/T-CG) in R3, conferred cross-resistance to both types.
- For VERPE, heterozygous Trp-574 conferred cross-resistance.
- For CHRSE, combinations of homozygotic (CTA) and heterozygotic (C/A-C/T-A or C-C/T-A or C-T/A-A) mutations for Pro-197 conferred sulfonylurea-resistance only.

Alternative (auxin mimic) herbicides were highly effective on these ALS-resistant populations. These results are the first confirmed cases of ALS resistance in VERPE and CHRSE, internationally.

Utilizing an Unmanned Aerial System (UAS)-Based Phenotyping System to identify Quantitative Trait Loci (QTL) linked with the waterlogging response in a two-row spring barley collection

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Barley (Hordeum vulgare L.) is a crucial crop for global food security. Yet, the escalating frequency of extreme rainfall events due to climate change, threat barley production. In this context, the selection and breeding of resilient varieties capable of maintaining high yields under such abiotic stresses become imperative for ensuring food security.

However, traditional phenotyping methods are not only laborious but also expensive, often acting as a bottleneck in breeding programs. UAS presents a promising solution due to their speed, cost-effectiveness, and robust capabilities in plant phenotyping.

In this study, European Heritage Barley core collection, comprising 230 genotypes of two-row spring barley were cultivated at the UCD Lyon field, subjected to waterlogging stress. Utilizing two types of UAS equipped with RGB and multispectral cameras, we conducted image-based phenotyping.

Drone image analysis revealed significant reductions in various indices related to biomass and yield under waterlogging stress conditions. Through GWAS, we identified several QTL associated with these traits, facilitating the identification of candidate genes linked to waterlogging response.

The outcomes of this study will shed light on the molecular mechanisms governing barley's response to waterlogging and will enhance the efficiency of plant breeding programs providing establish optimized methodologies for UAS-based phenotyping.

The role of inflorescence photosynthesis in competitive ability and fecundity of an agricultural weed, Avena fatua

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Avena fatua (common wild oat) is a weed affecting the yield of cereals, such as wheat and barley. Its combination of rapid growth and tall statue (high competitive ability) with abundant seed production (high fecundity) make it particularly problematic. Based on the hypothesis that inflorescence photosynthesis contributes to carbon capture for seed production, we explore photosynthetic gene expression in inflorescence organs and the impact of source-sink manipulation on seed formation. In addition, we investigate competitive interactions with barley aiming to identify barley varieties and management options that reduce the competitive impact of A. fatua. First analysis of mRNA-Seq comparing inflorescence organs (glume, lemma, palea and awn) to leaves shows higher expression of genes involved in lipid oxidation but lower expression of some photosynthetic genes. De-awning of plants resulted in a decreased number of seeds and total seed weight compared to defoliation, suggesting a role of awns in seed production and seed carbon gain. Initial analysis of competition with spring barley indicates only minor impacts on barley growth under low competitive pressure, despite A. fatua growing taller than the barley. Further work will investigate the impact of higher planting densities on barley varieties with varying height and tiller numbers.

Genetic improvement of birch species for sustainable forestry in Ireland

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Native broadleaf trees; Downy birch (Betula pubescens) and Silver birch (Betula pendula), are increasingly valuable in forestry due to their short rotation period of 40-50 years compared to other native broadleaves. In Ireland, birch was not a grant-aided species for afforestation, due to poor stem quality in naturally regenerated birch and inadequate survival/growth rates of imported plants. A “Pilot project for genetic improvement of Irish Birch” started in 1998, with further funding from CoFoRD and FORGEN. Three progeny/provenance trials were established in 2001 to evaluate seed lots, and tree growth over multiple growing seasons.

An indoor downy birch seed orchard was established in 2009 at Teagasc, housing clones from 56 individual trees selected after six growing seasons in field trials. In 2012, a further 90 ‘plus trees’ were added to the orchard, and in 2013, it achieved 'qualified' status under

an EU directive on the marketing of forest reproductive material. In 2014, Teagasc partnering with None-So-Hardy Nurseries Ltd, supported by DAFM, established a clonal indoor seed orchard for commercialisation, facilitating the production and supply of improved Irish birch planting material to growers. Current research focuses on genetic diversity studies, and field trials to achieve ‘tested’ status for seed orchard.

Genetic characteristics of plus tree oaks in Ireland and the UK.

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Oaks (Quercus robur L. and Q. petraea (Matt.) Liebl.) are highly valuable trees across the British and Irish Isles but their utilisation in the lumber industry as well as their afforestation usage has been recently underappreciated. However, recognition of their value towards environmental stability, the woodland economy and biodiversity has been growing in recent years and the process of tree improvement through breeding has begun. This process begins with the selection of plus trees which exhibit superior traits such as growth rate, stem form and wood quality. The long-term goals of many tree improvement programmes are to develop genetically improved varieties for forestation whilst maintaining the genetic diversity of the breeding stock. In this study, 192 plus trees selected from potential plus tree breeding stock in addition to 288 progeny trees were used to assess the genetic characteristics, diversity, and degree of hybridisation of future stock using single nucleotide polymorphism (SNP) sequencing and morphological characteristics of leaves. Comparative populations across the species range were used to inform on the conclusions from the results.

The role of endophytes as biological controls against apple replant disease

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Apples are a culturally-important crop in Ireland, valued at €131 million at retail sale value, and are the only food crop in Ireland with the potential to offset CO2 emissions through carbon sequestration. However, the establishment of new orchards is greatly limited by the occurrence of diseases, such as apple replant disease (ARD). ARD is caused by a consortia of microbes within the soil, that have been selected for by previous apple plantations, and results in a strong depression of plant and root growth, particularly in young apple saplings. Soil microbiome analyses of the Lamb-Clarke Heritage apple orchard maintained at UCD has provided valuable insights into ARD-causing microbes that are present within the orchard. A library of endophytes have also been cultured from ornamental fruit trees growing within the windbreaks of the orchard. Through dual-culture experiments, a number of these endophytes have been shown to limit the growth of ARD-soil microbes. Further research will

assess the use of these endophytes as a root-drench treatment to protect young apple sapling roots against ARD.

Unlocking the green elixir: GA3 priming effects and Cannabis sativa growth and development trajectories

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Cannabis sativa (hemp) is a multipurpose crop plant with applications across various industrial sectors. Hemp is predominantly a dioecious plant where monoecious cultivars have been generated via intentional breeding. Gibberellic acid (GA3), a phytohormone, regulates various growth and developmental processes in plants, for instance, seed germination and development, flower initiation, and fruit development. Previously, it was shown that the GA3 application on hemp plants tends to produce male flowers when applied at a specific time and a specific stage; however, the effects of GA3 pretreatment of seeds on hemp growth and development are largely unknown. For this purpose, we use seeds of different hemp cultivars, surface sterilize them, and treat them with different GA3 concentrations to determine the effects of GA3 pretreatment on plant growth and development. The plants developed from GA3-treated seeds show a marked increase in their internodal lengths and have more tendency towards maleness as compared to control plants. Thus, GA3 pretreatment of seeds can modulate the gene expression at a very early stage with priming effects on hemp growth and development.

The use of Ascophyllum nodosum extracts biostimulants improves crop quality through enhanced micronutrient use efficiency.

Dr Elomofe Ikuyinminu[1], Ms Ferga Hamilton[1], Dr Oscar Goni[1,2], Mr Matt Clancy[1], Dr Lukasz Langowski[1], Dr Shane O'Connell[1,2]

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Microelements such as iron (Fe), zinc (Zn), manganese (Mn), and boron (B) have vital roles in a plant’s life cycle, regulating essential cellular processes, such as photosynthesis, respiration, enzyme activation, transcription, and promote the transition from the vegetative to reproductive phase. Despite its importance, micronutrients deficiency in soil is a prevalent problem in agriculture. In current work, we investigated the effect of different Ascophyllum nodosum extracts (ANEs) biostimulants to stimulate micronutrient use efficiency and enhance related crop quality traits. The initial efficacy screening program was carried out using winter wheat seedlings under different nutrient conditions. The best performing ANE from this first screening was assessed in multi-year wine grape (cv. Cabernet-Sauvignon) field trials. We observed an accumulation of macro- and micronutrients in different grapevine tissues in response to the ANE biostimulant applied by foliar spray in plants growing under two nutritional conditions (with and without application of microelements). Interestingly, ANE treatment also modulated those grapevine berry quality markers associated to a more efficient micronutrient assimilation: °Brix, titratable acidity and phenylpropanoid compounds. Showing that the use of specific ANE biostimulants combined with good practices of fertiliser application might be a feasible solution to provide consistent crop quality to growers.

Control of silique photosynthesis in the Brassicaceae family

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Silique photosynthesis (SP) has been linked to seed oil and protein content in several species of the Brassicaceae. A better understanding of its regulation at the molecular level can help researchers to modulate these outputs. We have identified several transcription factors that appear to negatively regulate the establishment and progression of SP in Arabidopsis thaliana. Expression of these transcription factors declines by late stage 12 in the gynoecium, which leads to the expression of photosynthesis associated nuclear genes (PhANGs). In this study, the photosynthetic activity in gynoecia and siliques of the wildtype and mutant plants will be assessed using different parameters like chlorophyll levels and PhANG expression. We also further investigate the molecular mechanisms regulating the expression of MUTE in the gynoecia, a crucial gene in stomatal differentiation. We aim to further understand the transcriptional regulation of MUTE in the gynoecia by creating mute mutant alleles in A. thaliana using CRISPR-Cas9 and complimenting them with constructs with modified transcription factor binding sites. Together this work will provide a physiological molecular framework to study SP in members of the Brassicaceae.

Increasing Nitrogen Use Efficiency with Ascophyllum nodosum biostimulant PSI® 362 in winter wheat in field conditions allows for 25% reduction in nitrogen fertiliser application.

Dr Lukasz Langowski[1], Dr Oscar Goni[1,2], Dr Elomofe Ikuyinminu[1], Dr Shane O'Connell[1,2]

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Wheat is a globally significant crop that provides more than 30% of the calories of the global population. Unfortunately, nitrogen use efficiency (NUE) of wheat is reported to be between 35-45%, with the balance being lost to the environment. Therefore, there is great N application requirement to produce high yielding and quality wheat crop. It has previously been demonstrated that the application of a novel biostimulant (PSI® 362) derived from Ascophyllum nodosum has a direct effect on barley and grass grown in field conditions, and winter wheat seedlings grown in sterile conditions, improving N uptake and assimilation. Current study focused on assessing whether results obtained for wheat in controlled conditions could be translated to the field. Multiple tests were performed in Germany where intensive agriculture models resulted in major ground water pollution. Trials in 2021-2022 and 2021-2023 seasons showed that targeted application of PSI-362 (e.g., as a coating on mineral fertilizer) increased NUE in winter wheat grown under 75% and 80% N input. PSI-362 treated crops showed increased nitrate uptake or soluble protein content. Allowing the crops to grow under reduced N regime, while maintaining yield. This study demonstrates that formulated biostimulants can work as effective solution to enhance NUE.

ElmAsh: Towards conservation and breeding for disease tolerance of two native broadleaf tree species in Ireland

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Native trees are an integral component of the ecosystem, fostering biodiversity, carbon sequestration, and ecosystem services. In Ireland, native tree species cover 19% of the forest area. Among those, Common ash (Fraxinus excelsior) and Wych elm (Ulmus glabra) stand out as particularly important native broadleaf tree species. Since ash dieback first emerged in 2012, caused by the fungus Hymenoscyphus fraxineus, the ash population has suffered significant damage. Similarly, Dutch Elm Disease (DED) has plagued elm trees for over a century, caused by fungi Ophiostoma ulmi and Ophiostoma novo-ulmi, and transmitted by the elm bark beetle. The ElmAsh project aims to identify and propagate tree genotypes that exhibit higher levels of tolerance/resistance to the diseases. The key objectives include:

1) Investigate various propagation techniques to speed up the multiplication of disease tolerant ash using seed as well as vegetative explants from tolerant genotypes.
2) Study the microbiome of both tolerant and susceptible ash genotypes to isolate culturable microbes that could potentially serve as biocontrol agents for combating ash dieback.
3) Establish a germplasm collection of healthy elm trees for screening against Dutch Elm Disease.

These efforts will significantly contribute towards conservation and restoration of Elms and Ash trees in Ireland.

The effect of nitrogen management on radiation interception, grain yield and yield components of autumn-sown oats

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[1]Teagasc

Genotype selection and nitrogen management can affect oat (Avena sativa L.) yield in high-yield potential environment, yet their influence on yield components remains unclear. Field experiments were conducted at Teagasc Crops Research Centre to evaluate yield response of autumn sown oats to nitrogen (N) management and to understand relationships between radiation interception, grain yield and yield components. Three autumn sown oat varieties (Husky, Isabel and Barra) were tested under seven N regimes (0-240 kg/ha) in a split plot design. Radiation interception measurements were made during the growing season, while grain yield and its components were quantified at harvest. Radiation interception at anthesis increased with total N applied and strongly related to grain yield and grain numbers. Grain yield increased with N rate and strongly related to grain numbers and grain weight per panicle. Mean grain weight decreased significantly with increased N ($p < 0.05$). Panicles numbers were not influenced by N management ($p > 0.05$) but significantly influenced by variety. Nitrogen management should target maximum radiation interception during anthesis to increase grain yield. Panicles numbers are not significantly responsive to N doses. Nitrogen has a large influence on canopy size of oats resulting in an increase in radiation intercepted.

Effects of light intensity and temperature on the growth, maximum quantum yield and chlorophyll content of Ulva spp.

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The green seaweed Ulva sp. is considered a promising and sustainable resource for various industries, including food, pharmaceuticals, and biorefineries, due to its chemical composition rich in high-value compounds. Its ability to grow under a wide range of environmental conditions makes it suitable for cultivation in various systems, such as multi-trophic aquaculture systems, photobioreactors, and both land-based and open-sea farming.

However, optimising cultivation systems is imperative to ensure consistent and high-quality yields necessary for commercial exploitation. To achieve this, understanding the influence of abiotic factors on Ulva sp. growth and composition is essential. We are focusing on identifying the environmental parameters for increased production of compounds of interest, particularly those influencing the production of polysaccharides. In spring 2024, indoor experiments conducted at CTAQUA (Cadiz, Spain) explored the effects of light intensity and temperature on two Ulva species: a tubular one (U. cf. intestinalis) and the blade-like Ulva ohnoi. Results include assessments of maximum quantum yield, chlorophyll content, and growth, providing valuable insights into the physiological responses of Ulva sp. to environmental stimuli.

Investigating the functional strategies underlying the 'weediness' of grass weeds

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Weeds are, if left unmanaged, the most serious problem faced by farmers around the globe, causing higher crop losses than pests and pathogens. The grass weed Avena fatua (wild common oat) is closely related to Avena sativa (oat) and reduces crop yields of, e.g. wheat and barley, through competition.

Our work intends to characterize the traits that lead to the weediness in A. fatua. Through experiments documenting functional traits and strategies we are comparing populations of A. fatua from around Irish farms, predominantly tillage based.

Early findings indicate minimal differences in traits such as leaf area, dry matter content, and specific leaf area among various populations. Ongoing experiments aim to further investigate traits of A. fatua and elucidate strategies based on the competitive-stress tolerant-ruderal (CSR) system. Moreover, comparisons are being made between A. fatua and species of tillage crops including wheat (Triticum aestivum), barley (Hordeum vulgare), oat, and other significant grass weeds, using data from the TRY database. Initial results suggest that A. fatua exhibits higher specific leaf area than the other species.

Our future research strives to answer questions related to the functional strategies that lead to elevated weediness in A. fatua and its performance under environmental stress.

The effect of autumn closing date on white clover production over winter

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Ensuring adequate proportions of white clover in grazing swards is a key objective of pasture-based systems. The objective of the current study was to access the impact of autumn closing date on over winter white clover agronomic performance and persistence. A 5 by 2 factorial design study was established on a grass/clover sward with 5 autumn closing dates (25-Sept, 9-Oct, 23-Oct, 6-Nov and 20-Nov) and 2 spring grazing dates (15-Feb and 15-Mar). Within each plot five Individual stolon were identified and marked using coloured wire after each closing date. Every 3 weeks from closing to grazing in spring, stolon length, number of growing points, number and length of petioles, size of centre leaf and light availability at ground level. Herbage mass and clover content were determined at defoliation in spring. Earlier closed swards had a significantly ($P<0.001$) lower stolon length and the number of growing points on individual plants compared to later closed swards. Earlier closed swards had a greater herbage mass in spring ($P<0.001$) and lower sward clover content ($P<0.01$). Closing swards earlier in autumn, reduced light availability to the base of the sward thus reducing stolon length and growing pints, lowering overall sward clover content and persistence.

Improved mapping, monitoring and conservation of Irelands ancient woodlands.

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Ireland's forest strategy 2023-2030 emphasizes the preservation of woodlands in Ireland, particularly those that have been continuously forested since at least the 17th century. These ancient woodlands, once common but now fragmented and rare, hold substantial biodiversity and cultural significance. Despite their importance, there remains a significant gap in understanding their distribution and conservation needs. This project is committed to advancing the identification, mapping, and protection of these ancient woodlands. Employing a blend of field ecology (such as the presence of ancient woodland indicator vascular plant species), palaeoecological techniques (such as analysing pollen records from soil cores), digitization of historical maps, and examination of historical documents, we aim to build a thorough framework for assessment. In a comprehensive case study of the Leitrim and Kilkenny regions, we identified 245 woodland stands, covering 1124 hectares, that are ancient or potentially ancient. Almost half of these woodlands are in an unfavourable conservation state, largely due to the impact of invasive species and overgrazing. By collaborating with stakeholders, this project promotes policies that protect these crucial natural resources. This effort is a fundamental step towards fulfilling the National Inventory of Ancient and Long-established Woodlands in Ireland.

Active versus passive rehabilitation of degraded peatlands-growth and physiological responses of birch Betula Pubescens to peat depth

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In the last century, Ireland’s intact peatland area declined from 1,200,000 hectares to approximately 100,000 hectares, primarily due to industrial-scale harvesting of peat. Industrial peat extraction involves the complete removal of vegetation and the creation of drainage ditches causing the loss of functioning peatlands. However, the last two decades have seen increased recognition of the need to rehabilitate peatlands in Ireland, and particularly to restore their status as a carbon sink to aid climate change mitigation efforts. In peatlands where industrial extraction of peat has ceased, without intervention, these degraded bog ecosystems can rapidly transition to wooded landscapes due to the natural regeneration of fast-growing native trees. Factors facilitating the natural regeneration of native tree species on post-industrial peatlands are poorly understood. The overarching aim

of this project is to assess the factors contributing to the successful natural regeneration of native forests on post-extraction peatlands. At an experiment site with varying microtopography and peat depth, an in-situ experiment was established to assess the role of seed input, soil moisture, nutrient status, and microclimate on the early establishment and growth of regenerating birch Betula Pubescens on post-extraction peatlands. Ultimately, this project will inform future peatland restoration and rehabilitation approaches in Ireland.

Nuclear Dynamics During Seed Priming

Ms. Nora Pasquali[1], Dr. Sara Farrona[1]

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This research explores the impact of seed priming on Arabidopsis thaliana, with an emphasis on understanding the nuclear dynamics underlying memory maintenace. Seed priming techniques generally consist of inducing seed metabolism by imbibition and thereafter submitting the plant to a dehydration procedure right before radicle protrusion. We hypothesize that the retention of seed priming effects is localized in the shoot apical meristem (SAM). Therefore, we aim to unravel the transcriptomic and epigenomic changes in the SAM that contribute to the lasting effects of seed priming in A. thaliana. To test this hypothesis, a series of priming experiments using polyethylene glycol (PEG) as an osmopriming agent will be conducted. An initial whole seedling RNA-seq will be performed to identify candidate genes to the seed priming memory response, which will then followed by the collection of RNA-seq, ATAC-seq, and ChIP-seq data from the SAM by means of Fluorescence Activated Nuclei Sorting (FANS). Additionally, we aim to identify in-silico whether the cis-regulatory elements of the candidate genes for seed priming memory are involved in regulating the seed priming response. This research is significant as understanding the mechanisms of establishing seed priming memory could lead to the development of novel crop improvement strategies.

Investigation of the interaction of Mycorrhizal and Seaweed extracts and enriched blue and red wavelength light on the rooting of Crassula ovata and Ficus benjamina

Mr. Joseph Croke[2], Ms Kathrin Reimer[1]

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Vegetative propagation by stem cuttings is one of the most used propagation methods for the commercial production of indoor plants. Rising costs to nurseries and the need for more sustainable production systems of ornamental plants have led many producers to investigate alternative methods how to improve and shorten the rooting process. Seaweed and mycorrhizal fungi have been shown to enhance root formation in certain plants due to their root promoting abilities. Supplemental light treatments with red and blue spectrum could also potentially increase or reduce root formation. In this study, interactions of the application of seaweed, Mycorrhiza or IBA stimulants with four different light treatments, blue & red LED enriched spectrum, restricted (semi darkness) and ambient light on the rooting process of Crassula ovata and Ficus benjamina were investigated. Initial results indicated blue wavelength enrichment with no stimulant treatment rooted Crassula cuttings within 7 days. Blue and red enrichment had the highest survival rate after 30 days. IBA developed the most roots in natural light. Ficus showed signs of root formation in 80% in a combination of red light and IBA by Day 17. Enriched blue wavelengths resulted in well-developed optimum root systems after 30 days.

Investigation of interactions of different root zone temperatures with wood fibre peat alternatives for growing the nursery stock crops Petunia × atkinsiana and Bacopa monnieri

Mr Alastair Swanton[1], Mr. Joseph Croke[1]

[1]Munster Technological University

Nursery Stock industry in Ireland, worth €251 million farm gate value (2020), is in transition away from using peat, to environmentally friendly alternatives of root media for crop cultivation, assisting in protecting Irish peatland habitats that have vital biodiversity importance and also are Europe’s largest single carbon store. This study investigates the optimization of growth and quality parameters of Petunia × atkinsiana and Bacopa monnieri bedding crops through varied root zone temperatures (RTZ) and alternative growing media. Weekly analysis of plant height, width and leaf number and crop quality were performed. Results obtained indicate trends showing that increased root zone media temperature accelerated crop growth in both species, compared to ambient RZT, potentially reducing time of production for growers, increasing nursery floor profits/ M2/ year and offering better control of harvest date. Weekly data indicated peat-based media outperformed commercially used alternative wood fibre enriched media in crop growth and time to harvest. Results indicate significant value in investment in root zone warming technology but also that more work is required to assist the nursery stock industry towards transition to more sustainable root zone media alternatives to peat as a crop cultivation substrate.

InnoVar: Next generation variety testing for improved cropping on European farmland.

Mrs. Hazel Brown[1], Dr. Lisa Black[1], Prof. Fiona Doohan[2]

[1]AFBI, [2]UCD

Feeding an increasing global population in the face of global climate change is a challenge for the agricultural sector and governments alike. With increasingly fewer agricultural chemicals available to mitigate against biotic and abiotic stresses, it is necessary for new crop varieties to have traits of resilience and sustainability. Developing new varieties with more desirable characteristics is critical, but so are their regulation.

InnoVar, Next-generation variety testing for improved cropping on European farmland, is a Horizon 2020 'Research and Innovation Action' project. Using wheat as a test crop, InnoVar will devise and demonstrate improved, efficient methods of integrating new methods into plant variety testing processes and incorporating variety information into decision-making on-farm.

Creating the concept of high-performance low-risk (HPLR) varieties within the realm of value for cultivation and use (VCU) testing would help focus on this pressing need while introducing European harmonisation of VCU testing. InnoVar is developing tools and models to enhance current variety testing practices by exploiting high-tech genomics, imaging, and machine learning technologies. Next-generation variety testing will help countries and breeders focus on the challenge of feeding the next generations.

Cultivation of high-protein plant biomass using an agri-food wastewater for a circular economy

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The water fern, Azolla filiculoides (Azolla), is a small, floating, aquatic plant that can exhibit rapid growth even on wastewater with a high crude-protein content (25-30%). The incorporation of Azolla into a wastewater management scheme could support wastewater valorisation and promote a closed plant-nutrient cycle. Within the laboratory, preliminary investigations were performed to cultivate Azolla on wastewater sourced from a large commercial meat processor. Azolla was grown on various concentrations of wastewater (Control, 5%, 25%, 50%, 100%), three pH levels (pH 5, 6, 7.8), and different treatments (daily pH adjustment vs. adjustment on the initial day only) for seven days. The relative growth rate of Azolla tended to be similarly high across all concentrations, while pH of 5 and 6 displayed similar growth compared to Azolla grown on the unadjusted pH (pH 7.8). The data demonstrated that when 100% of wastewater with pH6 without daily pH adjustment, the highest removal rate of phosphorus and nitrogen reached 91.6% and 26.4%, respectively. These results indicate that abattoir processing wastewater can be a suitable cultivation medium for Azolla. The results of the study underpin the promising development of Azolla phytoremediation and high-protein biomass production in agri-food wastewater treatment.

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