Green Biosciences Examples of Year 4 Research Projects

***Type of project:* Education & Public Engagement (E&PE) project**

***Title:* The SeedPop! project – evaluation of an activity to promote sustainability and plant science**

***Supervisor:* Sara Farrona**

Background

The SeedPop! is an Education and Public Engagement (E&PE) project that aims to connect young people with scientists from Higher Education Institutions engaging them in STEM. The SeedPop! Project will introduce young students to the science of plants and food crops, placing these topics within the context of a rapidly changing environment and the growing need for more sustainable agricultural solutions. The SeedPop! project aims to help students understand how environmental factors, particularly salinity, a harmful environmental stress that farmers face, affect plants with a focus on seeds, a cornerstone of our agricultural and food systems. Students will also explore how science can drive the development of environmentally friendly solutions to secure future food production aligning with the Sustainable Development Goals (SDGs).

The SeedPop! project focuses on the development of an E&PE activity based on a germination kit. The kit contains all the materials to develop the activity together with the educational resources for teachers, such as the learning plan as well as learning objectives and outcomes.

Project Aim

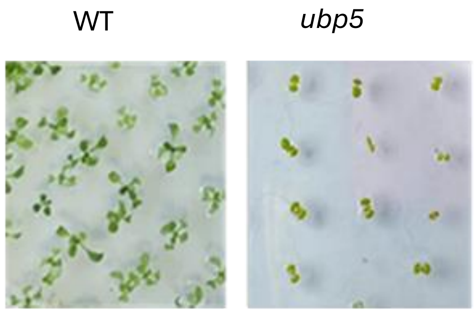
Through this project you will contribute to evaluate the SeedPop! project and its impact on teachers and pupils. You will use qualitative and quantitative data collected during the pilot phase. The analysis of feedback, collected in schools using a short questionnaire, and also the analysis of the observations recorded by the SeedPop! team members will allow you answer several evaluation research questions, including student engagement and project effectiveness in allowing students in 5th and 6th class to acquire knowledge about the importance of seeds in food systems, global issues such as climate change and food security, the importance of SDGs. You will also evaluate if the project has increases teachers' confidence in facilitating hands-on STEM activities.

Type of project: Lab-based research project

Title: Regulation of seed germination, a key plant trait, by UBIQUITIN PROTEASE 5

Supervisor: Sara Farrona

Background



Seeds are cornerstones of global food systems. Seed germination is a critical developmental process in plants and has long been a target for agri-biotechnological strategies aimed at ensuring uniform and reliable crop establishment. Our research has recently identified UBIQUITIN PROTEASE 5 (UBP5) as a key regulator of seed germination in the model plant *Arabidopsis thaliana*.

UBP5 is a deubiquitinase that regulates gene expression by removing ubiquitin from histone H2A (H2Aub). H2A is a core component of the nucleosome and its ubiquitination acts as a repressive chromatin mark. UBP5-dependent removal of this mark is therefore essential for the activation of transcription. Results from our group have demonstrated the central role of UBP5 in plant development: *ubp5* mutants, generated using CRISPR/Cas9, display impaired growth and developmental defects (Godwin et al., 2024). Consistent with this role, UBP5 is highly expressed during seed development, and transcriptomic analyses show widespread misregulation of thousands of genes in *ubp5* seeds (Nedounsejian et al., unpublished).

Project Aim

This lab-based, experimental project will explore the role of UBP5 in seed germination. Students will carry out *in vitro* germination assays to compare the germination phenotypes of *ubp5* mutants with wild-type and UBP5-GFP complemented lines. In addition, they will assess how *ubp5* seeds respond to gibberellins (GA), a key hormone promoting germination, and to abscisic acid (ABA), a major repressor of germination in comparison to the same control plants. Germination will also be tested in the presence of paclobutrazol, an inhibitor of GA biosynthesis.

Ultimately, this project will provide fundamental insights into how UBP5 regulates seed germination—a trait of major agricultural importance.

Through this project you will investigate the regulation of seed germination, one of the most important stages of the plant life cycle and will learn key plant molecular biology techniques also acquiring a solid knowledge in data analysis

Type of project: ***Lab-based research project***

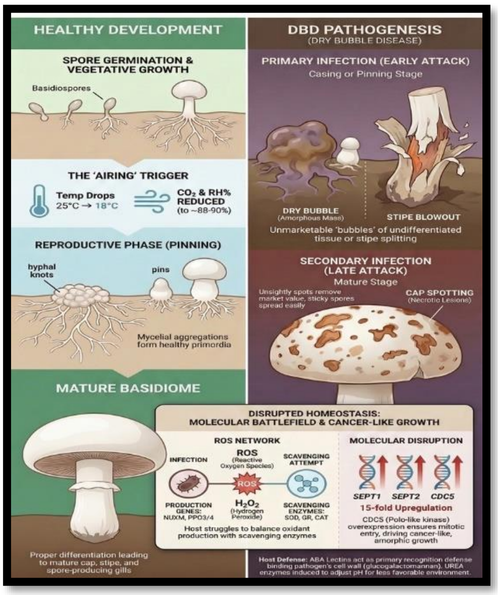
Title: ***Oxidation enzymes in white button mushrooms and dry bubble disease***

Supervisor: ***Galina Brychkova***

Background

The white button mushroom (*Agaricus bisporus*) is an economically important crop for the Irish horticultural sector. However, it is severely affected by dry bubble disease caused by the mycoparasite *Lecanicillium fungicola*.

L. fungicola triggers strong transcriptional upregulation of reactive oxygen species (ROS)-producing enzymes. Infected tissues exhibit elevated ROS levels, linking disrupted ROS homeostasis and the characteristic "bubble" symptoms of the disease (Quiroz et al., 2024). In *A. bisporus* postharvest biology, oxidative enzymes are already well established as key determinants of browning, membrane integrity, and senescence through their role in controlling ROS accumulation.



Beyond ROS, reactive carbonyl species (RCS) act downstream as mobile and protein-modifying signalling molecules in plants and fungi. These compounds contribute to oxidative stress signalling, programmed cell death, and virulence. In pathogenic fungi, detoxification of RCS is required for normal development, stress tolerance, and pathogenicity, while altered RCS levels can drive ROS accumulation, apoptosis, and growth defects, suggesting RCS as a key but unexplored layer in the interaction between *A. bisporus* and *L. fungicola*.

Project Aim

Through this lab-based project you will investigate oxidative signalling during the development of dry bubble disease. You will gain experience in plant/fungal pathology techniques, molecular biology, biochemical assays, and data analysis. You will also quantify ROS and RCS biomarkers as well as morphological changes associated with bubble formation.

Ultimately, this project will provide new insights into the biochemical and molecular basis of dry bubble disease in A. bisporus, with potential implications for improving mushroom health and productivity in commercial systems

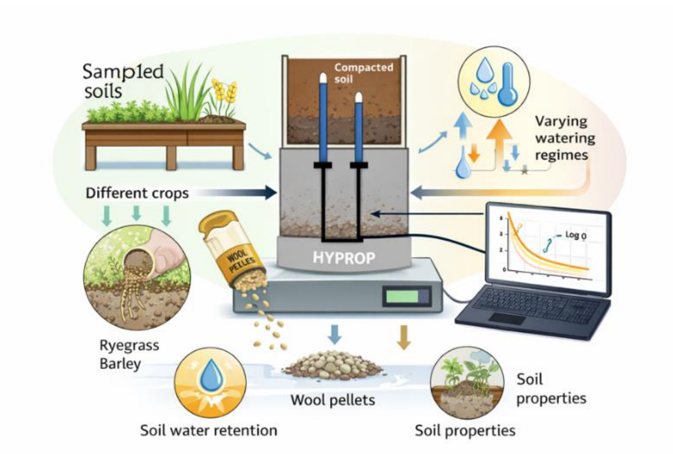
Type of project: ***Lab-based research project***

Title: ***Soil conditioner effect on water retention and soil aeration, and contribution to crops performance***

Supervisor: ***Galina Brychkova***

Background

Wool pellets are a novel organic soil amendment made from processed sheep's wool and are attracting growing interest as a sustainable tool for crop production. Their fibrous structure creates a rough surface that can help deter soft-bodied pests such as slugs, while a surface layer of pellets may also suppress weed growth by reducing the light and air available to germinating seeds.



Wool pellets also have interesting nutritional properties. They supply nitrogen (N) and potassium (K), but relatively little phosphorus (P), useful in soils where phosphorus is already present at high levels. This could make wool pellets a more environmentally sustainable option than some conventional fertilizers, particularly in areas where excess phosphorus can contribute to water pollution.

Another key feature of wool pellets is their high water-holding capacity. When wetted, they can absorb and store large amounts of water, then release it slowly into the surrounding soil. This may help plants cope with short periods of drought and reduce the need for irrigation. However, their effects on different cereal crops and under different watering conditions are still not well understood.

Project Aim

This project will investigate whether wool pellets can improve soil conditions and crop performance in cereal systems. Using different cereals, you will gain hands-on experience in measuring soil moisture dynamics, bulk density, porosity, infiltration, and soil aggregation, as well as assessing nutrient availability and plant responses such as germination, seedling vigour, biomass production, and root development.

Through this project, you will investigate how wool pellets as an innovative organic tool that can be a more sustainable solution, while gaining valuable experience in soil science, plant biology, and experimental data analysis

Type of project: ***Lab-based research project***

Title: ***Characterization of the Rumen Microbiome in High vs. Low Methane-Emitting Beef Cattle***

Supervisor: ***Sinéad Waters***

Background

Beef cattle play an essential role in food security, being a reliable source of protein and essential vitamins. This is largely due to the rumen —the largest of the four stomach compartments— and its microbiome, which digests plant material to provide energy for maintenance and meat production. However, methane (CH_4) is produced as a byproduct of this digestion.

Methane is a potent greenhouse gas, with a global warming potential much higher than that of CO_2, making it a key target for mitigation strategies. Since the rumen microbiome drives methane production, recent studies have focused on differences of rumen microbiome between high and low methane-emitting cattle. Understanding these differences can support breeding programs aimed at selecting low-emitting animals, reducing the environmental impact of the Irish beef industry.

This project will therefore focus on exploring differences in the rumen microbiome between high and low methane-emitting beef cattle.

Project Aims

- To discover which microbes live in the rumen of low-methane cattle and how they differ from those in high-methane cattle
- To understand how these differences might be used to make beef production more environmentally friendly

The student will work with rumen samples collected from a beef cattle performance trial conducted by the Irish Cattle Breeding Federation (ICBF). Laboratory work will include DNA extraction from the rumen samples, preparation for 16S rRNA sequencing, and downstream bioinformatic analysis.

This project will allow you to investigate the role of key microbial groups in the rumen of beef cattle that contribute to methane emissions, while gaining a solid background in data analysis

***Type of project:* Lab-based research project**

***Title:* More photosynthesis equals more growth? Taking green and red seaweeds as models**

***Supervisor:* Ronan Sulpice**

Background

Ireland is place for an amazing number of seaweed species, including Ulva spp. (sea lettuce), and *Palmaria palmata* (dulse). The production of farmed aquatic plants (mostly macroalgae) has risen four-fold since 2000 and stable cultivation of macroalgal biomass is becoming increasingly important in food, feed & bioproducts supply. In addition, seaweed cultivation is seen as a sustainable way to obtain much needed plant biomass, as it does not compete for land, and fix nutrients and CO_2, thus combatting eutrophication of coastal areas and acidification of our oceans.

Growth of seaweeds, like other photosynthetic organisms, is fuelled by photosynthesis.

Project Aim

The project will address two main questions:

1. How photosynthesis traits, i.e. chlorophyll fluorescence, O_2 release, and CO_2 assimilation agree when growth conditions or genotypes vary?
2. To which extent the efficiency of photosynthesis translates to increased biomass when growth conditions or genotypes do vary?

Seaweeds are recognised for their high productivity (growth), and photosynthesis is a key for providing organic compounds for growth. At present, chlorophyll fluorescence, and sometimes O_2 releases, are used to estimate photosynthesis rate. However, CO_2 assimilation is the ultimate parameter to use for assessing photosynthetic rate. In this project, we will compare how those three parameters agree together, using different environments, and/or different genotypes, and then those parameters will be compared to growth rates.

This project will provide crucial fundamental knowledge to establish tools for proper estimation of photosynthetic rates of Ulva and Palmaria, and will help refining models estimating CO_2 capture by seaweeds in marine waters

***Type of project:* Data Analysis Project**

***Title:* Trade-offs between nutrition, environmental impacts and cost in householder food practice in Galway**

***Supervisor:* Anne Mullen**

Background

Though the urgency of food systems transformation is widely accepted, responses have overwhelmingly been top-down and focused on agricultural and food production. The power of householders to transform food systems is poorly explored. Blunt messaging around reducing red meat consumption and food waste prevails, and food environments – built environments around us that dictate our food practice - do not always support consumers in making sustainable choices for human and planetary health. Our research has uncovered great enthusiasm, innovation and ingenuity among householders in Galway in mitigating the environmental impact of their food practice and now we want to quantify that potential in terms of human and planetary health.

Project Aim

You will join the PhD student Nicole Olweean in analysing data collected from householders in Galway on their current food practices and the changes they would make for sustainability. Our group will quantify the differences between current and desired food practices in terms of nutrition, environmental impacts and cost to the householder. You will also contribute to writing the results of the study as a report, scientific paper and – should time allow it – a policy brief.

You will join the Food Systems Lab led by Anne Mullen, and work closely with PhD student Nicole Olweean and MSc Agrifood Sustainability and Technology student Rose Wafer. You will gain skills in data analysis, interpretation and science communication for households, academics and policymakers

Type of project: ***Lab-based research project***

Title: ***Development of gene-edited legume varieties with improved tolerance to abiotic stress***

Supervisor: ***Felipe Quiroz***

Background

Legumes are essential crops for sustainable agriculture because of their nutritional value, role in biological nitrogen fixation, and contribution to lower-input farming systems. However, legume productivity is frequently limited by abiotic stresses such as drought, salinity, and heat, which are becoming more severe under climate change. Despite the potential of gene editing for crop improvement, progress in legumes has often been constrained by the difficulty of plant regeneration and transformation, which are highly genotype dependent in many species. Our research is addressing this challenge through the development of a genotype-independent transformation protocol in pea, creating new opportunities for the efficient application of CRISPR/Cas-based approaches in legumes. This platform can accelerate both functional gene analysis and the development of improved germplasm.

This project will focus on applying CRISPR/Cas-mediated gene editing and transformation technologies to support the development of new legume varieties. Depending on project progress, the work may involve *in vitro* tissue culture, transformation, molecular screening, and/or early phenotypic evaluation of edited or transformed materials under controlled stress conditions.

Project Aim

This lab-based project focuses on the development of legume molecular biology tools for crop improvement. The work involves the optimisation and application of a genotype-independent transformation platform in legumes, together with the generation and/or evaluation of edited plant material targeting improved abiotic stress tolerance.

The project provides training in plant tissue culture, transformation, molecular biology, plant stress, experimental design, data collection, and data interpretation.

Through this project, experience will be gained in plant tissue culture, transformation, molecular biology, and gene editing, together with experimental design, data collection, and data analysis in legume crops

***Type of project:* Computer/Lab-based research project**

***Title:* Network analysis of genes involved in microbe-legume nodulation interactions**

***Supervisor:* Peter McKeown**

Background

Legumes and other plant engage in nitrogen-fixing bacteria such as Rhizobia, providing biologically-available nitrogen without the use of energy-intensive fertilizers. We have analysed the genes involved in the symbiosis, identifying previously uncharacterised 'nodal' genes likely to be at the centre of regulatory modules.

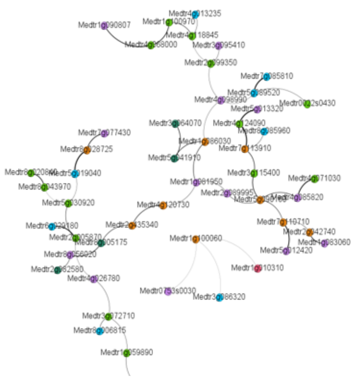


Figure. Core Nodulation Network in sample legume genome based on shortest path connector links

We have also demonstrated the patterns of purifying and positive selection which act upon these genes and which have shaped the evolution of nodules with differing efficiencies in different plant clades.

Project Aim

In this project, an analysis of the amino acids subject to selection will be carried out, using a combination of wet-lab and bioinformatic approaches. Selection analysis will be performed in PAML.

Students with particular interest in Horizontal Gene Transfer may also be able to develop skills in codon usage analysis to confirm suspected incidences of HGT of microbial genes into the plant partner. Interests in molecular evolution and some experience in bioinformatics are assets for this FYP. This work will inform evolutionary analyses ultimately aimed at optimising nitrogen fixation in plants and reducing dependences on artificial fertilizers so will also be of interest to students with broader perspectives in sustainability issues.

You will gain experience in molecular evolution and will acquire a blend of wet- and dry-lab skills while working in nitrogen fixation, a key trait in beneficial plant-microbial interactions

Type of project: ***Lab-based research project***

Title: ***Cytoplasmic effects on heterosis ('hybrid vigour') in plants***

Supervisor: ***Peter McKeown***

Background

Photosynthesising organisms like plants can contain three genomes in every cell, derived from the nucleus, mitochondrion and plastid.

We have demonstrated that interactions between nuclear genomes in lines where the cytoplasmic genomes have been 'swapped' between lines can lead to bigger seed being produced, a useful trait for crop breeding and of interest for understanding parental commitments to offspring.

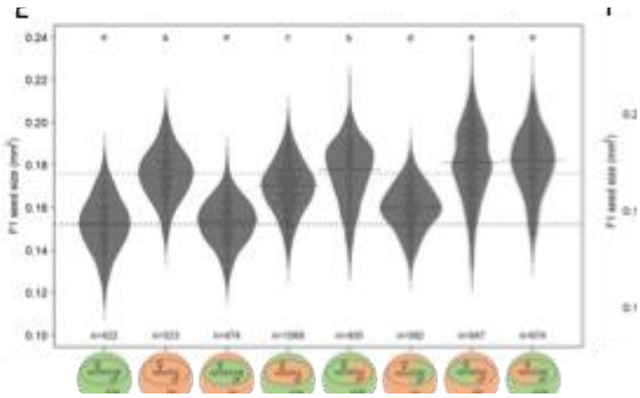


Figure. Seed size distributions in cytoswapped lines.

Project Aim

This will be a primarily lab-based research project working on plant molecular genetics, in the context of our research on heterosis. This project will examine lines of the model plant, Arabidopsis, across its growth cycle, determining the phenotypic effects of these unusual changes.

Plant yield is key for tackling food insecurity and, therefore, a paramount agricultural trait. Your research with cytoswapped Arabidopsis lines aims to discover fundamental and applied knowledge of heterosis and seed production

***Type of project:* Data analysis project**

***Title:* Biorefinery life cycle assessment**

***Supervisor:* David Styles**

Background

Biorefineries based on anaerobic digestion (AD) have been proposed as a core part of bioeconomy expansion, to process biomass into multiple useful products including energy. Understanding mass flows and emission through biorefineries is critical to evaluate their environmental sustainability, via life cycle assessment (LCA). A recent model developed in our research group (LCAD 2.0) enables users to model AD-biorefineries based on basic input and output data (Figure 1).

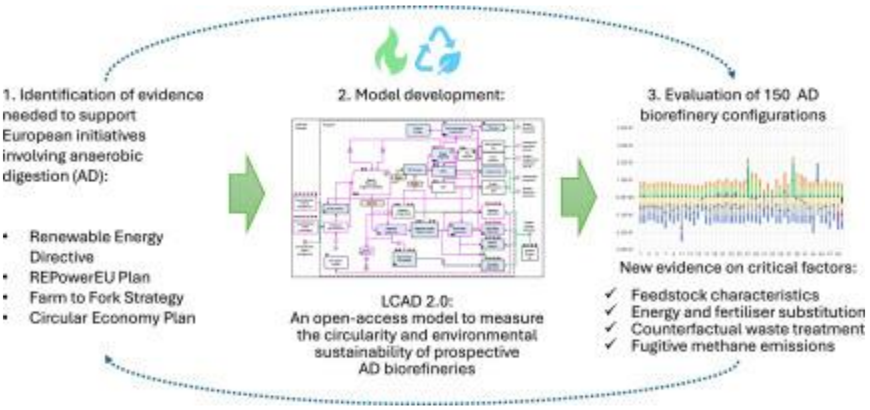


Figure. LCAD2.0 model, developed by Martinez-Arce et al. (2026). https://www.sciencedirect.com/science/article/pii/S092134492600131X

Project Aim

Collating data on one or more novel biorefineries, and using those data to run the LCAD2.0 model, to evaluate the environmental sustainability of the system. Data could be obtained from stakeholder consultation and/or literature review (e.g. papers and reports describing biorefinery configurations). The study would involve running the Excel-based model, and extracting data to undertake a full LCA – in OpenLCA software or in MS Excel.

As a complementary element of research, or as a derivative project, a student could undertake a techno-economic assessment of one or more biorefinery concepts.

Through this project you will evaluate the environmental sustainability of the bioeconomy, and gain experience in life cycle assessment and data management