

All sessions are plenary and held in the Van Emden Lecture Theatre (Edith Morley building),
University of Reading, Whiteknights Campus, RG6 6EL

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Wednesday 14th Feb - Morning

8.15-9.00 Registration, coffee and pastries and poster hanging in rooms 125 & 126 outside Van Emden Lecture Theatre

9:00-9:05 Welcome by Prof Donal O’Sullivan (local organizer)

Session 1: Nutrition & Quality (Part 1)

Session Chair: Dr Paola Tosi (University of Reading)

9:05-9:45 Keynote Speaker: Prof Marta Vasconcelos (Univ Católica Portuguesa)

[“Legume nutrition paradoxes: from the grain to the gut”](#)

9:45-10:00 Cathrina Edwards (QIB)

[“Impact of food processing on the digestion and metabolic effects of pulses”](#)

10:00-10:15 Rosanne Maguire (Warwick)

[“Systems thinking to envision a food system that serves public health using novel varieties of common bean”](#)

10:15-10:30 Rispah Ng’ang’a (QIB)

[“A Technofunctional and Nutritional Study of Pea Seed with Reduced Antinutritional Proteins”](#)

10:30-11:00 Coffee/tea break

Session 1: Nutrition & Quality (Part 2)

11:00-11:40 Keynote Speaker: Prof Luisa Trindade (Univ Wageningen)

[“Breeding legumes for improved quality for the food industry”](#)

11:40-11:55 Peter Jackson (Reading)

[““Raising the Pulse’: systems analysis of the environmental, nutritional and health benefits of pulse-enhanced foods”](#)

11:55-12:10 Mark Bal (JIC)

[“Two auxins are better than one – Chlorinated auxin in pea fruit development”](#)

12:10-12:25 Surbhi Rana (JIC)

[“Auxin Transport in Pea Fruit Development: Unravelling 4-Cl-IAA Distinctions”](#)

12:30-13:30 Lunch and poster viewing in rooms 125 & 126 outside Van Emden Lecture Theatre

Wednesday 14th Feb - Afternoon

Session 2: Trait Genetics & Genomics (Part 1)

Session Chair: TBA

13:30-14:10 Keynote Speaker: Dr. Thomas Wood (NIAB)

[“Characterising natural genetic diversity to support the development of improved disease resistance in temperate and tropical pulse crops.”](#)

14:10-14:25 Mahmut Tor (Worcester)

[“Towards RNA-based downy mildew control in pea plants”](#)

14:25-14:40 Nicolas Trenk (JIC)

[“Putting the root rot on the spot: Characterising genetic sources of resistance against pea”](#)

14:40-14:55 Jamie-Leigh Carter (Teagasc)

[“Faba Bean Chocolate Spot Resistance Responses in Diversity Panels”](#)

14:55-15:20 Coffee/tea break in rooms 125 & 126 outside Van Emden Lecture Theatre

Session 2: Trait Genetics & Genomics (Part 2)

15:20-16:00 Keynote Speaker: Dr. José De Vega (Earlham Institute)

[“Identifying adaptations and admixture in common bean: why do we need pangenomes and genomic platforms?”](#)

16:00-16:15 Shradha Saraf (EBI)

[“Legumes in EnsemblPlants”](#)

16:15-16:30 Thomas Harvie (Reading)

[“Prospects for the genetic improvement of protein traits in faba bean”](#)

16:30-16:45 Mark Chapman (Southampton)

[“Genomic advances in underutilised legumes”](#)

The Funding Landscape

16:45-16:55 Dr. Emma Markham (BBSRC, UKRI)

“BBSRC funding opportunities for legume researchers”

16:55-17:05 Paul Laniran (InnovateUK, UKRI)

“Funding opportunities at Defra-funded Farming Innovation Programme”

17:05-19:00 Poster viewing session in rooms 125 & 126 outside Van Emden Lecture Theatre

19:00 Conference dinner - Meadow Suite, Park House

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Thursday 15th February - morning

8.30-9.00 Coffee and pastries, poster viewing

Session 3: Cropping Systems and Nitrogen Fixation (Part 1)

Session Chair: Dr Jake Bishop (University of Reading)

9:00-9:40 Keynote Presenter: Prof. Euan James (James Hutton Institute)

["Development and use of rhizobial inoculants to improve Biological Nitrogen Fixation by pulse crops in the UK"](#)

9:40-9:55 Katharina Schiessl (SLCU)

["Light-sensitive Short Hypocotyl \(LSH\) genes confer symbiotic nodule identity in *Medicago truncatula*"](#)

9:55-10:10 Clare Hurst (Warwick)

["CLE sigNal peptides: A potential target for optimising nitrogen efficiency in legumes"](#)

10:10-10:25 Carolina Isidra-Arellano (Kew)

["EPFL peptides are involved in legume nodulation"](#)

10:30-10:55 Coffee/tea break

Session 3: Cropping Systems and Nitrogen Fixation (Part 2)

10:55-11:10 Pete Iannetta (JHI)

["Faba bean as a foundation for climate smart crop- and feed-systems"](#)

11:10-11:25 Christine Watson (SRUC)

["Full of beans: A survey of attitudes and production practices in Europe"](#)

11:25-11:40 Thomas Wilkinson (ADAS)

["Nitrogen Climate Smart - The role of and approach to farmer engagement in valorising arable pulse cropping benefits in the UK"](#)

11:40-11:55 Imelda Uwase (Reading)

["Cereal-legume intercropping alters soil microbial processes driving carbon and nutrient cycling"](#)

12:00-13:00 Lunch

Thursday 15th February - afternoon



PCGIN Annual Stakeholder Meeting

Session 1

Chair: David Lloyd, Germinal

13:00 Welcome, PCGIN and industry perspective, introduction to the programme (David Lloyd, Germinal)

13:05 Introducing the network and the resources it delivers (10 minutes each)

- Genomic and genetic resources for enhanced disease resistance in pea (Sanu Arora, JIC)
- Toolkits for enhanced disease resistance in faba bean (Tom Wood, NIAB)
- Enhancing seed quality traits through genetics (Ahmed Warsame, JIC)
- Extended genetic diversity in faba bean (Donal O'Sullivan, Reading)
- PCGIN 10-year review (Andrew Thompson, Cranfield)

14:10 Perspectives for PCGIN 2024 and beyond (18 minutes each)

- The war against bruchids – genetic resistance? (Nadim Tayeh, INRAe)
- Crop diversification and the agronomic and environmental benefits (Christine Watson, SRUC)
- Successful gene editing in pea (Pankaj Bhowmik, Saskatoon, Canada)

15:10-15:25 Tea/ coffee break

Session 2

Chair: Simon Berry, Limagrain

15:25 Industry perspective, future breeding challenges & discussion (10 minutes each)

- Pulses for the future – protein crops which fix nitrogen (Paul Billings, Openfolde)
- Yield enhancement factors for pea and faba bean (Charlotte White, ADAS)
- The rise of novel and healthy food uses for pea (Chris Harrison, Novofarina)
- Novel and sustainable industrial products (Luke Browning, Xampla)

16:10 Highlights from students & early-career researchers (4 minutes each)

- Neglected legume crops (Nadia Radzman, SLCU)
- Early detection of root disease organisms (Alba Pacheco Moreno, JIC)
- Crop sensing and machine learning (Leah Howells, PGRO)
- Natural and induced variation in seed phytic acid in faba bean (Callie Rice, Reading)

16:30 Meeting close

Legume nutrition paradoxes: from the grain to the gut

¹Vasconcelos, M.W., ¹Pinto, E.C., ¹Ferreira, H., ¹Geraldo, R., ¹Duarte, R. & ^{1,2}Iannetta, P.P.

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²James Hutton Institute, UK

Adopting eco-friendly diets will demand more plant-based food sources, particularly in the global north. However, social, economic, and cultural barriers jeopardize our goal to shift towards more sustainable dietary patterns. Legume grains are undeniably rich sources of nutrients, but their consumption is also enveloped in a few nutrition-linked paradoxes. This talk will try to address three of these and create some food for thought.

1. Legumes have been proposed as one of the most environmentally, economically, and nutritionally sustainable plant-based protein food sources. However, the current protein craze witnessed in EU markets needs critical thought, and legumes are much more than protein.

2. Legumes are rich in phytochemicals that are often negatively connotated as anti-nutrients. However, these may offer health benefits, influencing the human gut microbiome and demonstrating anti-inflammatory and antioxidant properties. Should we rename them to convey a more positive message?

3. It is speculated that the daily intake of around 100–150g of cooked grain legumes can improve the nutritional quality of a diet and reduce several cardiovascular disease risk factors. But has this been convincingly demonstrated, and for which population types?

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Programme

Impact of Food Processing on the Digestion and Metabolic Effects of Pulses

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² Imperial College London, U.K. ³ King's College London, U.K.

Legumes have several nutritional properties that are of interest for supporting gut and cardiometabolic health. Pulses (non-oilseed legumes) contain a balance of dietary fibre, protein and starch, and are nutritionally well-suited to meeting the nutritional needs of the UK public. Furthermore, regular intake of pulses is associated with reduced risk of obesity and type 2 diabetes. Despite these benefits, UK consumer intake of pulses remains low. Increasing the use of pulse ingredients in mainstream pre-processed food products could improve consumer intakes. However, most processing techniques can also cause major structural changes with implications for how nutrients are digested, absorbed, and metabolised. Currently the nutritional value and health effects of processed pulse-based foods have not yet been widely studied.

We have conducted a series of studies using *in vitro* digestion models and human randomised controlled trials to investigate mechanisms by which food processing influences the digestion and metabolic responses to pulses. These studies were mainly conducted in 'chickpeas' *Cicer arietinum* L. (Kabuli-type) and focused on cotyledon cell wall intactness, building on our earlier observations of cell fracture or separation tendencies of legumes during dry vs. hydrothermal processing ^[1]

The *in vitro* digestibility studies showed that chickpea preparations consisting of damaged cells had a higher rate and extent of starch digestion compared with intact cells. In a study where human participants were fed differentially processed chickpea porridges with identical nutrient compositions, we found that processing-induced changes to plant cell wall intactness altered the structure and composition of intestinal digesta, leading to significant differences in blood glucose and gut hormone responses. In a separate human study, we also showed that incorporation of whole chickpea cells into white bread led to large and significant reductions in glycaemic responses, and dose-dependent increases in gut hormones GLP-1 and PYY ^[2].

In conclusion, these studies demonstrated that intactness of the cell walls of chickpea cotyledon during digestion is a key factor that controls the release of starch during human upper-gastrointestinal transit and impacts postprandial responses involved in glycaemic control and appetite regulation. Furthermore, the desirable low-glycaemic properties of pulses were found to be compromised when foods were made from dry-milled pulse flour, which contained mainly damaged cells. These mechanistic insights have led us to develop a legume-based ingredient – a unique whole cell legume flour called 'PulseON[®]', which is being pursued commercially to deliver the next generation of healthier processed convenience food products. Overall, these studies demonstrate how the structural transformation of pulses during food processing can have a significant impact on postprandial metabolic responses. The findings are important for realising the nutritional potential of pulses when used in processed food products.

References

1. Edwards CH, et al.. *Nature Food* 2: 118-126, 2021. DOI: [10.1038/s43016-021-00230-y](https://doi.org/10.1038/s43016-021-00230-y)
2. Bajka BH, et al. *Am J Clin Nutrition* 117: 477-489, 2023. DOI: [10.1016/j.ajcnut.2022.12.008](https://doi.org/10.1016/j.ajcnut.2022.12.008)

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Systems thinking to envision a food system that serves public health using novel varieties of common bean.

¹*[Maguire, R. M.](#), & ¹Holub, E.B.

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Does our 'five-a-day' food system serve public health? The current high-volume-low-diversity supply chain does not provide the essential ingredients, but this is not sufficient for public health as evidenced by rising trends of diet-related diseases in the UK. The importance of food diversity and prebiotics (soluble fibre) as key factors for life-long personal health has been highlighted by recent media attention and major evidence-based publications. Diversifying the culinary landscape is therefore critical, and pulses provide the most plausible, desirable, immediate and significant options for health (Didinger and Thompson, 2021) and sustainability gains (Van der Weele *et al.*, 2019).

According to the Family Food survey, 95 g (cooked weight) of pulses were consumed on average per person per week in UK households in the year 2020/21 (Defra, 2023). Data is not available for breakdown of all pulse types, except the separation of the popular processed meal of British style baked beans (78 g canned navy beans, cooked in tomato sauce, equating to ~40 g cooked beans) and canned peas (14 g, which are traditionally eaten as mushy peas) from all other whole pulses (32 g canned, 9 g from dry). This falls drastically short of NHS Eatwell guidelines for 80 g per person/day and the Eat Lancet recommendation of 100 g per person/day. Consuming pulses, especially when cooked whole and eaten as part of a meal, provides an easy solution to address soluble fibre deficits (NHS, 2022), as well as increases phytonutrient intake, and can provide opportunity to consume other healthful ingredients (Winham *et al.*, 2020).

In the BeanMeals project (funded by the UKRI Transforming UK Food System programme), we have been applying multiple systems thinking methods to develop systemic innovations that could improve the balance of health, social, economic, and environmental outcomes by increasing pulse diversity in our food system. For a case study, the multidisciplinary team has been exploring the food system of primary schools, with the research extending across policy, into school canteens and down to household levels. Two new UK registered varieties of common dry bean (*Phaseolus vulgaris*) have been used to disrupt and stimulate thinking about bean production and consumption. The varieties Godiva (a blonde kidney-size bean) and Capulet (similar to imported navy beans) were developed from a wide diversity cross at the University of Warwick specifically for conventional farm production in the UK.

Closed-loop mapping and Viable Systems Modelling have been used to design a Social Enterprise that could provide a direct feedback loop between cooks and farmers. Critical back-casting is being used to improve participatory engagement needed to deliver equitable, accessible and affordable supply of these new varieties. Cooks initially in Midland communities (including households and catering businesses) have been identified as Agents of Change that are critical for providing the demand for dry, whole ingredients needed to incentivise grower uptake to introduce a new field crop into an existing operation. The learning from BeanMeals will help inform the TUKFS toolkits needed to systemically innovate a system, and in particular scale up any 'diversity' ingredient for the table, including additional new varieties of pulses or other crops.

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A Technofunctional and Nutritional Study of Pea Seed with Reduced Antinutritional Proteins

¹Ng'ang'a, R.N., ²Rayner, T., ¹Perez-Moral, N., ¹Cockram, G., ¹Ryden, P., ¹Booth, C., ²Østergaard, L., ¹Wilde, P., ²Domoney, C., ¹Edwards, C.H.

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Sustainable and nutritious protein sources are becoming increasingly essential due to a growing global population and the rising popularity of plant-based diets. Legumes, such as pea (*Pisum sativum* L.), are excellent alternative protein choices due to the overall nutritional richness of their seeds and environmental sustainability of the crop. However, the industrial application of legume-based proteins is so far limited by sub-optimal techno-functional performance. Furthermore, pulses contain antinutritional proteins, which can hinder nutrient bioavailability. This research aimed to evaluate the techno-functional and nutritional properties of proteins isolated from two distinct pea lines: a wild-type control pea and a mutant line carrying null mutations for three proteins with poor nutritional characteristics. The seeds of the wild-type and mutant pea lines were ground, and the isolated protein used to create emulsions and foams. The emulsions were characterized based on their particle size, zeta potential, microstructure, and stability over time. Additionally, foams were characterized based on their foamability and stability. To gain further insight into the surface activity of pea proteins, the pendant drop method was used to measure their surface tension and interfacial properties. The findings revealed that proteins from both pea lines effectively stabilized emulsions over a 24-hour period. Emulsion stability was observed to have a positive correlation with the following factors: small droplet sizes, high zeta potential, and specific oil and protein concentrations. Minor differences were observed in the foaming properties of the two pea protein isolates. However, it was noted that foaming stability depended on high protein concentrations, a threshold that was not achieved in this study. In conclusion, this research demonstrated the similar techno-functional properties of wild-type and mutant pea lines, underscoring their potential for industrial use. Future research will utilize static in vitro simulation of gastrointestinal food digestion (INFOGEST 2.0) to evaluate the impact of pea mutations on starch and protein digestibility of cooked food items. Lastly, the study will assess the reduced allergenic potential of the mutant pea, further expanding the understanding of these promising protein sources.

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Breeding legumes for improved quality for the food industry

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Natural resource depletion and climate change pose challenges in meeting future food demand for the anticipated population growth by 2050. Increased consumption of animal proteins, driven by rising incomes and urbanization, contributes significantly to environmental issues such as land and water use, greenhouse gas emissions, acidification, and eutrophication. To address this, a crucial shift from meat-intensive diets to plant protein-based diets, is essential for achieving climate change mitigation targets and ensuring food security. The European food market has witnessed a notable rise in plant-based food retail sales, particularly in meat and dairy analogues. Legumes stand out as a promising source of plant proteins for the Northern European region. However, their cultivation in the North is currently limited due to unstable yields, posing risks for farmers, and suboptimal bean quality for the production of meat and dairy analogues. In my presentation, I will introduce the breeding tools we are developing to enhance legume varieties, with a focus on faba beans, peas, and lupins, catering to the specific needs of the food industry.

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‘Raising the Pulse’: systems analysis of the environmental, nutritional and health benefits of pulse-enhanced foods.

[Peter Jackson](#)¹ on behalf of the ‘Raising the Pulse’ consortium

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The Raising the Pulse project, funded at £2 million from 2022 to 2025, adopts a systems approach to promote healthier and environmentally sustainable pulse-inclusive diets across the UK. Using faba bean flour in addition to wheat flour in white sliced bread, the project aims to showcase overcoming barriers to pulse adoption on a wider scale. Key highlights to date include:

1. **Varietal Impact:** Varieties of faba beans exhibit significant differences in nutrient density and land requirements, emphasising the role of variety selection in influencing health and environmental impacts associated with faba bean-derived food products.
2. **Scalable Milling Method:** The project established a scalable method for milling faba beans into baking flour, revealing major variations in nutrient density across different milling streams. This underscores that protein and iron contents can vary significantly based on specific variety-milling stream combinations.
3. **Nutritional Benefits:** Analysis of UK National Diet and Nutrition Survey data demonstrated that pulse-inclusive diets in the UK are linked to higher energy, fibre, essential vitamins, and micronutrients, while showing lower total and saturated fat and sugars.
4. **Consumer Behaviour:** A systematic review of consumer behaviour towards pulses indicated that health and environmental considerations strongly influence attitudes, with acceptance levels varying significantly based on demographics and lifestyle.
5. **System Mapping:** The project mapped all components of the bread-related food production system, from 'farm to folk,' in preparation for developing a predictive, system-wide model.

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Two auxins are better than one – Chlorinated auxin in pea fruit development

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Legumes (family Fabaceae) comprise the third-largest family of flowering plants and second-largest family of eudicots. Though morphologically extremely diverse, legumes are united by their unicarpellate (single-chambered) fruits, known as pods. Legume pods act as the portal connecting the parent plant to its offspring (the seeds) and represent a fascinating and agronomically significant model of parent-offspring resource allocation.

Across plants, the phytohormone auxin (indole-3-acetic acid, IAA) is essential to global plant development including post-fertilisation fruit growth and seed filling. As a general rule, fruit do not synthesise most of their own auxin and their growth is dependent on the active export of auxin from successfully fertilised seeds. Thus, a lack of seed auxin export gives a mechanism for spontaneous fruit abortion in the event that a flower is not successfully fertilised (e.g. due to temperature stress, pollinator dearth, etc.)

The UK's major legume crops pea (*Pisum sativum*) and closely related faba bean (*Vicia faba*) are unusual among plants in that they produce not only IAA but a chlorinated variant 4-chloroindole-3-acetic acid (4-Cl-IAA). This hormone duplication is evolutionarily recent (~20 million years ago) and is not universal across legumes, which gives a unique opportunity to study the evolution of neo-hormonal signalling systems. In pea, 4-Cl-IAA levels are low in vegetative tissues but accumulate to high levels in developing seeds and fruit. This suggests 4-Cl-IAA is important for fruit growth.

Our lab has taken a combined approach of exogenous hormone application assays, biochemistry and transcriptomics to elucidate both the biosynthesis of 4-Cl-IAA and its *in planta* developmental functions. Excitingly, pea fruit respond differently to IAA and 4-Cl-IAA by an unknown mechanism. The two hormones appear to be antagonistic in that 4-Cl-IAA promotes pod growth while IAA (unexpectedly) is weakly inhibitory to pod growth. Understanding the mechanism by which pea fruit discriminate between these two auxin variants is a major focus of the lab.

We are also currently studying pea endosperm for its halogenase activity, which we have detected *in vitro*, in the hopes of identifying the chlorinating enzyme responsible for 4-Cl-IAA biosynthesis. As over 30% of prescription drugs are halogenated, we speculate that identifying this enzyme may be of relevance to the chemical synthesis sector. Halogenation in plants is poorly understood, and so we have taken a bottom-up approach of enzyme assays and proteomics to identify candidate enzymes for 4-Cl biosynthesis.

Finally, we have been studying the role of GRETCHEN-HAGEN3 (GH3) enzymes, which are endogenous auxin inactivators, in the context of IAA/ 4-Cl-IAA in pea. Through the use of synthetic inhibitors of GH3 activity, we have recently developed a working model for how IAA and 4-Cl-IAA are synthesised, transported, decoded and ultimately inactivated during pea pod elongation.

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Auxin Transport in Pea Fruit Development: Unraveling 4-Cl-IAA Distinctions

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The plant hormone auxin plays a pivotal role in diverse facets of plant growth and development. Within the plant kingdom, five naturally occurring auxins exist: indole-3-acetic acid (IAA), 4-chloroindole-3-acetic acid (4-Cl-IAA), phenylacetic acid, indole-3-butyric acid (IBA), and indole-3-propionic acid (IPA). In the Fabaceae family, encompassing species such as peas and others in the Fabeae and Trifolieae clades, a chlorinated auxin variant arises, denoted as 4-Cl-IAA, characterized by a chlorine atom attached to position 4 of the indole ring. This specific auxin, 4-Cl-IAA, is implicated in fruit development.

Previous research has shown that developing seeds exhibit elevated auxin levels compared to pericarp tissues, suggesting a potential role of seeds as an auxin source for pea fruit development. Intriguingly, only 4-Cl-IAA, not IAA, demonstrates the ability to stimulate growth in deseeded pea pericarps. Thus, intricate spatiotemporal regulation of auxin distribution, particularly via polar auxin transport is of paramount importance for pea fruit growth and development. We investigate whether and how auxin transporters differentiate between these two auxins.

Our preliminary findings reveal that 4-Cl-IAA is transported approximately 10 times faster than IAA in oocyte transport assays. Gaining a fundamental understanding of the mechanisms that distinguish the actions of these two auxins will significantly contribute to our comprehension of molecular mechanisms controlling legume fruit growth and the evolutionary complexity within legume genomes.

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Characterizing natural genetic diversity to support the development of improved disease resistance in temperate and tropical pulse crops.

¹Wood, T. A., ¹Webb, A., ¹Gostkiewicz, K., ¹McAdam, S., ¹Davis, H., ¹Thomas J. E., ² Reynolds, T., ³Santaella, M., ³Gereda, J., ³Wenzl, P., ⁴Arora, S., ⁴Domoney, C., and ⁵Tör, M.

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Legume crops are in a perpetual battle with a range of pathogenic organisms, which can negatively influence productivity and quality when control strategies prove ineffective. Integrated management approaches utilizing specialized agronomic, genetic and chemical approaches are the most commonly used strategies for controlling disease in pulse crops in Northern Europe. More frequent periods of climatic instability, coupled with the loss of chemical controls, are leading to greater demands for new, effective sources of genetic resistance for reducing the effects of disease in crops. Plant breeders aim to mitigate the losses caused by plant pathogens by selecting for new, better-adapted varieties through a systematic process of testing different combinations of alleles to identify the best performing lines. Access to novel genetic diversity is therefore a key element to maintaining crop performance in response to rapidly evolving pathogen populations.

Collections of diverse germplasm, including wild relatives and adapted cultivars (i.e. landraces) can provide important reservoirs of novel disease resistance, helping to support crop improvement initiatives. Unfortunately, novel sources of disease resistance are often identified in backgrounds that are not well-suited to the UK climate, meaning they can be overlooked due to the time and cost required to introgress novel alleles into breeding programs.

Efforts and insights into characterizing novel sources of disease resistance against major pathogens of faba bean (*Vicia faba*) and common bean (*Phaseolus vulgaris*), such as chocolate spot, downy mildew, anthracnose, and web blight, will be discussed. We will demonstrate how classical pathology, genetics and genomic techniques have been combined to identify, characterize and in specific cases to map important sources of diverse genetic resistance in pulse crops, creating valuable resources for breeders and researchers. We will demonstrate the utility and limitations of bi-parental mapping populations for characterizing complex quantitative resistance and describe efforts to develop more advanced association genetics approaches to overcome this.

We will also discuss how genomics has been applied to improve understanding of how genetic variation in crop pathogens is contributing to disease and how this can influence virulence and race-structure in downy mildew of pea and faba bean (*Peronospora viciae* f. sp. *pisi* and *P. viciae* f. sp. *fabae*, respectively). We will demonstrate how the recent re-sequencing of contrasting *P. viciae* f. sp. *pisi* race-types can be utilized effectively to identify differences in effector complement, how mildew isolates group according to their geographic origin when compared phylogenetically, and also highlight some of the potential limitations of differential screening in genetically uncharacterized host material for defining race-types defined by major gene-for gene resistance.

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Towards RNA-based downy mildew control in pea plants

¹Tör, M., ¹Göl, D., ¹Okechukwu, E., ¹Osborn, R., ¹Ünal, G., ¹Jin, W., ¹Fu, W., ¹Hong, Y., ²Studholme, D., ³Castillo-Machuca, I., ³Sherif, S., ³McDowell, J., ⁴Webb, A. and ⁴Wood, T.

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⁴NIAB, UK

Peas (*Pisum sativum*) serve as vital components in sustainable farming due to their rich nutritional profile. However, downy mildew disease, caused by the pathogen *Peronospora viciae* f. sp. *pisi* (*Pvp*), poses a significant threat to pea yield and quality.

Current control methods, relying on pesticides and genetic strategies, face challenges. In our collaborative projects, we investigated pathogenicity and developmental genes in downy mildew pathogens, employing a model system *Arabidopsis-Hpa* (*Arabidopsis thaliana-Hyaloperonospora arabidopsidis*), and focusing on the pea-*Pvp* and lettuce-*Bremia lactucae* pathosystems.

Using chemically synthesized short, synthetic, double-stranded RNAs (SS-dsRNAs), we targeted over 100 genes in *Hpa*. Notably, 47 SS-dsRNAs halted germination, while 32 increased it. Additionally, 25 SS-dsRNAs inhibited infection, 13 increased sporulation, and 42 decreased sporulation compared to the controls.

Transferring the SS-dsRNAs-mediated gene silencing approach to *Pvp*, we identified orthologs of *Hpa* genes inhibiting infection. Plant pathology and molecular biology techniques, including infection assays and qRT-PCR, confirmed the observed inhibition of *Pvp* on pea plants. Further, we conducted infection inhibition studies with chemically synthesized and *E. coli*-produced dsRNA of various lengths. Our findings provide promising evidence for the development of Spray Induced Gene Silencing (SIGS) to control downy mildews on peas and other crop plants.

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Putting root rot on the spot: characterising genetic sources of resistance against pea root diseases

Nicolas Trenk¹, Jitender Cheema¹, Alba Pacheco-Moreno¹, David Gilbert¹, Jane Thomas², Claire Domoney¹, Ellen Sizer-Coverdale³, Noel Ellis¹, Sanu Arora¹.

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A major constraint to worldwide pea production is a soil-borne pathogen complex mainly consisting of *Aphanomyces euteiches*, *Fusarium spp.*, *Pythium spp.* and *Rhizoctonia solani*. These pathogens cause damping-off, seedling blight and root rot, resulting in significant yield losses. With limited effective chemical treatments, genetic resistance emerges as the most promising control strategy. Previous studies on partial resistance to the complex member *Fusarium solani* f. sp. *pisi* (Fsp) identified a major QTL on linkage group II as well as two minor QTLs on LG III [1]. However, the underlying genetic factors still need to be elucidated. The aim of this work is to identify novel as well as characterise existing sources of resistance to root rot pathogens utilising the genetically diverse *Pisum* germplasm collection available at the John Innes Centre, a subset of which has recently been sequenced.

For efficient Fsp resistance screening of the germplasm, we developed multiple axenic high-throughput phenotyping approaches. Initial screens of 300 accessions have revealed significant phenotypic variation, which was summarised into a 5-level scoring scale capturing the extent of lesion restriction. This ranged from soft and rotten tap roots with severely impeded lateral root formation to only minor discolouration with unimpeded lateral growth. A 10-day time course experiment involving microscopic analysis with fluorescent staining (WGA-AF-488) of fungal colonisation in root cross-sections of susceptible and partially resistant genotypes confirmed the correlation with the phenotype. Moreover, contrasting phenotypes were observed in several lines which have biparental crosses available. Notably, a partially resistant landrace and a susceptible cultivar are parents of a recombinant inbred line (RIL) population. A pilot experiment involving QTL mapping of 207 RILs with 18,349 markers was able to identify a significantly associated peak on linkage group II.

The initial results are being followed up by further screening of a larger number of RILs from the biparental population, particularly those with recombination in the peak-region to fine map the underlying genetic factors. This is further supplemented by an RNA-seq study investigating differential expression at various crucial infection timepoints identified through our histological studies. Additionally, the observed phenotypic variation across the panel provided further confidence in utilising the genetic diversity of our germplasm collection effectively with high-throughput phenotyping methods. Future work will involve Genome-Wide Association Studies (GWAS) and validation of identified QTL. Further work on the microscopic elucidation of disease progression using various staining techniques will provide insights into the plant-pathogen interactions underlying partial resistance.

References

1. Coyne, C.J., et al., *Confirmation of Fusarium root rot resistance QTL Fsp-Ps 2.1 of pea under controlled conditions*. BMC Plant Biology, 2019. 19.

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Chocolate Spot Response in Faba Bean: Comparative Assessment of Two Disease Assays for Detecting Intermediate Resistance in Diversity Panels

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Faba beans are an inexpensive, readily available source of protein, complex carbohydrates, vitamins, and minerals, making them a valuable food and feed commodity. Their rising importance in Europe has increased demand for knowledge surrounding biotic stresses affecting their yield.

Chocolate spot (CS) is one of the major diseases compromising yield stability in faba bean, especially in the British Isles. Presently, growers heavily rely on fungicides for maintaining yield, and long rotations are required to keep inoculum levels low. However, with more severe fungicide policies and increased demand, alternatives, such as CS resistant cultivars, need to be investigated, to secure faba beans as a viable European protein crop.

This study aims to assess rapid disease screening methods for identifying genetic sources of resistance to CS. The ProFaba diversity panel, consisting of 220 faba bean lines previously genotyped and yield-tested in European field conditions, was used for screening studies.

An Irish isolate of *Botrytis fabae*, the lead causal species of CS, was used in all levels of disease screening. We will discuss the results of different levels of screening assays, with detached leaf and whole plants in controlled conditions and whole plants in field conditions. Preliminary results of a genome wide association study (GWAS) are also presented utilizing scoring data and quantitative outputs of disease image analysis. Additionally we will explore the results of a CS field trial involving twenty faba bean varieties in the context of Irish conditions. While no complete resistance to CS was observed, preliminary quantitative trait loci are proposed for further investigation into the faba bean genome

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Identifying adaptations and admixture in common bean: why do we need pangenomes and genomic platforms?

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Our group is focused on identifying beneficial adaptations in landraces that can be incorporated into improved genetic backgrounds. We are also developing genomic resources and tools to support crop breeding programmes.

As the impact of climate change becomes more apparent, it is increasingly important to improve the fitness and genetic diversity of crops. One approach to achieve this is through the integration of adaptive introgressions from related or same species. Common bean (*Phaseolus vulgaris*) is an ideal model to study spontaneous gene flow between genetic pools because it has been independently domesticated twice, resulting in the Andean and Mesoamerican gene pools. We are examining a diversity panel of nearly 150 common bean accessions, particularly those from Colombia and nearby regions, where the two gene pools converge. Our aim is to investigate the relationship between population structure and photoperiod sensitivity, a trait that is likely linked to early agricultural selection. We have also developed alignment-based methods to identify genome-wide hybridization and introgression, which we intend to link to this trait's QTLs.

In addition, we are collaborating with breeding partners trying to boost genetic gain through genomics. Our research demonstrates that the use of haplotype-resolved reference genomes can greatly benefit GWAS and Genomic Selection. I will explain how the use of long-read and Hi-C technologies has effectively resolved the "assembly problem" regardless of ploidy and heterozygosity levels. Furthermore, it has opened doors for the development of multi-accession references or pangenomes, which I will compare to single and no reference association mapping. Finally, I will introduce the "Legume Generation" consortium and a new Legume Trial Data Platform that we are developing in collaboration with more than 30 breeding institutions as part of it.

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Legumes in Ensembl Plants

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Ensembl Plants is an integrative resource presenting genome-scale information for the analysis and visualisation of plant genomic data. Ensembl produces genome databases and can be freely accessed through our web browser, API and BioMart tools.

We currently host over 125 species with more than ten legumes including soybean, pea and cowpea. The faba bean genome has been added recently into Ensembl Plants while the assembly for *Medicago truncatula* has been updated. Our platform provides access to genome annotations and comparative genomics analyses including homology predictions and multiple genome alignments. We plan to increase the number of legume genomes available and work with the community to incorporate key species and data sets to support legume research and breeding.

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Prospects for the genetic improvement of protein traits in faba bean

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Faba beans are valued, mainly, as a protein source in food and in feed. Producing varieties with more, and better quality, protein would therefore seem a natural objective for breeders. Yet, while breeding efforts have delivered steady gains in yield, any improvements in protein content made over the last decades have been much less apparent, and very little attention has been given to protein quality. This is in spite of a clear industry appetite for higher protein varieties and a growing interest in the nutritional and processing qualities of faba protein. Though the reasons for this apparent lack of progress may be manifold, two obvious hindrances are the high costs associated with protein phenotyping and potential trade-offs between desirable traits such as high protein content and high yield. In light of these considerations, we sought to gain a detailed understanding of the correlations between seed protein phenotypes and important agronomic traits in diverse germplasm, and to evaluate the potential of marker-assisted/genomic selection in improving faba protein.

To these ends, more than 200 inbred lines covering much of the genetic diversity available to European breeders were phenotyped for amino acid contents, protein sub-unit composition, protein content, sulphur content, yield, seed weight and days until end of flowering. Targeted genotyping was performed using single primer enrichment technology, yielding ~750,000 good quality SNP markers. With these data in hand, correlations between traits and their respective variance components were estimated using Bayesian multivariate mixed models. GWAS and genomic prediction were conducted using linear mixed models and Bayesian whole genome regressions.

Our results were consistent with widespread genetic correlations both within protein traits and between protein traits and agronomic traits. Though some of these correlations indicated potential genetic trade-offs, in all such cases there existed substantial genetic variation orthogonal to the trade-off axis. That said, the undesirable correlation between protein content and low yield was not limited to the genetic effects, the estimated correlation of the genotype by environment effects being -0.5. Certain trade-offs may, therefore, be difficult to avoid completely "in the field". In contrast to these potential trade-offs, we also found strong evidence of positive genetic correlations between desirable protein quality traits and protein content. GWAS discoveries included both novel and replicated marker-trait associations, some of which could be put to practical use in marker assisted breeding schemes, especially for protein quality. Similarly, we were able to generate genomic prediction models with practically useful predictive accuracy for highly complex traits, with a relatively simple GBLUP model explaining ~23% of the protein content variance in hold-out samples.

Our results suggest viable improvements can be made with no penalty on genetic yield potential and point to paths by which such trade-off free gains can be made. Weighing up the costs and benefits, marker based selection schemes will probably be more easily and immediately used in breeding for protein quality. If genomic selection is to substantially replace phenotypic selection for protein content, larger populations may be required for model training, particularly if very broad swaths of diversity are to be accessed. In less diverse populations of similar size, gains from genomic selection may be made more easily.

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Genomic advances in underutilised legumes

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Humans rely on a surprisingly narrow amount of genetic diversity (both in terms of the range of crops, and the varieties of each) for their food. In addition to these staple crops, there are hundreds of underexplored minor crops, representing opportunities for further investigation in terms of nutrients and climate resilience. In this talk, I will discuss recent advances made for these underutilised legumes from a range of viewpoints, and how we might be able to combat the barriers to their full utilisation.

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**UKLRC 2024 Annual Conference &
PCGIN Annual Stakeholder meeting
Programme**



The Funding Landscape

16:45-16:55 Dr. Emma Markham (BBSRC, UKRI)

“BBSRC funding opportunities for legume researchers”

16:55-17:05 Paul Laniran (InnovateUK, UKRI)

“Funding opportunities at Defra-funded Farming Innovation Programme”

Development and use of rhizobial inoculants to improve Biological Nitrogen Fixation by pulse crops in the UK

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Pea (*Pisum sativum*) and faba bean (*Vicia faba*) are the most important grain legumes grown in the UK and are a valuable source of dietary protein and fibre for humans and animals. They are capable of forming a root nodulating symbiosis with Nitrogen (N)-fixing soil bacteria called “rhizobia”, and this symbiosis can provide them with all their N-requirements without any need for additions of N-containing fertiliser. The amount of N fixed by faba bean ranges from 100 - 400 kg Ha⁻¹ depending on the climatic conditions [1]. This means that in addition to their commercial value as crops they may also present a substantial saving in terms of offset-fertiliser costs. If managed appropriately they may leave a substantial residue of N in the soil (50 - 100 kg Ha⁻¹) for the following non-legume crop. Pea and faba bean are also closely related to lentils (*Lens culinaris*), vetches (*Vicia* spp.) and vetchlings (*Lathyrus* spp.), and all are nodulated by the same type of rhizobia, *Rhizobium leguminosarum* species complex sv. *viciae* or “Rlv”. All these species of legume will nodulate spontaneously in UK soils, which contain substantial populations of Rlv, suggesting that there should be no need for the application of rhizobial inoculants. However, even when nodulation appears to be adequate for the needs of the plants it is not certain that the most effective strains of Rlv (in terms of N-fixation) are the ones that occupy the root nodules; this sub-optimal N-fixation response is considered to be one of the reasons for the commonly reported erraticism in UK faba bean yields. A programme has been undertaken to screen effective Rlv strains from high-performing (in terms of N-fixation) faba bean and pea plants from several sites in the UK. Some of these can significantly out-perform the current commercially available inoculants under greenhouse conditions. These data are discussed in terms of whole genome sequences of Rlv strains with a range of symbiotic performances on pea, faba bean and lentils. In addition, data supporting the introduction of novel N-fixing legumes like soybean (and their specific rhizobial symbionts) into northern cropping regions like Scotland are also presented [2].

[1] Maluk et al. (2022) Fields with no recent legume cultivation have sufficient nitrogen-fixing rhizobia for crops of faba bean (*Vicia faba* L.). *Plant and Soil* **452**: 365-368.

[2] Maluk et al. (2023) Biological Nitrogen fixation by soybean (*Glycine max*), a novel, high protein crop in Scotland, requires inoculation with non-native bradyrhizobia. *Frontiers in Agronomy* doi: [10.3389/fagro.2023.1196873](https://doi.org/10.3389/fagro.2023.1196873)

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LIGHT SENSITIVE SHORT HYPOCOTYL (LSH) GENES CONFER SYMBIOTIC NODULE IDENTITY IN *MEDICAGO TRUNCATULA*

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Legumes grow specialized root nodules to host beneficial nitrogen-fixing bacteria that provide the plant with ammonia in exchange for carbon. These symbiotic nodules are distinct from lateral roots in morphology and function as they comprise of cells that can accommodate nitrogen-fixing rhizobial bacteria intracellularly and provide favorable conditions for the biological nitrogen fixation process.

Nodules initiate from the inner tissue layers in response to the perception of rhizobial bacteria at the root surface via cytokinin-mediated upregulation of the nodulation-specific transcriptional regulator *NODULE INCEPTION (NIN)*. Our previous findings that the initiation of lateral roots and nodules converges at a common developmental program^[1] led to the hypothesis that an additional nodule-specific program is required to determine nodule organ identity on top of the shared root-like initiation program.

Here, we show that two members of the *LIGHT SENSITIVE SHORT HYPOCOTYL (LSH)* transcription factor family (*MtLSH1* and *MtLSH2*), predominantly known to define organ boundaries and meristem complexity in the shoot, function as regulators of nodule organ identity. *MtLSH1/2* are upregulated during early stages of nodule development in a cytokinin- and *NIN*-dependent manner and are expressed in dividing cells. Our loss of function analysis of *lsh1/2* demonstrated that these regulators are required for the development of functional nodule primordia that can support the intercellular cortical infection, the intracellular colonization, and nitrogen-fixation by the bacteria.

Furthermore, molecular functional analysis revealed that *LSH1/2* control components of the auxin-cytokinin cross talk and function upstream of and together with the previously identified nodule organ identity genes nuclear factor *Y-A1 (NF-YA1)* and *NODULE ROOT1/2 (NOOT1/2)* to recruit a program with pleiotropic functions in the shoot to differentiate nodules from lateral roots and to determine nodule organ identity. The principal outcome of *LSH1/LSH2* function is the production of cells able to accommodate nitrogen-fixing bacteria, the unique nodule feature. We conclude that the coordinate recruitment of a pre-existing primordium identity program, in parallel to a root initiation program, underpins the divergence between lateral roots and nodules.

REFERENCES:

[1] Schiessl et al., *Curr Biol* 29 (2019). [2] Schiessl et al., *bioRxiv* 528179 (2023).

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CLE sigNal peptides: A potential target for optimising nitrogen efficiency in legumes

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The Autoregulation of Nodulation (AON) mechanism regulates nodule numbers and activity in *Medicago truncatula*. CLAVATA3/ESR (CLE) peptides have been implicated to have a role as a signal in AON. CLE34 has previously not been studied as was first described as a pseudogene without a functional CLE domain in *Medicago truncatula* ecotype A17 due to the presence of a stop codon. However, 99% of other accessions, such as ecotype R108, do not have this stop codon.

The aim of our work is to characterise the CLE34 peptide in *Medicago truncatula*, following the hypothesis that it plays a role in AON and focusing on a hypothesised functional CLE34 in ecotype R108. Alongside this, CLE35 still has yet to be characterised extensively, and is closely related to CLE34, akin to the roles of CLE12 and CLE13, thus may have an overlapping role with CLE34.

Medicago truncatula R108 mutants with insertions in the *MtCLE35* gene have been genotyped and *MtCLE34* mutant plants continue to be genotyped. A split root method is currently being adapted to use to study local and systemic signaling involving *MtCLE34* mRNA and peptide levels/location when inoculated in high and low efficiency strains of rhizobia and in different nitrate soil concentrations.

Preliminary data in the Gifford lab led to the hypothesis that CLE34 and CLE35 are both signals of external nitrogen, thus targeting these genes for future crop improvement studies may lead to generating plants with altered AON, and therefore are capable of producing nodules and having increased yield even in high-nitrogen soils. We therefore hypothesise it will be a possible target for future crop improvement of legumes for higher nitrogen efficiency and therefore larger crops.

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EPFL peptides involve in legume nodulation.

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For almost a century, synthetic nitrogen fertilizers have reaped enormous benefits for crop yields and human life. However, their production and use accelerate anthropogenic climate change and cause extreme soil and water pollution worldwide. Legume crops, such as pulses and beans, are central to global food security and agricultural soil health due to their nitrogen-fixing root symbioses with rhizobial soil bacteria. This symbiosis, which takes place in specialized root nodules, gives legumes access to atmospheric nitrogen for photosynthesis and growth, reducing the need for nitrogen fertilizers, improving soil fertility, and maintaining legume crop yields. However, legume nitrogen fixation efficiency is variable and highly sensitive to environmental stresses such as droughts. In recent decades, there has been an increasing effort to understand and improve the process of nodulation and nitrogen-fixation.

Several plant-derived peptides are now known to control the legume-rhizobia symbiosis, including the CLEs (CLAVATA3/ESR), NCRs (nodule-specific cysteine-rich), and CEPs (C-terminally encoded peptides), among others. Conspicuous by their absence, however, is another family of small secreted peptides, the Epidermal Patterning Factors, or EPFs, better known for their ancestral above-ground roles in processes such as stomatal and vascular development. For example, EPFL9 (EPF-Like 9) is a positive regulator of stomatal development. Recently, we found that these EPFL peptides are also involved in nodulation in *Medicago truncatula*. The involvement of these stomatal-associated EPFs in *Medicago truncatula* rhizobial responses raises tantalizing questions of shared or divergent mechanisms and evolutionary relationships in nodule development programs across the legumes.

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Faba bean as a foundation for climate smart crop- and feed-systems

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Towards enhancing the sustainability and resilience of the UK's crop- and feed-systems, this presentation summarises the objectives and initial insights from a key project undertaken by the Agroecology Group (Department of Ecological Sciences), of the James Hutton Institute (JHI) and associated partners.

There is a focus on the DEFRA-funded, '*Nitrogen efficient plants for Climate Smart arable cropping systems*' or 'NCS' Project (www.ncsproject.co.uk; 2023-27), which comprises 18 industry and research partners to empower the production and processing of UK-grown faba beans. Their approach aims to reduce the GHG emissions of UK agriculture by 1.5 Mt CO₂e per annum, which is 54% of the maximum potential reduction (2.8MT) of the UK ag-industry ([Defra Agri Climate Report, 2021](#)). Half of the reduction (0.7 MT CO₂e) would be attained by replacing 50% (1.8 MT) of imported soybean meal (SBM) with home-grown beans. The remainder of the CO₂e savings achieved mainly via reductions through avoided synthetic nitrogen (N) fertiliser use and N-losses, plus faba bean-based feed formulation. The innovation pipeline to achieve this will be described, including with the details on how you may get involved in NCS-Project activities, and outputs.

In addition to quantifying the potential GHG savings from legume-based feed systems, it is also critical to account for other system attributes, such as ecosystem-services, or -functions, including water quality and soil processes. Therefore, we elaborate on recent findings that highlight the importance of long-term cropped system monitoring, and methodological approaches that integrate ecosystem-impact and -function metrics. Data from JHIs 'Centre for Sustainable Cropping' Life Cycle Analysis (LCA) of cropped systems is used to inform and develop the larger scale 'land use risk assessment' model, GOBLIN ([10.5194/gmd-15-2239-2022](https://doi.org/10.5194/gmd-15-2239-2022), and [10.1038/s41893-022-00946-0](https://doi.org/10.1038/s41893-022-00946-0), respectively). This innovative and ambitious approach aims to allow the assessment of ecosystem-impacts and -functions to be made across scales; and to identify how these may be best-harmonised using scenario analysis.[10.1038/s41893-022-00946-0](https://doi.org/10.1038/s41893-022-00946-0)

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Full of beans: A survey of attitudes and production practices in Europe

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The yield gap is often used to explain why grain legumes occupy such a low proportion of arable land in Europe. Pedoclimatic conditions, sub-optimal management, and limited experience of producing grain legumes are widely accepted as contributing to the yield gap. In 2020/2021 the SUSCROP Legume Gap project carried out a large-scale online farmer survey to explore the relationship between yields and a wide set of pedoclimatic, management, structural, and knowledge factors and to identify areas where farmers require more knowledge. The survey focused on faba and soya in Finland, France, Germany, Latvia, the Netherlands, Poland, Spain, Sweden and the UK. In total, there were 216 responses for soya bean and 547 for faba bean from farms distributed widely across the countries.

The survey questions investigated farm types and land use, farmer demographics including education, experience of growing grain legumes and management practices commonly employed for soya and faba (e.g. irrigation, mechanical weeding, inoculation). Questions were also included on what sources of information farmers used as well as rating the contribution of grain legumes to their cropping systems/farms.

Analysis of the survey data is ongoing using classification and regression tree analysis. So far, the hypothesis that higher experience and knowledge is associated with higher yields has been confirmed for both crops. Farmers identified droughts, weed infestations, and soil characteristics as critical factors determining crop yields. Management of weeds, pests and diseases was particularly important for faba growers. In terms of farmers desire for knowledge, faba bean growers were particularly interested in understanding crop growth while knowledge about market outlets was important for soya producers. The survey results highlight the opportunity to support farmers new to growing grain legumes through advisory services with knowledgeable specialist advisors. Success in early years is likely to encourage producers to go on producing these crops. This is particularly important for crops which are relatively new in Europe, such as soya bean, and could be important for introducing new crops in more Northerly areas as the climate changes.

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Nitrogen Climate Smart - The role of and approach to farmer engagement in valorising arable pulse cropping benefits in the UK

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The potential benefits of including pulse crops in the rotation, such as those to following crops and soil fertility, have been shown by several projects and initiatives. Due to the need for rotational breaks the theoretical maximum for arable land cropped by pulses is 20% of the total, however, the area of pulses cropped in the UK remains below this. Estimates suggest that reaching this potential could contribute to a reduction of 1.5Mt CO₂e per annum (54% of the maximum CO₂e reduction potential for UK Agriculture) through reducing the amount of nitrogen fertilizer applied to rotations and also by reducing the impact of importing soy for animal feed.

The Nitrogen Efficient Plants for Climate Smart Arable Cropping Systems (NCS) is a four-year research programme involving 200 UK farms and 18 partners, funded by the Defra Farming Innovation Programme and delivered by Innovate UK. It aims to 1) model the impact of increasing pulse cropping frequency in the UK in terms of rotational GHG emissions via life cycle assessment using a mixture of real farm data and experimental platforms. 2) aid the uptake of pulse cropping in the UK by providing guidance to farmers on pulse arable production, as well as pulse end uses (focusing mostly on validating the incorporation of faba beans as a livestock feed as a means to create an end market).

This presentation will introduce how the NCS project aims to connect researchers and industry with farmers to collect on farm data and support pulse production. Tried and tested industry initiatives for on farm data collection (the Yield Enhancement Network and Farm Carbon Calculator) will be combined with farmer and industry led field based research to develop a community of engaged farmers sharing cropping data for use in LCA analysis whilst simultaneously exploring the on farm potential benefits of pulses and best practice. This farmer led testing will then be communicated through the web based Pulse Performance Enhancement Platform (PulsePEP), both disseminating outputs and also engaging the wider community of farmers, researchers and industry to contribute their own on farm data and knowledge on best practices. We encourage members of the conference across industry and research to join us in the PulsePEP community.

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Cereal-legume intercropping alters soil microbial processes driving carbon and nutrient cycling

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Intercropping involves growing multiple crops together in the same field. Intercropping cereals and legumes can promote sustainable agriculture through synergies that enhance ecosystem services such as biodiversity, climate resilience, while reducing weed competition and fertilisers inputs relative to monocultures. Research has focused on plant-plant interactions underpinning intercropping benefits; however, little is known about how intercropping affects plant-soil interactions that shape soil microbial processes critical for soil functioning and crop productivity.

Through laboratory experiments, we examined the influence of barley-pea intercropping on soil microbial processes involved in carbon and nutrient cycling. We quantified the effect of barley-pea intercropping on microbial decomposition of soil organic matter (SOM), a sink and source of carbon (C) and nutrients, through continuous ¹³C-labelling. Barley-pea intercropping generally decreased SOM decomposition rates compared to barley and pea monocrops during the vegetative growth stages. By combining continuous ¹³C-labelling with phospholipid fatty acid (PLFA) analysis, we showed that barley-pea intercropping increased net microbial assimilation of root-derived C compared to the average of monocrops, particularly under sustainable soil management. This indicated that barley-pea intercropping decreased SOM decomposition through increased microbial assimilation of roots substrates.

We also evaluated key microbial physiological and functional traits indicative of microbial resource use efficiency, acquisition and utilisation. While barley-pea intercropping did not increase the efficiency of soil microbes to convert root-derived substrates into biomass, it increased microbial catabolic diversity, enhancing the ability to metabolise diverse organic compounds. On the other hand, intercropping predominantly decreased potential activities of carbon, nitrogen and phosphorus acquiring enzymes. Overall, intercropped pea had a predominant influence on microbial processes, likely through enhanced N-rich rhizodeposition.

These findings provided evidence of belowground mechanisms underpinning the beneficial effects of cereal-legume intercropping on soil functioning. However, our understanding of plant-soil interactions in cereal-legume intercropping systems remains limited and requires further on-farm research in collaboration with farmers.

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