PCGIN

Pulse Crop Genetic Improvement Network

PCGIN Newsletter - November 2024

Welcome to the PCGIN Newsletter, bringing you news about research on pulse crops funded by Defra, stakeholder activities and our annual network event. We aim for 2 – 3 newsletters per year.

In this first edition, you can read about:

- The new 5-year PCGIN programme and the main topics of research
- The principal investigators of the programme
- Annual stakeholder meeting, 27 February 2025
- The latest research findings and publications

In future issues we will highlight research staff funded by PCGIN and their great efforts to make new discoveries for the genetic improvement of peas and beans.

What is PCGIN and what is new?

The Pulse Crop Genetic Improvement Network (PCGIN) is one of 5 GINs funded by the Department for Environment, Food & Rural Affairs (Defra). The networks facilitate knowledge exchange between research organisations and industry stakeholders in the UK. The research is informed by problems ‘in the field’ and the participating research organisations provide genetics expertise and resources to breeders, growers and end-users for future commercialization. Furthermore, PCGIN provides links with, and involvement in, legume crop research programmes world-wide.

The new PCGIN programme, running for 5 years from 1 July 2024 to 30 June 2029, is similar to its predecessors in that it is shaped with input from the PCGIN stakeholder base, including an annual stakeholder meeting and industry representatives on the management team. The programme maps onto Defra’s 4 overarching priorities, which are:

- to enhance productivity and food security;
- to enhance environmental sustainability including pest and disease resistance;
- to build resilience to climate change; and
- to improve nutritional and other quality traits.

While continuing the good work on diseases and nutritional traits, the new PCGIN will invest in:

- legumes other than faba bean and pea for the UK, such as lentil and common bean (*Phaseolus vulgaris*);
- collaboration with the Met Office to address challenges from climate change; and
- establishment of a service pipeline for gene editing of faba bean and pea.

Research highlights of the new PCGIN

Pea and faba bean pests and pathogens

In the previous PCGIN project, JIC and NIAB focused on identifying QTLs for downy mildew resistance in both pea and faba bean, as well as foot rot resistance in faba bean. In the new phase of PCGIN, we plan to leverage these loci to support breeding efforts by designing molecular markers and functionally validating some of the underlying genes through gene editing. Additionally, we aim to explore and identify resistance to foot rot and viruses using the pea diversity panel, discover additional sources of foot rot resistance in faba bean, and establish nested-association populations for characterising genes conferring resistance to downy mildew and fusarium foot rot.

Bruchid beetle in faba bean

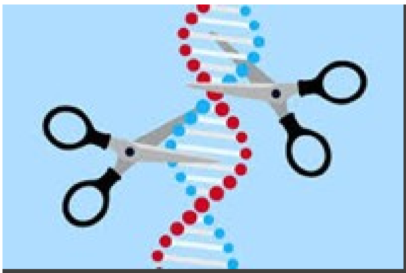
This common pest is becoming more widespread in England and has been found in Scotland recently, although at very low levels. Climate warming and loss of natural predators are thought to be the main factors. Currently, control with insecticides is ineffective. To complement research in France into finding sources of genetic resistance, a PhD student with Donal O’Sullivan at the University of Reading will undertake a molecular study of resistance mechanisms. In addition, a microscopy study into physiological barriers (e.g. thickness of the pod wall or seed coat) at Aberystwyth University will help find clues of how to stop the larvae getting into the seeds.

Seed quality traits

During the previous PCGIN, the groups of Claire Domoney, Janneke Balk and Donal O'Sullivan screened faba bean and pea collections for natural diversity in protein levels, protein composition, phytate and other nutritional traits. Several genetic loci for these traits were found. In the coming two years, the data will be consolidated and genetic markers made available online. We will also organise a workshop with PGRO, attached to the stakeholder meeting on 27 February, to identify premium seed quality traits of interest.

Climate change

This will create challenges for growing pulses in the UK but also opportunities. Together with the other GINs, we will work with Met Office researchers to predict how higher temperatures and changes in rainfall in different UK regions could affect planting dates, possible expansion of legume crops (e.g. lentils, chickpea, common bean), but also pests and diseases. In parallel, the JIC Germplasm Unit and PGRO will explore genetic traits for growing lentils in the UK. We will also screen for drought tolerance, root architecture and heat tolerance during flowering in faba bean and pea.



Gene editing

The legislation of the Precision Breeding Act in England opens new opportunities for crop improvement and could shorten the breeding pipeline from ~10 to ~5-6 years. Unfortunately, gene-editing in pulses is difficult because of a bottleneck with introducing the genetic toolkit into the plants. In the new PCGIN, NIAB and JIC will focus on faba bean and pea, respectively, to develop efficient pipelines for gene editing, targeting genes for downy mildew resistance and specific quality traits.

Meet the PCGIN research leaders...

Janneke Balk, John Innes Centre

Janneke is the new PCGIN award holder, with Sanu Arora as co-lead (see Sanu’s profile below), taking over from Claire Domoney who expertly headed PCGIN for the past 13 years. Janneke started her own research group at the University of Cambridge in 2005 and moved to JIC in 2011.

Combining fundamental and applied research, she is interested in how plants take up iron and other nutrients from the soil and distribute this to leaves and seeds. This includes iron accumulation in pea seeds and iron delivery to nitrogen fixing nodules. She has been involved with PCGIN since 2021, to unravel the genetics underlying protein, starch, sugars and other compounds in pea seeds.

Janneke is originally from the Netherlands and did her undergraduate degree at Wageningen University. She is from a farming background: Her granddad grew common beans up to 1980 and a 19th century ancestor won prizes for breeding a dark brown ‘capuchin’ pea variety!

Website: Janneke Balk

Sanu Arora, John Innes Centre

Sanu is co-lead of the new PCGIN with Janneke Balk. She started her independent research group in November 2021 at JIC and has since been working within PCGIN.

Her research focuses on understanding the molecular foundations of key diseases affecting the pea crop, including downy mildew, root rot and viruses. Using *Pisum* germplasm and advanced genomic tools, she is developing novel gene discovery methods to harness the genetic diversity present in natural populations. This work aims to identify novel genes and alleles to introduce into modern cultivars to build a resilient pea crop. Sanu is also pioneering the development of rapid diagnostics for soil microbiome composition.

In addition, Sanu collaborates closely with European legume researchers and leads the pea innovation community within the "Legume Generation" project. This initiative focuses on developing resilient pea cultivars adapted to diverse environments. Sanu is originally from India and has collaborated closely with agricultural institutes focused on pulse breeding.

Website: Sanu Arora

Donal O'Sullivan, University of Reading

Donal has been involved in legume improvement since his 1997 PhD on common bean anthracnose and has been a co-investigator of PCGIN since 2010. His research team has been at the forefront of developing and characterising high quality inbred diversity collections and mapping populations for faba bean, as well as developing pioneering bean genotyping platforms, high density genetic maps and ultimately complete sequencing of the 'giant' bean genome. These tools have been put to good use in the discovery of the precise DNA sequence variants explaining zero tannin, pale hilum and low vicine quality traits. In the course of the present PCGIN cycle, the group will further refine the 'toolkit' by developing a large collection of sequenced mutagenized bean lines and screen these for more complex traits such as heat, drought and bruchid resistance, as well as protein and micronutrient content.

Beyond discovery genetics, Donal co-leads the £2m 'Raising the Pulse' project which takes a systems approach to removing barriers to better utilisation of faba beans in food manufacture and leads a new 'Fabaplus' BBSRC Follow-on Fund project which aims to breed novel high protein bean varieties.

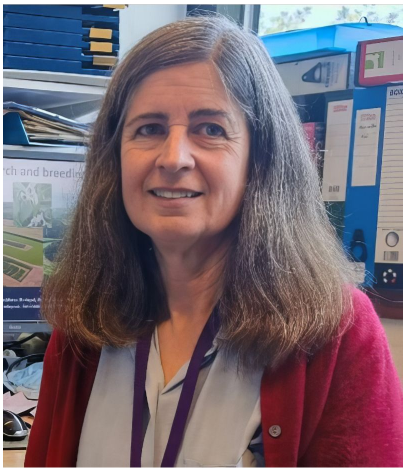
Website: Donal O'Sullivan

Tom Wood, NIAB

Tom is a senior program leader in the Plant Pathology Department and has worked on PCGIN since 2012. Tom’s research utilizes genetics and genomics techniques to improve understanding of host-pathogen interactions in faba and common bean. This is achieved through characterizing novel sources of resistance to facilitate the breeding of better adapted varieties and by elucidating the genetic mechanisms regulating virulence in various important diseases. Recent work has included using classical genetic mapping to identify molecular markers linked to resistance to chocolate spot caused by *Botrytis fabae* and fusarium foot rots within PCGIN, developing association genetics resources for discovering multiple novel sources of resistance to downy mildew in diverse faba bean collections and investigating differences in downy mildew race structure. Tom has acted as PI and Co-I for a range translational research projects, collaborating with academic and industry partners to support crop improvement efforts both in the UK and overseas, including efforts to optimize genetic transformation procedures for faba bean.

Website: Tom Wood

Catherine Howarth, IBERS, Aberystwyth University



Catherine leads the Grains for Health and Pulse Breeding teams at IBERS. Her research focuses on the use of genetic and physiological tools to understand the genetic control of agriculturally important traits, in particular improving the seed quality and abiotic stress tolerance of peas, beans and oats and the application of novel breeding and phenotyping technologies to incorporate these traits into improved plant varieties. She has considerable experience of leading large multidisciplinary projects and collaborating with industry and has been Principal or Co-Investigator on a series of projects involving academic and industrial partners. Seven winter faba bean varieties currently commercialised and marketed by Senova were bred by Catherine's team at IBERS as part of a long term collaboration with UK Pulses which is a joint venture between Senova and Wherry's. These include the variety Vespa which dominates UK production of winter faba beans. She is also involved in a number of EU-funded projects exploiting genetic diversity in peas and beans and their potential for increased cultivation by European farmers, determining their ecosystem services and developing new food products.

Website: Catherine Howarth

Becky Howard, PGRO

Becky Howard is the R&D Manager for PGRO and has worked in the legume industry for 30 years. She has experience of managing large, collaborative projects (UKRI/ AHDB), and oversees PGRO's efficacy trials team and laboratory services. Becky has trials management experience with specialisms in general agronomy, agricultural entomology and plant pathology of UK legumes. Her research has focussed on insect pests of UK pulses including the development of prediction and monitoring tools, and integrated techniques to manage pests and diseases for improved crop productivity. The team at PGRO carries out research to improve pulse agronomic knowledge and increase crop productivity, conducting the research on behalf of farmers. The organisation was established by growers in 1944

and as the UK's centre of excellence for peas and beans, PGRO has a long and highly valued track record of providing authoritative, up to date information and project work based on solid, reliable research. PGRO is a non-statutory levy body supported by grower members, and the UK trade.

PGRO website - Becky Howard

PCGIN Stakeholder meeting

When: Thursday 27 February 2025, approx. 10.00-17.00

Following the UK Legume Research Community meeting, 25-26 February

Where: Kew Gardens, Richmond, London

Programme and sign-up information to follow

Research findings and publications

There is always a lot going on in the participating research organisations!

For every newsletter we will select a small number of topics to highlight, especially linked to new research publications or reports. Here we focus on:

- **New faba bean germplasms with resistance to root rot and foot rot**
- **Genetic resources: induced mutant populations in faba bean and pea**
- **Pea protein: mapping loci for variation in protein composition**

In the next issue, we will look at:

- Working with the Met Office to model climate impacts on UK legume crops;
- Trials of UK-adapted lentils, common bean and chickpea;
- The Precision Breeding Act and gene-editing.

New faba bean germplasms with resistance to root rot and foot rot

Faba bean plants with severe symptoms of root rot (above) and moderate resistance (below).

Tom Wood and his team at NIAB have been selecting faba bean lines with resistance to *Fusarium* sp. that cause root rot and foot rot. In the 3rd generation offspring (F3), ‘families’ of resistant lines were selected. They are crossing lines with good resistance to lines with better agronomic traits. The lines will be transferred to NPZ Ltd for breeding while the results are written up to be published.

(Milestone 85 of the previous PCGIN programme, completed in September 2024)

Genetic resources: induced mutant populations in faba bean and pea

Collections of faba bean and pea varieties have, over the years, been great resources for breeders to improve specific genetic traits, such as disease resistance, sugar and starch properties or seed coat colour. These collections were brought together in the previous century by researchers who travelled all over the world (thanks the British empire…), capturing material from different climate regions that were partially domesticated by local growers.

With a better understanding of genetics in the 1980s, researchers started to induce DNA mutations using chemicals or radiation. Lots of interesting phenotypes were found, but it has been difficult to find the mutated genes because of the large size of pulse genomes. Now that the genomes have been sequenced, the groups of Donal O'Sullivan and Janneke Balk are developing new mutant populations in faba bean and pea, respectively, using PCGIN funding. The mutagenesis of faba bean was funded by the previous PCGIN, whereas the initial work on pea has been funded by BBRSC and will be continued under the new PCGIN. Part of each collection will be sequenced, either the combined coding gene sequences or the whole genome.

For pea, please contact Janneke Balk, Janneke.balk@jic.ac.uk, if you are interested in mutations (alleles) in specific genes. From January onwards we will be able to do TILLING on the population.

(Milestone 87 of the previous PCGIN and new milestones for 2025)

Pea protein: mapping loci for variation in protein composition

Pea seeds are a valuable source of plant proteins for human and animal nutrition. In addition, pea protein has ever more industrial applications, for example for meat and dairy alternatives. Pea protein is a mix of different seed storage proteins and their relative abundance affects digestibility and functional properties. Thus, understanding the genetic basis of seed protein composition is crucial to enhance both protein quality and nutritional value through breeding.

Ahmed Warsame in the Balk group has characterized variation in seed protein composition in a diversity panel of 209 pea lines. The lines were grown at the John Innes Centre field station for two consecutive years in 2021 and 2022. Using association mapping, variation in proteins was compared with genetic knowledge of each line, in the form of high-density DNA markers along the entire pea genome. Lots of whizzy computing then found several regions in the genome that are likely to contain genes of interest for protein variation. Candidate genes include those for specific seed proteins (convicilins, legumins, lipoxygenases) and genes involved in protein biosynthesis, trafficking, and modification. This comprehensive genetic mapping study serves as a foundation for future breeding efforts to improve protein quality in pea and other legumes.

The paper has been submitted for publication and can be viewed here:
https://doi.org/10.1101/2024.07.04.602075