Legume Generation

Boosting innovation in breeding for the next generation of legume crops for Europe

Progressing the breeding of pea

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Legume Generation Report 11

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Legume Generation

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Contents

Summary

This report sets out the progress that has been made up until August 2024 in Legume Generation in boosting the breeding of pea.

The Pea Innovation Community (PIC) was established to address pressing challenges in pea cultivation while unlocking the crop's potential for sustainable agriculture and protein diversification. Since its launch, the PIC has made substantial progress in building a coordinated research community, generating genomic and phenotypic resources, and establishing the community infrastructure required for pre-breeding. In particular, we have made progress in:

(i) community building with active engagement across academic, public-sector, and commercial partners;
(ii) characterising the *Pisum* diversity panel, consolidating genomic data and establishing a reference set for trait discovery;
(iii) delivered multi-trait phenotyping across various environments, generating robust datasets on key traits relevant to climate resilience and yield; and
(iv) established a pipeline linking phenotypic data with genotypic information, enabling preliminary trait–genotype analyses and preparing the groundwork for marker development, thereby creating new opportunities for integrating pea into both public and private breeding pipelines.

In the next steps, we will focus on expanding and integrating the multi-location trial datasets, advancing trait–genotype association analyses using pangeome approach, and developing new collaborative partnerships to extend the reach of PIC resources. These activities will support the generation of markers and pre-breeding lines for deployment within partner breeding programmes. The collaborative model has fostered new academic–industry partnerships, training opportunities, and international exchanges that will strengthen innovation capacity in legume research beyond this project.

Beyond the immediate benefits to breeding programmes, we believe we will contribute to food security and sustainable development by:

- supporting the development of climate-resilient pea varieties by establishing a platform for sharing genomic data, diversity panels, and trial results; and by

- building a collaborative community of breeders, researchers, and industry stakeholders can jointly define priorities and share outcomes. This community-driven approach increases the likelihood that innovations will be translated into practical breeding solutions.

Introduction

Pea is one of the first domesticated crops and remains an important legume with significant nutritional and environmental value. The combination of biological nitrogen fixation and the yield of high-quality plant protein for human consumption give pea an important role in sustainable agriculture and protein diversification. Different types of pea have been developed for various uses. However, the two main categories are dry (grain) pea and vegetable (green) pea. The Pea Innovation Community (PIC) is primarily focused on the genetic improvement of dry pea which is important due to its diverse applications in processing industries, ease of scalability, and growing market demand, particularly to reduce dependence on imported soya.[1]

Current challenges: Despite its many advantages, both yields and quality of pea are threatened due to the increasing frequency of climate extremes, particularly drought and heat stress. For example, in the UK in 2025, pea growers in eastern regions have reported up to a 30% reduction in grain yields due to exceptionally dry conditions following the warmest and driest spring in over 100 years.[2] Climate change is also driving higher levels of pest and diseases, further limiting productivity. Key challenges affecting pea production are summarised below in Table 1.

Table 1: Key challenges affecting pea crop production

Category	Main challenges
Climate stress	Drought, heat stress
Fungal/oomycete diseases	Root rot (soil fatigue), downy mildew, ascochyta blight
Pests and viruses	Viruses transmitted by insect vectors, pea moths

Emerging opportunities: Recent developments are creating a favourable environment for innovation in pea research and breeding. These include the availability of large-scale genomic resources, such as multiple reference genomes and fully sequenced diversity panels[3,4], as well as high-throughput phenotyping platforms that enable more precise trait identification, marker development and genetic selection. At the same time, the rapidly growing consumer demand for plant-based proteins is driving renewed interest in pea as a sustainable and versatile crop.

The PIC aims to bridge academic research and breeding practice by harnessing these genomic tools and germplasm resources, conducting trait-focused phenotyping, and fostering collaboration to develop tools to accelerate pea pre-breeding. Our approach integrates multi-location trials with partner institutions, comprehensive data analysis, and targeted studies on stress resilience, yield traits and disease resistance. A notable example of how academic research has translated into breeding impact is the work carried out at

[1] de Visser, CLM., Schreuder, R., Stoddard. F., 2014. The EU's dependency on soya bean import for the animal feed industry and potential for EU produced alternatives. OCL, Oilseeds and Fats, Crops and Lipids 21: D407. https://doi.org/10.1051/ocl/2014021

[2] BBC News. July 2025. Pea shortage fears over earliest harvest in years. Available at: https://www.bbc.co.uk/news/articles/c9dg2ll5172o

[3] Feng, C., Chen, B., Hofer, J., et al., 2025. Genomic and genetic insights into Mendel's pea genes. Nature 642, 980–989. https://doi.org/10.1038/s41586-025-08891-6

[4] Yang, T., Liu, R., Luo, Y., et al., 2022. Improved pea reference genome and pan-genome highlight genomic features and evolutionary characteristics. Nat. Genet. 54, 1553–1563. https://doi.org/10.1038/s41588-022-01172-2

JIC on pea morphology.[5] The identification and deployment of the *af* and *st* mutations led to the creation of the 'Filby' leafless pea and ultimately the widely adopted semi-leafless pea. This breakthrough not only solved mechanisation challenges but also delivered agronomic benefits, reshaping pea breeding and production in the UK.

Progress on key activities and results

We have worked on:

1. building the Pea Innovation Community (PIC);
2. establishing a *Pisum* diversity panel and line selection;
3. preparation and distribution of seeds to partners; and on
4. field trials at partners' locations

The following describes these activities in detail:

Building the Pea Innovation Community

We have successful built a network of academic researchers from six institutions and three breeding companies (KWS, DANKO, RAGT). The partners bring together pea genetic resources and their expertise in genomics, phenotyping, pathology, and breeding (Table 2). The John Innes Centre (JIC), with its long history of pea research in support of breeding, contributes its historical pea collection which forms a backbone for our innovation community. Aberystwyth University provides access to its high throughput phenotyping platform to enable screening of the diversity panel for complex traits such as drought tolerance. Researchers at SERIDA are evaluating diverse germplasm for local adaptation under organic farming systems, while experts from University of Oxford, IPK and SRU provide input into the design and implementation of phenotyping trails.

Our breeder partners contribute valuable practical knowledge of the crop. They identify gaps for pea improvement, conduct phenotyping trials across multiple locations, and help bridge these gaps by selecting promising lines. This work is establishing a pre-breeding programme for dry pea, with a particular focus on high yield, cold resistance, resilience to both diseases and climatic stress. The discussions during IC meetings provide a forum for experimental planning, germplasm exchange, and decision-making to guide next steps.

We have extended our collaboration beyond the core IC. For example, in the UK., we maintain regular interactions with partners in the Defra Pulse Crop Genetic Network (PCGIN), which supports the exchange of genetic material and strengthens international links. Engagement with stakeholders at annual meetings has created additional opportunities, including the establishment of a new doctoral studentship with one of our industrial partners. Starting in October this year, this project will investigate the genetic basis of downy mildew resistance in pea.

Table 2: Pea IC member profiles

[5] Tayeh N, Hofer J.M.I, Aubert G, et al. (2024), afila, the origin and nature of a major innovation in the history of pea breeding. New Phytol. 243, 1247-1261. https://doi.org/10.1111/nph.19800

Name	Role	Organisation
Klaus Oldach	Private-sector plant breeder; researcher	KWS
Donal Murphy-Bokern	Policy specialist; research director	DMB
Laurent Gervais	Private-sector plant breeder	RAGT
Ivo Rieu	Researcher	SRU
Eric Visser	Researcher	SRU
Ana Campa	Researcher	SERIDA
Juan Jose Ferreira	Public-sector plant breeder; researcher	SERIDA
Małgorzata Niewińska	Private breeding company	DANKO
Agnieszka Katańska-Kaczmarek	Private breeding company	DANKO
Amelie Detterbeck	Private seed sector association	EURS
Lars Østergaard	Researcher	UoO
Lars-Gernot Otto	Researcher	IPK
Jasmin Karer	Network	DS
Catherine Howarth	Researcher	ABER
Sanu Arora	Researcher	JIC

Pisum diversity panel and line selection

We selected a core diversity panel from the widely used John Innes *Pisum* Germplasm Collection (https://www.seedstor.ac.uk/). This collection comprises a wide range of wild and semi-cultivated material, together with landraces and cultivars originating from many regions around the world. Approximately 800 lines from this collection have been whole genome sequenced to an average coverage of 20x per accession.[3] From this wider resource, the Pea IC selected a core set of 256 lines based on multiple criteria: genetic diversity, parental representation of mutant and mapping populations, seed availability, and inclusion of accessions representing *Pisum fulvum*, *Pisum elatius*, *Pisum humile*, and *Pisum abyssinicum*, along with the majority being *P. sativum* landraces and cultivars. The genomic diversity of these accessions has been summarised in a *k*-mer matrix, which revealed phylogenetic relationships among the panel members (Figure 1). This *k*-mer matrix will serve as the foundation for genotype–phenotype association mapping to identify loci linked with key agronomic traits.[6]

[6] Gaurav K, Arora S, Silva P, et al. (2022) Population genomic analysis of *Aegilops tauschii* identifies targets for bread wheat improvement. Nat. Biotechnol. 40, 422–431. https://doi.org/10.1038/s41587-021-01058-4 (Journal Paper)

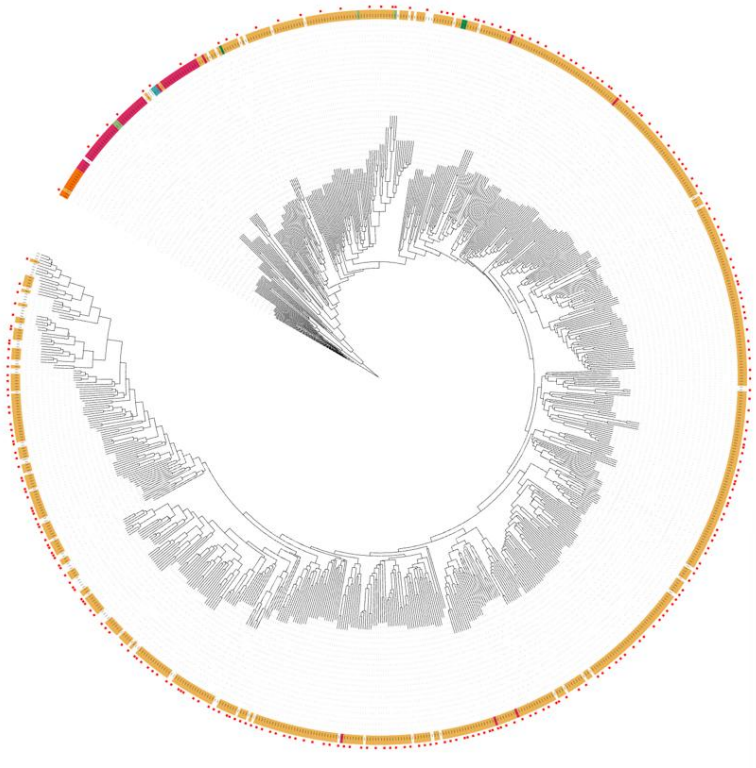

Figure 1. Phylogenetic relationships between pea accessions at the John Innes Centre. The subset of core lines selected for this project are highlighted with red dots in the outer circle.

Seed distribution to IC partners

In spring 2023, seeds from the selected core set of 256 lines were sown at the JIC field station for multiplication to ensure sufficient quantities for distribution to PIC partners. Pods were harvested during July-August, after which seeds were threshed, cleaned and packed. The seeds (50 seeds/accession) were prepared and shipped to partners at RAGT, KWS, DANKO, SERIDA and ABER in compliance with material transfer agreements (MTAs) and phytosanitary certification requirements. These seeds are now being used in both field and controlled-environment trials.

Field trials and trait scoring at partners locations (2024 and 2025)

The Pea Innovation Community (PIC) has established a coordinated multi-location trialling effort across Europe to evaluate the genetic diversity of *Pisum* accessions under a range of environments and management systems. Field trials were conducted at multiple sites, including the UK (John Innes Centre, Aberystwyth University), Spain (SERIDA, Asturias), Germany (KWS LOCHOW), Poland (DANKO), and France (RAGT). This broad geographic distribution (Figure 2 – map of trial sites) ensured that the diversity panel was exposed to a wide range of climatic conditions, soil types, and biotic stresses, capturing genotype × environment interactions relevant to pea cultivation across Europe. Most sites used replicated trials, with plot layouts adapted to local agronomic practices. At JIC, a randomised block design with three replicates was applied, while other partners used row or plot-based systems with one or more replicates. A common set of traits was recorded

across sites, including plant height, flowering time, emergence, flower colour, yield components (seed and pod number/weight, thousand seed weight), and disease symptoms (downy mildew, powdery mildew, viruses, root rots). Leaf tissue was collected from symptomatic plants for molecular characterisation of viral infections and downy mildew race typing. At some sites, harvested seed was retained for protein content.

Field trails were complemented with controlled-environment studies for drought phenotyping at Aberystwyth University (using automated watering systems) and root rot assays in controlled chambers at JIC.

Figure 2. Map of pea field experiments (SERIDA, JIC, RAGT, KWS, DANKO).

John Innes Centre, Norwich, England: In 2024, field trials were established for 256 pea accessions at the JIC field station in Bawburgh, on the outskirts of Norwich. Each accession was planted in three replicates following a randomised block design, with five seeds sown per replicate supported by wires. The trial received a pre-emergence herbicide treatment, followed by fungicide applications at early, mid, and late flowering. An insecticide was also included to manage pea moth. Weevil damage was observed as notching on the leaves with some genotypes appearing worse affected than others. Several traits were assessed, including flower colour and plant height, which served as control phenotypes for our GWAS pipelines since the underlying genetic loci are already known in pea. Additional traits scored resistance or tolerance of virus infection and downy mildew (DM) (Figure 3a, b). Plant tissue from symptomatic individuals was collected and stored at

–80 °C for subsequent molecular analyses to identify virus species and determine downy mildew race types. Yield-related traits were also measured at harvest, including seed weight and number of pods per plant (Figure 4a, b). Ten representative pods per accession were photographed to enable image-based scoring of pod shape variation.

The diversity panel was sown again following the same experimental design in 2025. However, emergence was poor due to significant rodent damage and root rot, primarily caused by *Fusarium* spp. Exceptionally dry and hot summer conditions led to an early harvest. No downy mildew symptoms were observed, although virus symptoms were again recorded.

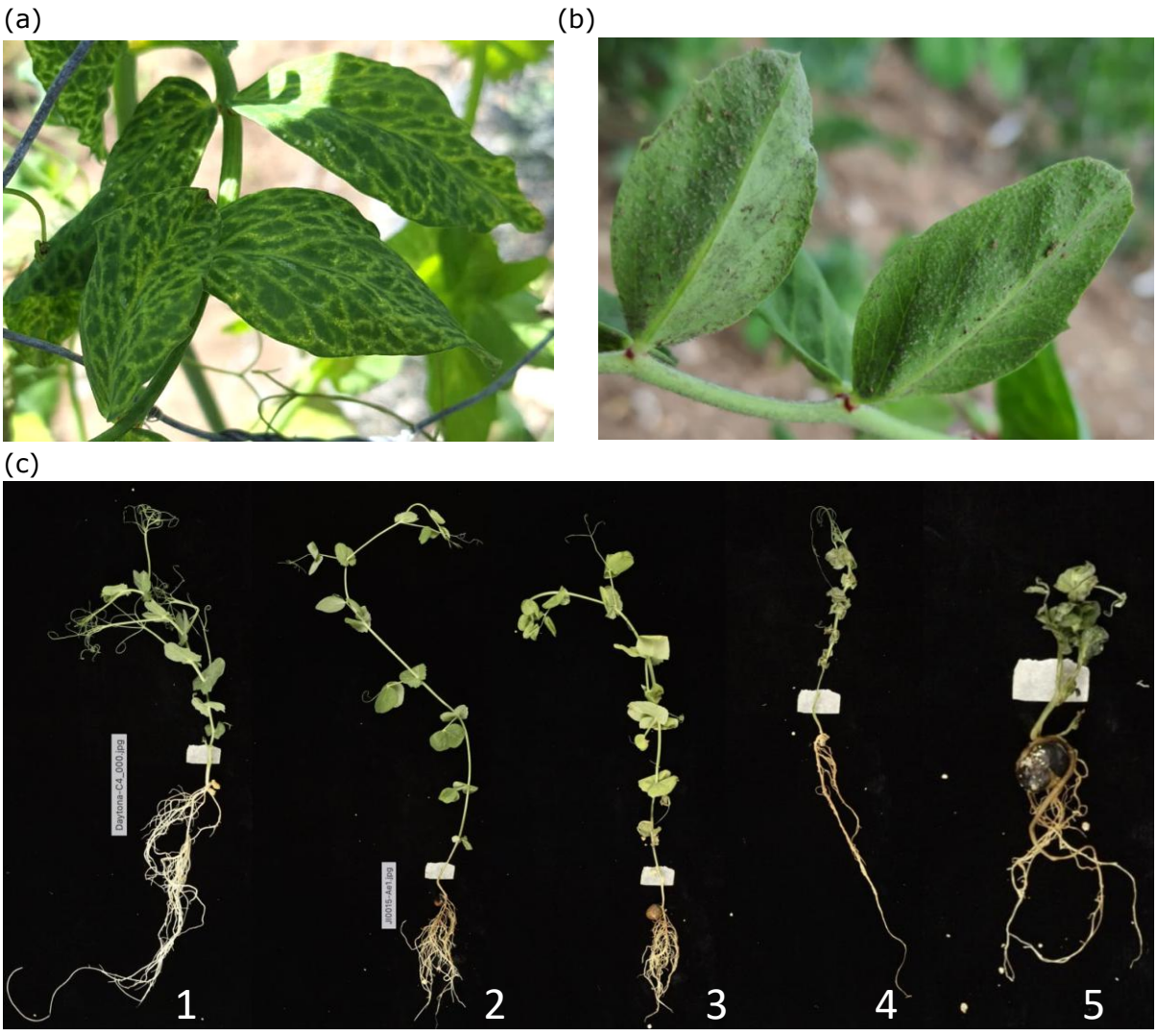

Figure 3. Disease scoring at JIC (a) virus and (b) downy mildew symptoms observed in the field trial. (c) Representative disease severity scale (1-5) for controlled phenotyping of pea accessions against Aphanomyces euteiches root rot.

Root rot, caused by a complex of fungal and oomycete pathogens, remains a major constraint to pea production, progressively rendering fields unsuitable for the crop. To

address this, controlled-environment phenotyping was conducted for *Aphanomyces euteiches* (Figure 3c). Most accessions showed an intermediate level of resistance, providing a basis for future resistance breeding.

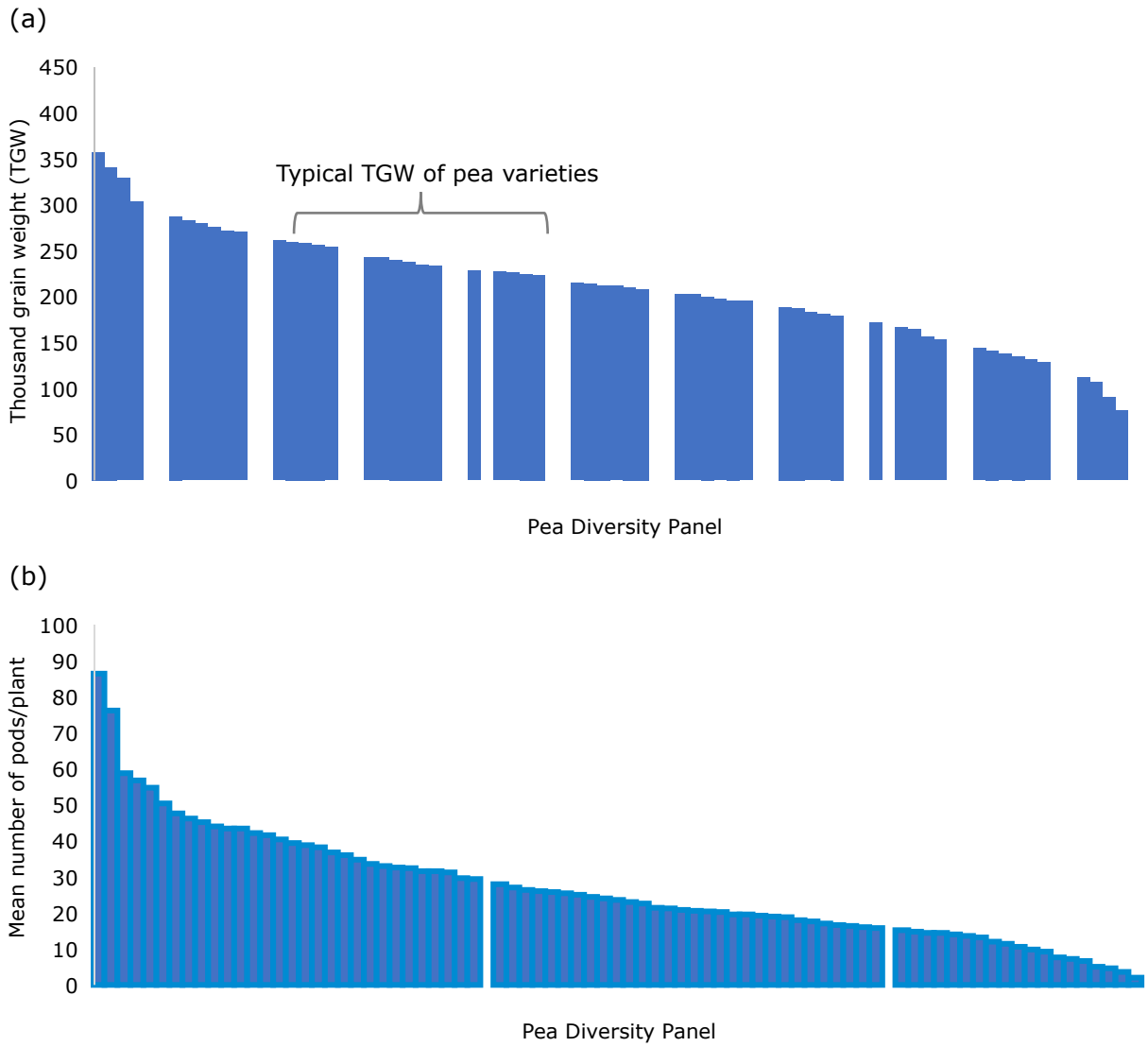

Figure 4. Yield traits scored at JIC field trials (2024). (a) Variation for thousand grain weight (TGW) and (b) pod number per plant.

SERIDA, North-west of Spain, Villaviciosa, Asturias: A total of 146 pea lines were sown at the SERIDA experimental station in 2024 at the end of February and harvested during summer, benefitting from a longer growth period compared with other Pea IC trial locations. The lines included 50 accessions from the JIC collection, 62 homozygous lines from the SERIDA collection, 18 additional SERIDA accessions, and 13 commercial varieties. The field trial comprised 280 plots (two replications), each with 10 plants planted at 1 m spacing. The trial was conducted under organic farming conditions using mulching. The main objectives were to multiply material, obtain homozygous lines, evaluate adaptation of the accessions to local conditions, and provide phenotyping and crop management training. Of the 280 plots, 19 failed to produce seed. Phenological and morphological

characterisation included observations of flowering and pod formation, growth habit, leaf and pod traits, flower colour, yield parameters, and presence/absence of pests and mildew.

Building on this initial work, the full diversity panel of 256 lines was sown in 2025, along with 11 commercial control lines and 24 local lines conserved within the SERIDA collection, to assess biotic stress responses and yield performance. Seeds (40 per line) were first sown in greenhouse trays (40-cell, peat substrate) and then transplanted to the field. The germination rate averaged 98% (Figure 5a, b, c). Trials were established as three replicates per line (R1, R2, R3), randomly distributed across the field, giving a total of 850 plots. Each replicate consisted of 10 plants arranged in two rows of five. The crop was managed under organic conditions with mulching and without irrigation. Phenological and morphological descriptors recorded were consistent with those assessed in 2024. In addition, yield parameters were collected, including dry biomass of harvested plants, weight of 10 dry pods, seed weight from 10 pods, total seed yield, 100-seed weight, and number of seeds in 10 pods.

The major challenge identified at this site was powdery mildew that affected 95% of lines. Only 13 resistant lines were identified (Figure 5d). This disease remains difficult to manage under organic conditions as no effective treatments are available. It caused progressive defoliation and significant yield loss. Downy mildew was also observed (Figure 5e), though incidence was lower than for powdery mildew, but still affected 76% of the lines. DM symptoms appeared early in the crop cycle but did not progress significantly through the season. Samples were preserved at –20 °C and sent to JIC on 28 July for race profiling. Ascochyta blight was also recorded at moderate incidence but with low severity and limited impact on yield. Its occurrence was particularly associated with periods of intense rainfall. Other diseases observed were rust and ascochyta blight (Figure 5f, g). Root rot and ascochyta were observed in 16% and 15% of the lines, respectively, while viral infections were detected at a much lower frequency (0.6%). In addition, leaf miner damage was found in 19% of the lines.

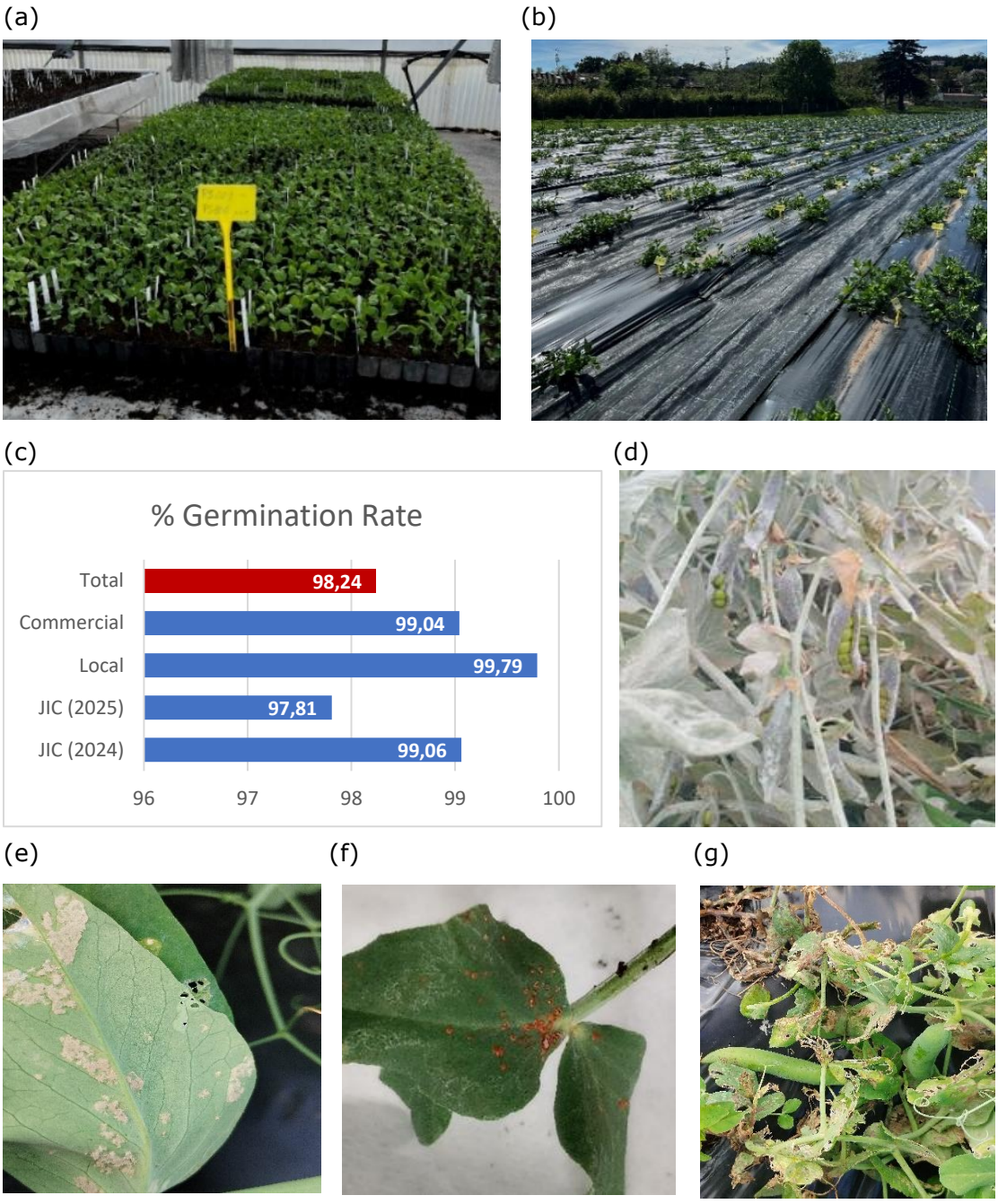

Figure 5. Field phenotyping during trial at SERIDA, Asturias (a) Seedbed prepared in the greenhouse, and (b) Field trial. (c) Percentage of germination rates obtained. Germination rate of the 50 JIC lines multiplied at the SERIDA during 2024 and ~250 lines JIC in 2025. Disease incidence recorded for (d) Powdery mildew, (e) Downy mildew, (f) Rust and (g) Ascochyta blight.

KWS LOCHOW GmbH, Northern Germany: The complete pea diversity set (256 lines) was cultivated near the KWS LOCHOW breeding station in Northern Germany. Sowing tool place at the end of March 2025, which is considered an early date for this region. Given the high frequency of wild-type leaf morphologies in the panel, *Camelina* was co-cultivated to provide support and allow pea plants to climb away from the soil surface. Because the

panel was already multiplied in 2024, microplots were established in 2025 using a sowing density of 80 seeds per m^2 for each genotype. Each genotype was planted once, as the main purpose of this trial was the identification and removal of potential contaminations among the different genotypes. Flower colour was scored across the panel and used to eliminate off-types from the plots. The plots were harvested in early August 2025. In parallel with the panel multiplication, a root-rot provocation site was initiated to enable repeated assessment of pea accessions for their response to *Aphanomyces* and *Fusarium* species. This provides an important resource for evaluating resistance to two of the most destructive pathogens affecting pea cultivation.

DANKO, Hodowla Roślin Sp. z o.o., Kościan, Poland: A field trail including 256 pea genotypes was sown in March 2025 at Kościan, Poland. The experimental design consisted of a single replicate with 5 rows per genotype, each row is 1 metre in length. The trial was managed throughout the growing season, and a wide range of traits were evaluated - (i) Morphological traits: including presence/absence of anthocyanin pigmentation, flower colour, leaflet presence, tendril form, plant height, and number of branches per plant. (ii) Phenology and agronomic traits: flowering start and end date, maturity date, lodging, and disease resistance. (iii) Yield components: For 10 randomly sampled plants per plot, pod number and weight, seed number and weight, and thousand seed weight were recorded.

In total, data were collected from more than 2,500 individual plants. Additionally, seed from each plot was harvested to secure material for future research, including protein content analysis. Considerable variation was observed across the panel in terms of morphological traits, health status, flowering and ripening times, and yield structure (Figure 6). Flowering commenced as early as 14 May, with the latest genotypes beginning to flower by 15 June. Harvesting began on 20 June and was completed by 24 July.

Figure 6. Field trial of pea diversity panel in 2025 at DANKO, Poland, showing variation during flowering and maturity.

RAGT, Louville:, a field trial with 256 pea genotypes was sown in March 2025 in two replicates at Louville, France. The main purpose was to bulk the seeds which will be used for disease evaluation and protein content measurement, providing valuable data on nutritional quality alongside disease resistance. At harvest, thousand kernel weight (TKW) was recorded across the panel.

Drought phenotyping, ABER: Abiotic stresses such as drought are difficult to manually impose consistently and reproducibly at large scale. To address this, we used the automated Photon Systems Instrument (PSI) conveyor-based phenotyping platform at the National Plant Phenomics Centre, Aberystwyth University. The system enables precise imaging and automated target watering of up to 2000 individual pots (Figure 7a). Following a preliminary experiment of a small number of accessions at a wide range of soil water treatments, 265 diverse pea accessions, ranging from 'improved' cultivars to wild type, were screened under three different levels of drought: control (60% soil water content, SWC), mild drought (30% SWC), and severe drought (20% SWC) (Figure 7b). With replication, this experiment comprised approximately 3,200 plants. Seeds were imbibed for 2 days at 15 °C, sown into pre-weighed pots, and scored for emergence. The automated watering system maintained each pot at its designated target weight, allowing accurate measurement of plant water use throughout the experiment. Growth was rapid and varied markedly across the diversity panel. Phenotypic data recorded include emergence, plant height, fresh weight, dry weight, and node number (Figure 7c). Under water-limiting conditions, the correlation between shoot height and dry weight was weak, indicating that height alone is not a reliable proxy for drought tolerance. Additional traits were observed, such as the production of leaf wax in many accessions subjected to drought. However, semi-wild accessions and traditional landraces did not show a clear wax-associated response, suggesting alternative drought adaptation mechanisms. Preliminary harvest data revealed substantial variation in drought responses across the panel. Water-use efficiency was calculated for each accession, these datasets will be integrated with genomic data to identify loci and markers linked to drought resilience, providing breeders with valuable resources for improving pea performance under climate stress.

(a)

(b)

30% 20% 15% 60% SWC

(c)

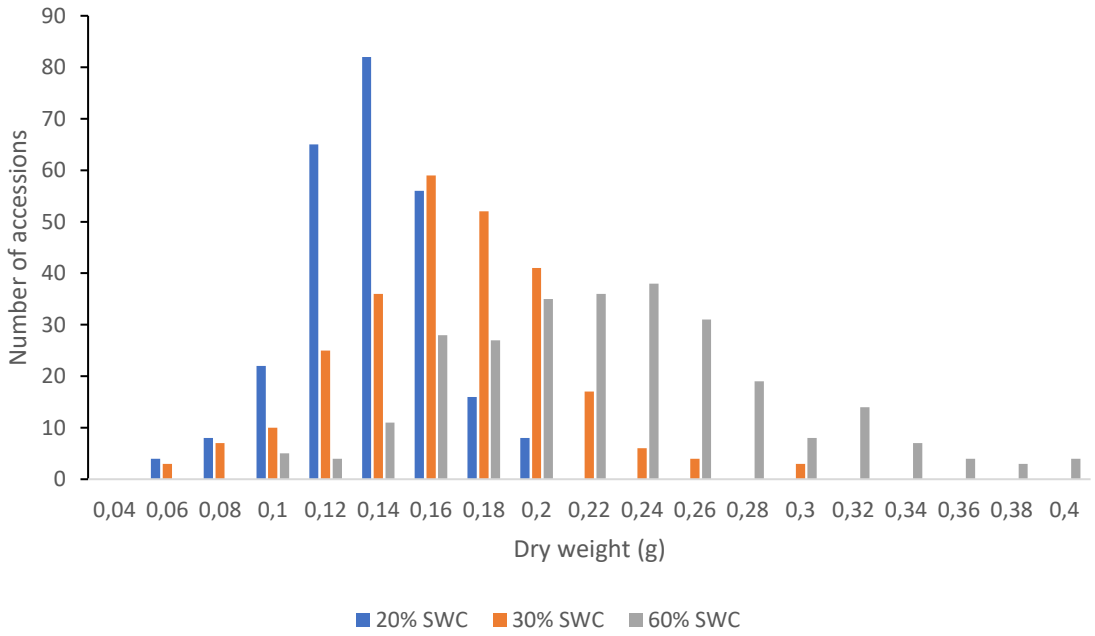

Figure 7. Drought phenotyping at Aberystwyth University using the PSI automated system. (a) Experimental setup showing pea accessions on the conveyor system in the National Plant Phenomics Centre. (b) Drought treatments (i) under control (60% SWC), (ii) mild drought (30% SWC), (iii) and severe drought (20% and 15% SWC). (c) Distribution of dry weight across diversity panel under different drought treatments.

Genomic data analysis, JIC: we have set up a *k*-mer based genome-wide association study (GWAS) pipeline to dissect trait-genotype relationships. This reference-free approach integrates multiple reference genomes, enabling the identification of presence/absence variants and structural polymorphisms that are often missed in single-reference analysis.[6,7] Such a strategy has proven particularly effective in highly diverse wild plant species, enabling fine-scale haplotype mapping even in the presence of substantial structural variation. For the *Pisum* diversity panel of 250 accessions, *k*-mers were counted from trimmed raw reads for each accession. These counts were then combined to generate a binary presence/absence matrix with >10 billion *k*-mers, highlighting the pangenomic diversity of *Pisum* species. To validate our *k*-mer GWAS pipeline, we used plant height measured at ABER as a control phenotype. *k*-mers with an association score of >4.5 were mapped to the *Pisum* reference genome Cameor that revealed a highly significant peak at the known locus controlling plant height on chromosome 5 (Figures 8). This confirms the robustness of our *k*-mer GWAS pipeline and its suitability for trait mapping in diverse pea populations.

[7] Arora S, Steuernagel B, Gaurav, K. et al. (2019) Resistance gene cloning from a wild crop relative by sequence capture and association genetics. Nat. Biotechnol. 37, 139–143. https://doi.org/10.1038/s41587-018-0007-9 (Journal Paper)

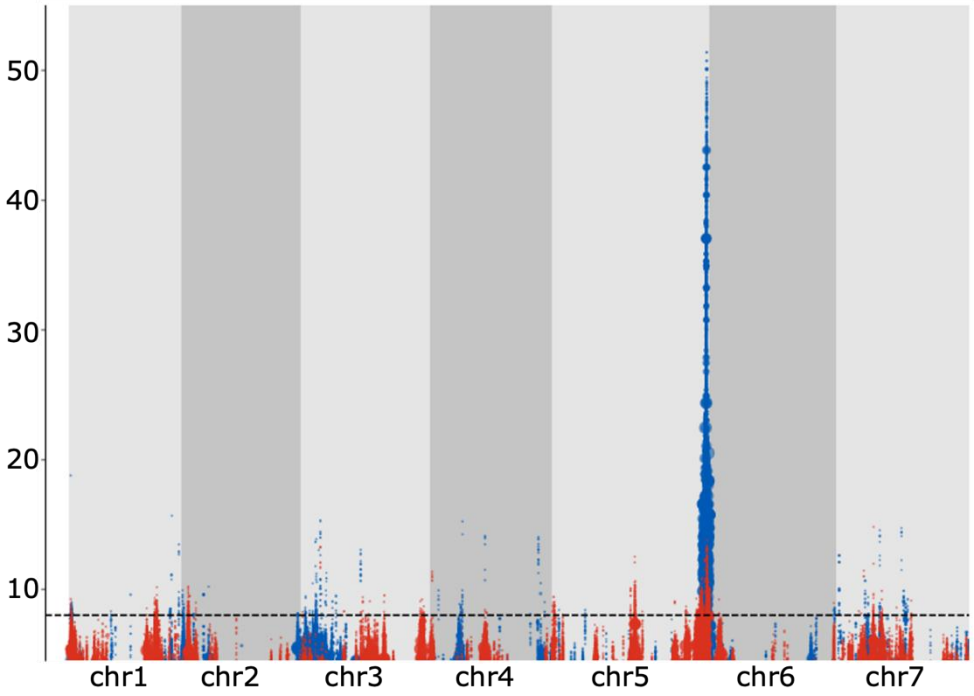

Figure 8. Validation of k-mer GWAS pipeline. Manhattan plot showing association of k-mers with plant height on chromosome 5.

University of Oxford: Pod characteristics are important for several aspects in pea and include for example size (length, width, thickness), number of seeds per pod and rate of pod filling. The cellular architecture of the pods determines traits such as edibility (like snap and snow peas) and seed dispersal (pod shatter). At the field station at Wytham (Oxford), we are growing four plants from each of the 250-line subpanel in the greenhouse over the 2025 summer/autumn at ~18°C. Plants have been sprayed with fungicide against powdery mildew. Pods are photographed at different developmental stages and subsequently fixed in formaldehyde for sectioning and phenotypic analysis of cellular arrangement under the microscope. Similar to the field trial at JIC, we will measure control phenotypes for the GWAS pipeline such as flower colour and plant height. In addition to this, the team at JIC carefully recorded pod phenotypes from the 2024-field trail, and photos from this phenotyping effort will be analysed at Uni Oxford and compared to pods from the green-house grown plants.

Outreach and engagement

In 2024–2025, breeder engagement and outreach activities were expanded through breeder's days at JIC, the DANKO Field Day in Szelejewo, and SERIDA demonstrations (Figures 9). These events brought together breeders, farmers, students, and stakeholders, providing opportunities to showcase ongoing research within the Legume Generation project, share trial results, and promote diversity of old and modern pea lines. Presentations were delivered at major conferences, including ICLGG 2024 and the Association of Applied Biology Legumes meeting, while training sessions on pea cultivation and protection supported knowledge exchange with growers. Dissemination was further

strengthened social media updates, ensuring broad visibility of trial progress and outcomes.

(a) (b)

Figure 9. Engagement and outreach activities (a) Breeder's days at JIC (b) DANKO field day in Szelejewo.

Conclusion

The Pea Innovation Community (PIC) has successfully established a collaborative, Europe-wide effort to unlock the potential of pea as a climate resilient protein crop. Our aim is to bridge the academic research and practical breeding. By characterising a genetically diversity pea panel and implementing coordinated field and controlled-environment trials, we have laid the foundations for trait discovery and pre-breeding in pea. We have demonstrated that integration of robust phenotyping with advanced genomic tools, particularly the *k*-mer GWAS pipeline, can uncover novel variation. Our trails across Europe and UK revealed critical challenges in adaptation, disease resistance, and resilience to climate extremes. Early findings, such as variation in responses to powdery mildew, root rots, and drought, demonstrate the potential to identify genetic determinants of resilience and productivity. This will be a valuable shared resource for the wider legume research and breeding community.

Going forward, we plan to focus on:

- Expanding trait–genotype analysis by integrating multi-location phenotypic datasets with genomic information to identify markers and haplotypes associated with key agronomic traits.
- Validating candidate loci through replicated trials, functional analyses, and integration into pre-breeding pipelines with industry partners.
- Selecting pea lines to initiate crosses with elite cultivars by breeders and use marker data for selection of lines.
- Broadening partnerships and capacity building, with an emphasis on training, fostering industry–academic collaboration, and strengthening international networks.
- Sharing data and tools with partners and beyond.