



Legume Generation

The Legume Generation Pea Innovation Community

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

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Pea is Europe's most widely-grown cool-season legume and is important in emerging novel food markets and for high value feed uses (e.g., aquaculture). Despite being a model for plant genetics, the rate of pea improvement has lagged behind that of cereals. Reversing this trend is of critical importance. Our partners are well positioned to draw on the extensive resources at JIC to combine different traits including developmental, morphological, stress-related and metabolic traits. The pea crop is impacted by increased incidences of biotic stresses (pests and pathogens); high sensitivity to abiotic stresses (drought, heat and lodging); and low availability of frost-tolerant pea cultivars for stable yield and expansion of the winter pea.

The **Pea Innovation Community** is a group of breeders and scientists from both commercial and academic organisations from five countries (Figure 1) working together in a tightly linked collaborative European network to generate new breeding material that has both economic and environmental benefits for growers and the public. Figures 2 and 3 illustrate how we will work together to bring about change in pea breeding.



Figure 1: (i) Pea flower and seed colour variation observed in the field (ii) Partners involved in the Pea Innovation Community

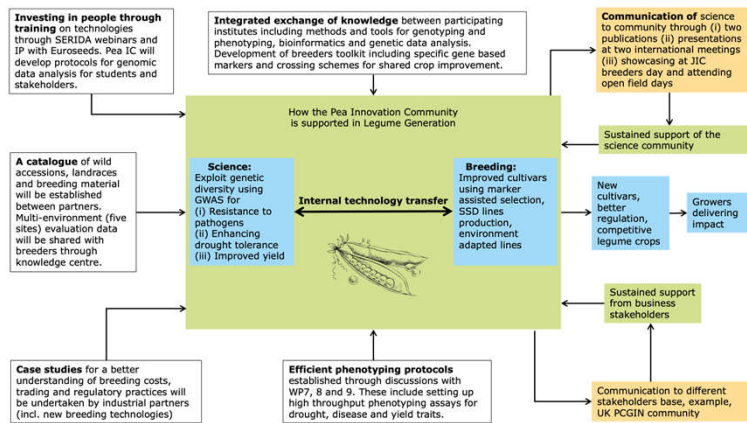


Figure 2: How the Pea Innovation Community is supported in the Legume Generation

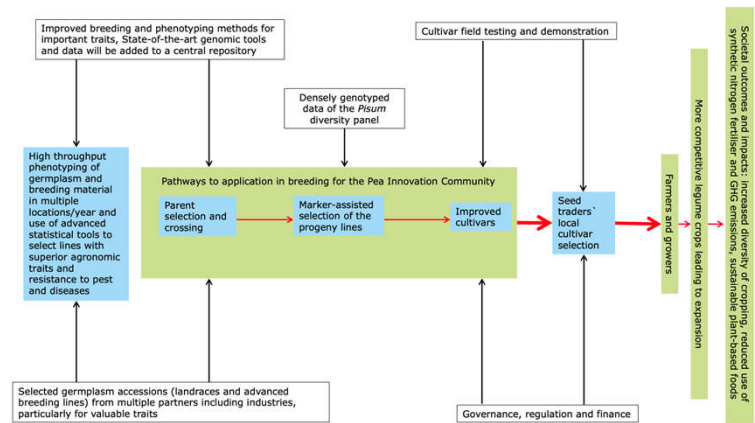


Figure 3: Pathways to application in pea breeding

Objectives, approaches and current activities

The goal is to boost the breeding of pea by exploiting genetic diversity of *Pisum* species guided and implemented by our Pea Innovation Community. The objectives include:

1. building the pea innovation community for the production of better adapted cultivars;
2. screening pea genetic diversity to find genetic markers for a wide range of traits; and
3. pyramiding desirable alleles into elite cultivars using marker-assisted-selection.

A core set of 250 lines (see red dots in Fig.4a) have been multiplied and shared with partners to further multiply and phenotype across different locations in Europe. The panel was grown in three replicates as treated and untreated plots at JIC in summer of 2024 and assessed for any disease symptoms, variation in emergence and flowering and currently being assessed for seed and pod traits to analyse yield variation. This panel will be phenotyped for pod and seed yield, fertility, lodging and drought resilience, winter hardiness and disease resistance traits in controlled environments and in multi-location trials (JIC, ABU, KWS, RAGT, DANKO, SERIDA). Complementing this, we are **establishing bioinformatics tools** to identify associated genomic regions and new alleles for breeding. This will support gene pyramiding/introgression using molecular markers to develop cultivars, which will be tested in multiple locations with partners.

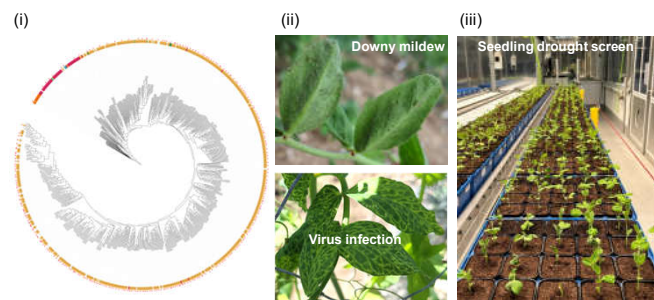


Figure 4: Pea diversity panel at the John Innes Centre (i) genetic diversity (ii) identification of disease traits (Downy mildew and virus resistance) variation during field evaluation (iii) drought experimental setup in controlled conditions. Future tasks will include multi-site trails, marker-trait identification, crossing and breeding to stack traits and training, communication and dissemination of results.



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