



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 (*Pisum sativum* L.) is the most widely grown cool-season grain legume across Europe and the UK, with growing importance for sustainable protein production, novel food markets, and high-value feed sectors. The pea crop is impacted by increasing pressure from biotic (pests and pathogens) and abiotic (drought, heat, and lodging) stresses, and low availability of frost-tolerant pea cultivars for stable yields and expansion of winter pea cultivation. Yet despite its historical role as a model organism for genetics, the rate of genetic improvement in pea has lagged far behind cereals, reducing farm-level competitiveness and discouraging growers from including pea in rotations. Targeted public investment in pre-competitive pea breeding research is essential to correct this imbalance.

The **Pea Innovation Community** (PIC), within the EU-funded Legume Generation project, addresses this challenge by connecting researchers and breeders across Europe and the UK in a sustainable framework for pre-competitive collaboration (Figure 1). Our strategic goal is to identify and deliver novel genetic diversity and validated breeding tools that improve pea yield, resilience, and disease resistance across a range of environments.

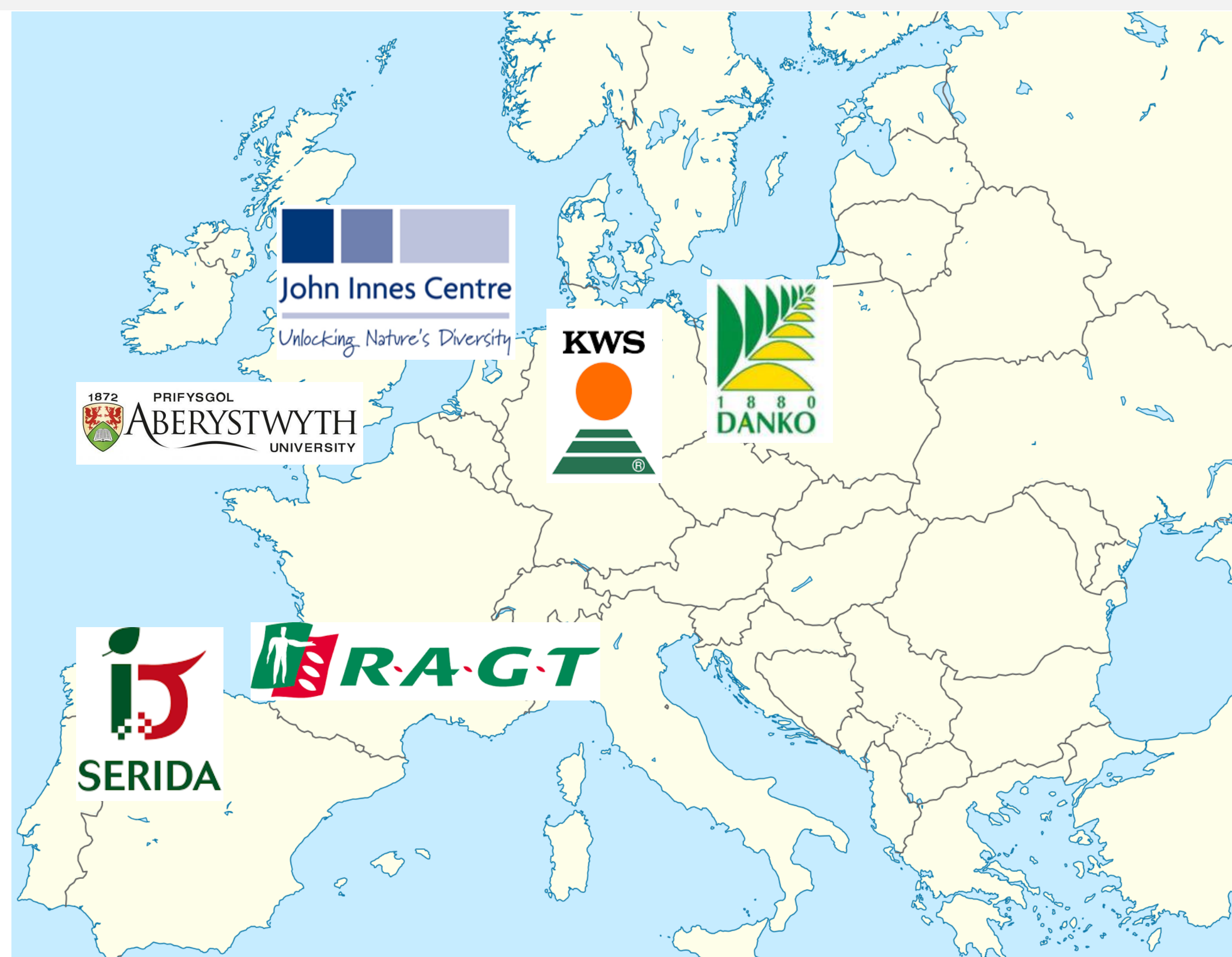


Figure 1: Partners involved in the Pea Innovation Community

To achieve this, we have established a curated diversity panel of ~250 accessions including wild *Pisum* relatives, landraces, and modern cultivars which are being phenotyped in multi-location field trials across the UK, Germany, France, Poland, and Spain (Figure 2). Controlled environment assays and high-throughput phenotyping complement field evaluations, targeting traits including drought and heat tolerance, resistance to root rots, powdery and downy mildew, and adaptation to autumn sowing (Figure 3). Using field and controlled-environment data, high-performing lines with key traits such as powdery mildew resistance and high thousand seed weight were selected as parents in crosses with elite cultivars developed by PIC partners.

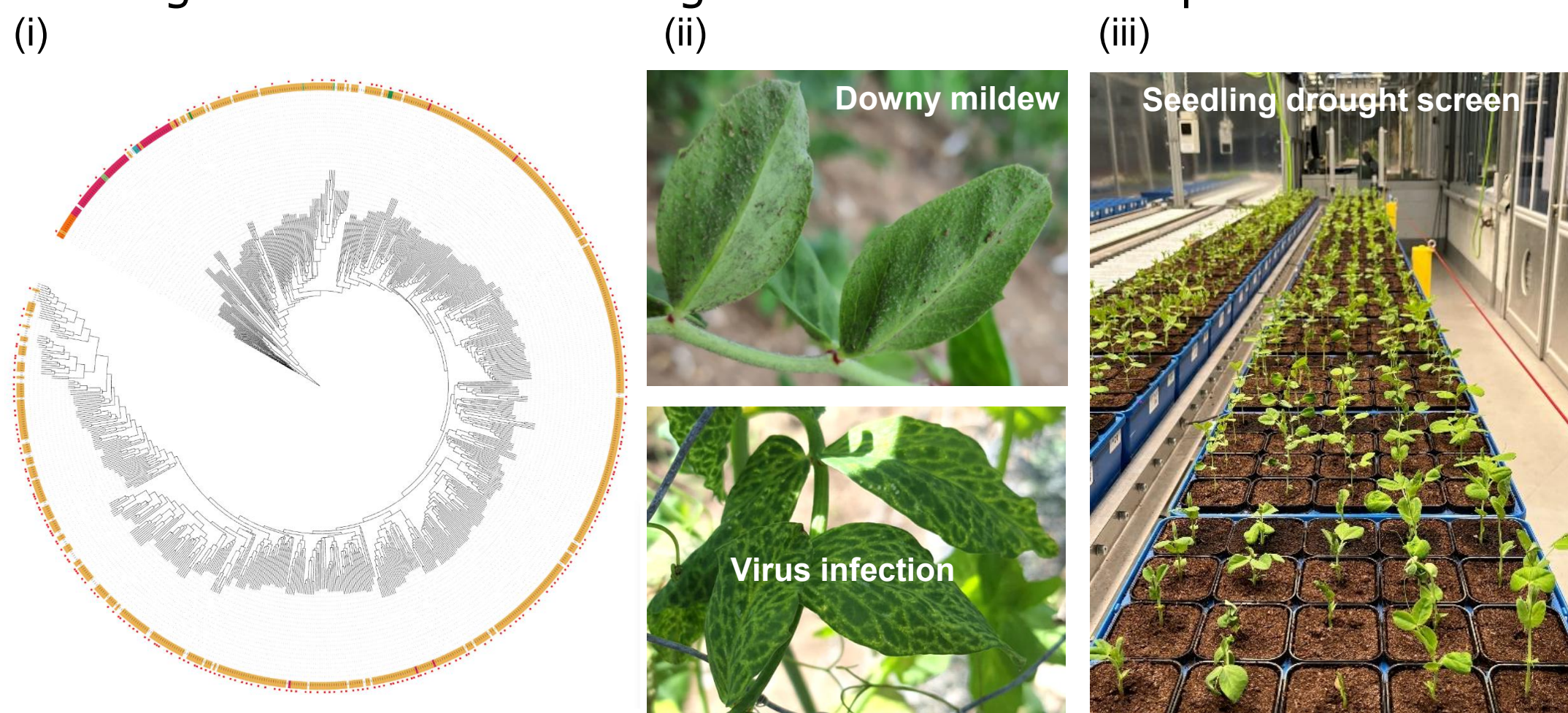


Figure 2: Pea diversity panel at the John Innes Centre. (i) Genetic diversity (ii) Variation in disease traits, including downy mildew and virus resistance, during field evaluation (iii) Controlled-environment drought experimental setup.

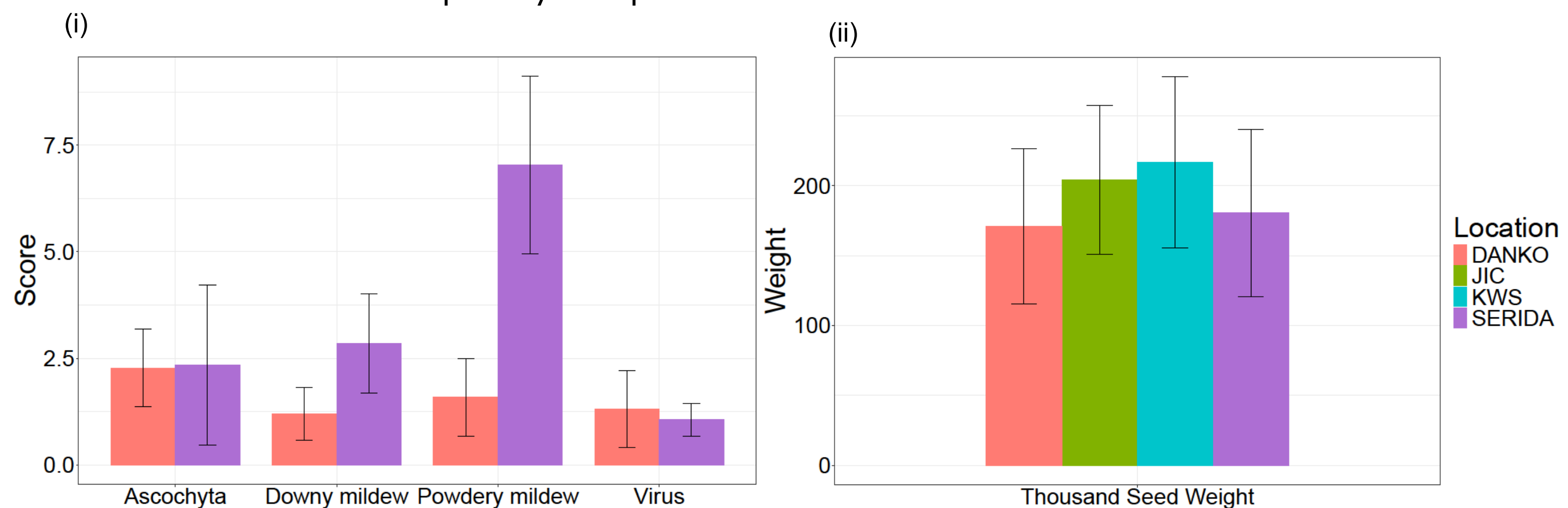


Figure 3: Results from 2025 field trials. (i) Disease scores for Ascochyta blight, downy mildew, powdery mildew, and virus symptoms collected at DANKO and SERIDA, showing differences in disease pressure and accession response, particularly for powdery mildew. (ii) Thousand seed weight was consistent across field trials at DANKO, JIC, KWS, and SERIDA.

High-depth whole-genome sequences across the panel enable pangenome-based GWAS, through which we have already identified novel loci for thousand seed weight, powdery mildew resistance, and seedling drought tolerance (Figure 4). Markers derived from these findings are being developed and will be shared with breeding partners for deployment in marker-assisted selection. These efforts are expected to result in high-yielding, disease-tolerant, and resilient pea cultivars.

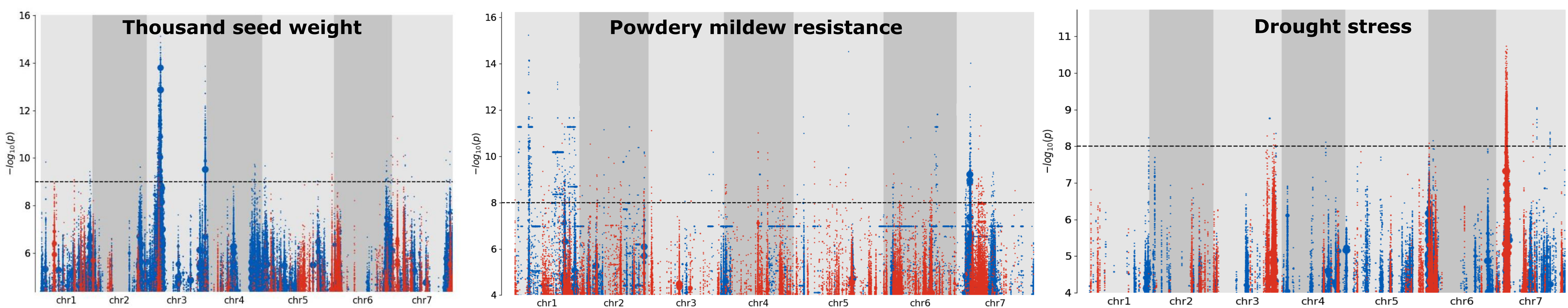


Figure 4. *k*-mer GWAS results from field and controlled-environment phenotyping for thousand seed weight, powdery mildew resistance, and drought stress. (i) Two loci on chr3 are associated with high thousand seed weight. (ii) A novel, rare locus on chr7 is associated with powdery mildew resistance. (iii) A locus on chr7 is associated with water loss over time under drought stress.



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