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INTEGRATIVE GENETICS & GENOMICS FOR MULTI-PEST RESISTANCE IN GRAIN LEGUMES

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OBJECTIVES

Grain legumes are key players in agro-ecological and food transitions, but are susceptible to multiple diseases and pests. *Aphanomyces* root rot, *ascochyta* blight, and seed weevils have been the most damaging and studied stresses in France over the last 20 years. Other pests, including weeds, aphids and sitona, are currently becoming problematic for grain legumes in the light of new regulations on pesticide use. Breeding varieties for multi-pest resistance is a major challenge for grain legume development.

A major objective of the French national project SPECIFICS (2021-2027) is to generate and integrate knowledge on the diversity, genetics, genomics and mechanisms of resistance to multiple pests for innovative grain legume cropping systems.



'SPECIFICS' WorkPackage1 AIMS AT:



- Characterizing genetic resources for resistance to multiple stresses and managing related information;
- Identifying genetic loci, genes, mechanisms underlying resistance to multiple stresses using GWAS and omics approaches;



- Using translational approaches to transfer knowledge on resistance determinants to and between grain legumes;
- Introducing relevant genetic loci into elite material to create multi-resistant pea lines.

MAIN ACHIEVEMENTS

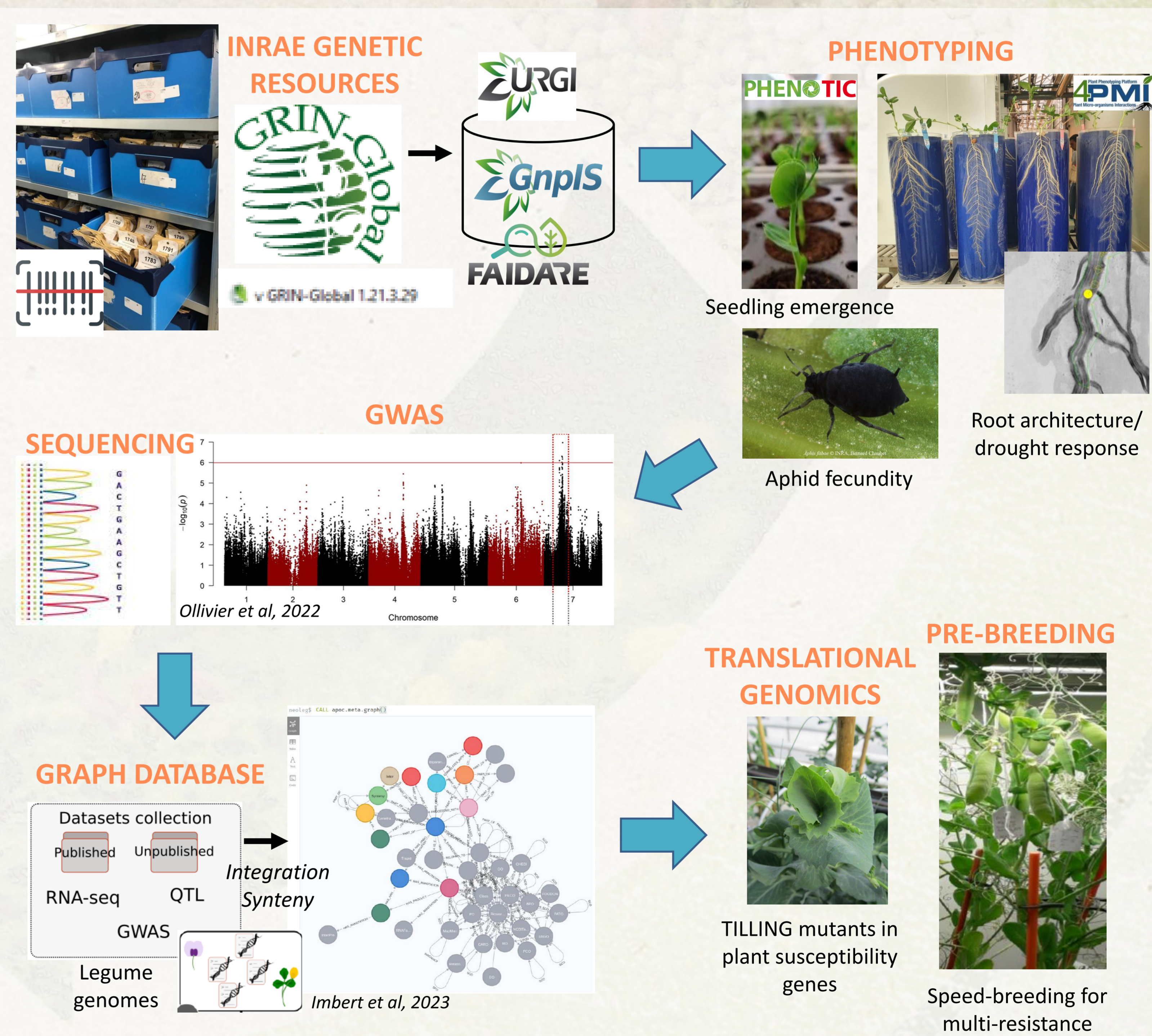
A Grin-Global database is being deployed to manage datasets related to pea and faba bean genetic resources hosted at INRAE (>12000 accessions, >22000 seed samples, >200 trait codes).

Automated or manual phenotyping of exome-sequenced pea and faba bean collections is performed for seedling emergence, drought tolerance, aphid resistance, as well as plant root and nodule architecture.

A NoSQL graph database is being developed to integrate QTL, RNA-Seq and gene annotation data for five legume species. The database aims at

connecting data obtained in the project and previously for resistance to diseases and pests, seedling establishment and pest or disease-related root/aerial architectural traits, in order to identify putative pleiotropic or syntenic genes.

Pea mutant lines in susceptibility genes conserved from other plant species and speed breeding introgression lines are produced to identify and combine key genes and loci for multi-pest resistance.



CONCLUSION

SPECIFICS is a driving force for acquiring knowledge and tools to accelerate grain legume breeding for pesticide-free cropping systems.

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