

Exploiting grass pea natural variation to understand stress resilience genetics

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Climate change is impacting agriculture differently across regions and crops. Major stresses include variable rainfall, reduced water availability, rising temperatures, frequent extreme weather events, and increased pest and disease outbreaks. These factors are expected to reduce crop yields, demanding alternative varieties or new crops to maintain a stable food supply. Traditional growing regions face significant challenges, prompting renewed focus on developing crop varieties resilient to prevalent biotic and abiotic stresses (Gonçalves et al, 2022).

Grass pea (*Lathyrus sativus* L.) is a model crop for sustainable agriculture (Vaz Patto et al, 2006). It tolerates extreme temperatures, drought and floods, and is resistant to several pests and diseases, making it suitable for various production systems and environments. The species shows high morphological and agronomic diversity, with two main ecotypes: Mediterranean (larger, light-colored seeds) and Asian (smaller, dark-colored seeds). However, even in this hardish crop, the increased climate instability imposes a reorientation of grass pea breeding to address new production challenges.

Identifying resilient traits sources in grass pea is crucial for current breeding efforts. Understanding the genetic control of these traits will enable pinpointing genomic targets for developing molecular tools to assist precision breeding for multi-stress resistance. Precision breeding uses molecular markers linked to resistance genes, making selection more efficient, faster, and cost-effective when compared to conventional methods. Understanding the genetic basis of resistance is thus essential for this approach. Genome-wide association studies (GWAS) are powerful approaches for exploiting natural variation in plant germplasm collections to identify allelic variants controlling complex traits.

In this keynote lecture, we will explore my research group's efforts to elucidate the genetic architecture of stress resistance traits in grass pea using worldwide natural variation. We will discuss the challenges of performing GWAS in this understudied crop. Success stories on the identification of the genetic basis of resistance to fusarium wilt (Sampaio et al, 2021a,b), powdery mildew (Martins et al, 2023), and rust fungi (Martins et al, 2022) will be highlighted, as well as future research directions (Gonçalves et al, 2024; Sanches et al, 2024). Particular emphasis will be given to the significance of previous phylogenetic and syntenic investigations, comparative mapping (Santos et al, 2021), and transcriptomic analysis (Almeida et al, 2014), in facilitating genetic research in grass pea. These genetic studies demonstrate the usefulness of exploiting natural variation in grass pea germplasm to identify genomic regions controlling stress resistance. Both known and novel resistance genes, along with several new resistant loci, were discovered. The favourable SNP alleles already identified may serve as important genomic tools for precision resistance breeding in grass pea.

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