**Leveraging Genome-Wide Association Studies (GWAS) for Enhanced Understanding and Breeding of Faba Bean: Insights from Two Distinct Panels on Agronomic Traits and Stress Tolerance**

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Faba bean (Vicia faba L.), a crucial legume crop for sustainable agriculture due to its nitrogen-fixing ability and high protein content, faces production limitations and instability due to various biotic and abiotic stressors. Furthermore, breeding efforts have been limited due to underdeveloped genomic resources.

To enhance breeding efficiency, this study employs a comprehensive GWAS approach on two distinct faba bean panels to identify candidate genes associated with key agronomic traits and stress tolerance, followed by cross-panel validation using genomic prediction.

The two panels, consisting of around 200 diverse faba bean accessions, with an overlap of around 50, was analyzed to uncover genetic markers linked to agronomic traits such as plant height, time to flowering and lodging, as well as disease-related traits. Using high-density SNP arrays, we identified several significant marker-trait associations that provide insights into the significant genetic components of these traits.

To validate these findings and predict their utility across different genetic backgrounds, we applied genomic prediction techniques. Cross-panel validation was conducted, where significant SNPs from one panel were used to predict the other panel. The integration of GWAS findings with genomic prediction not only confirms the robustness of the GWAS findings but also underscores the potential of identified candidate genes for targeted breeding programs. This strategy promises to accelerate the development of faba bean varieties with improved agronomic qualities, thereby supporting global food security and sustainable agricultural practices.