

From Genome to Field: Applying Genome Wide Association Study for Sustainable Ascochyta Blight Management in Faba Beans

Authors : Rabia Faridi, Rizwana Maqbool, Umara Sahar Rana, Zaheer Ahmad

Abstract : Climate change impacts agriculture, notably in Germany, where spring faba beans predominate. However, improved winter hardiness aligns with milder winters, enabling autumn-sown varieties. Genetic resistance to Ascochyta blight is vital for crop integration. Traditional breeding faces challenges due to complex inheritance. This study assessed 224 homozygous faba bean lines for Ascochyta resistance traits. To achieve $h^2 > 70\%$, 12 replicates were required (realized $h^2 = 87\%$). Genetic variation and strong trait correlations were observed. Five lines outperformed 29H, while three were highly susceptible. A genome-wide association study (GWAS) with 188 inbred lines and 2058 markers, including 17 guide SNP markers, identified 12 markers associated with resistance traits, potentially indicating new resistance genes. One guide marker (Vf-Mt1g014230-001) on chromosome III validated a known QTL. The guided marker approach complemented GWAS, facilitating marker-assisted selection for Ascochyta resistance. The Göttingen Winter Bean Population offers promise for resistance breeding.

Keywords : genome wide association studies, marker assisted breeding, faba bean, ascochyta blight

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