

GENETIC MAPPING OF ANTHRACNOSE RESISTANCE IN WHITE LUPIN

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White lupin (*Lupinus albus*) is a valuable grain legume with a high protein content and quality, contributing to soil fertility (Monteiro *et al.*, 2014, Lambers *et al.*, 2013). Its high yield potential could make it a sustainable alternative for imported soybean in Europe (Lucas *et al.*, 2015). However, lupin anthracnose, caused by the air- and soil-borne fungus *Colletotrichum lupini* severely limits cultivation as low levels of seed infestation can already cause total yield loss (Talhinhas *et al.*, 2016). Host resistance is crucial for managing anthracnose but a better insight into the genetic basis is required. We developed a high-throughput phenotyping tool that identifies field-relevant anthracnose resistance under controlled conditions. For inoculation, we identified a local, highly virulent *C. lupini* strain. Phylogenetic analyses revealed that the strain belongs to a globally dispersed genetic group corresponding to Dubrulle *et al.*'s (2020) *C. lupini* group II. Using the developed tool we phenotyped a diverse collection of 200 white lupin accessions, revealing a strong segregation between susceptible and resistant plants, potentially holding novel sources of resistance. Genotyping-by-sequencing was performed and the generated single-nucleotide polymorphic markers (SNPs) are currently being used for genetic mapping. Quantitative trait loci (QTLs) for anthracnose resistance will be presented aiding to improve and speed up white lupin breeding programs.

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