Development and validation of molecular markers tagging anthracnose resistance in white lupin (*Lupinus albus*, L.)

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White lupin (*Lupinus albus*, L.) has great potential to be utilized more in organic and sustainable agricultural systems. However, there are major obstacles in the production of this crop to overcome. One of these is the susceptibility against its main fungal pathogen, *Colletotrichum lupini*, which causes anthracnose disease, representing a serious threat to lupin cultivation worldwide, potentially leading to total yield loss in Swiss growing conditions. The trait of anthracnose resistance is polygenically controlled in white lupin, no complete resistance was observed and only few sources of resistance were identified until now. Efforts are constantly made to breed cultivars with increased resistance. To achieve this goal, developing and validating molecular markers for direct application of marker assisted selection (MAS) and genomic selection (GS) in variety development is pivotal.

This ongoing study (2022 – 2025) aims to develop MAS and GS strategies based on already published and still unpublished resistance loci. We present a newly performed genomic prediction analysis (predictive ability of up to 0.58) based on already available genotyping (9,940 SNPs) and phenotyping data (in controlled conditions) for a panel of 200 accessions. Marker selection was subsequently applied to define a set of 56 markers that allow to improve the prediction accuracy in the studied panel (predictive ability of up to 0.79) and that can be used as basis for implementation in breeding. We used these loci to develop KASP markers, which is a cost-effective genotyping assay with the potential to be upscaled to high-throughput platforms such as Standard BioTools™. We also developed markers for three significant SNPs described in the published GWAS by FiBL on the same panel, as well as for ten significant SNPs from an unpublished GWAS by LfL (panel of 254 accession, 24,534 SNPs, phenotyping under field conditions in Germany). Finally, we transformed two published dCAPS markers tagging the resistance source from Ethiopian germplasm into KASP markers.

We present the results on selection effectiveness of these markers from validation performed using a new panel of 62 accessions, including landraces, commercial varieties and breeding lines from FiBL (Switzerland) phenotyped under controlled conditions.

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