Summary

White lupin (*Lupinus albus* L.) is a valuable grain legume, especially for sustainable agricultural systems both for its nutritious seeds, and for their beneficial ecosystem services during the growing season. However, its profitable production in temperate regions is hindered by two major challenges, susceptibility to anthracnose disease (caused by the plant-pathogenic ascomycete *Colletotrichum lupini*), as well as high and unstable quinolizidine alkaloid content in the seed. This dissertation explores the current *status quo* of marker assisted selection for these two traits of interest, and through diverse molecular analyses, present novel, functionally validated molecular markers.

Through Bulked Segregant Analysis on an F_2 population segregating for two low quinolizidine alkaloid (QA) loci, a novel quantitative trait locus (QTL) was identified on chromosome *Lalb_Chr05*. This locus represents a new genetic source of reduced alkaloid content, independent of the well-characterized and introduced into breeding *pauper* allele. By combining genotyping for the known *pauper* locus conferring the low-QA chemotype, together with the newly identified QTL, 50 recombinants carrying stacked alleles from both loci were identified in the subsequent generation (F_3). These lines showed exceptionally low total alkaloid content (22.8 ±10.4 ppm), substantially lower than even the *pauper*-associated genotypes (171.7 ±18.5 ppm).

Regarding anthracnose resistance in white lupin, nine previously published molecular markers were validated in multiple panels from various environments. Additionally, re-analysis of existing datasets enabled (i) the discovery of five additional single nucleotide polymorphism (SNP) markers through genome-wide association study (GWAS) and (ii) the development of a genomic prediction (GP) model based on 42 SNP loci. A previously reported QTL on chromosome *Lalb_Chr10*, associated with resistance in the cultivar 'Frieda' was positively validated. Two markers showed consistent statistically significant associations across multiple panels, while seven were panel-specific. The GP model achieved high prediction accuracy in the training population (0.84 ± 0.13), but required re-training for unrelated panels to maintain high predictive performance.

Together, these studies provide complementary molecular tools for further white lupin improvement as a crop plant. The identification of a novel low-alkaloid QTL and development of associated markers enable enhanced selection for seed quality, while validated SNP markers and genomic prediction approaches strengthen the breeding for anthracnose resistance. The study highlighted the value of combining established loci with newly discovered variation, as well as the need to validate molecular markers in unrelated, and sometimes narrower genepools. These findings offer a robust integrated framework for accelerating the development of anthracnose-resistant white lupin varieties with high seed quality.