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Genetic and molecular analysis of stem rot (*Sclerotinia sclerotiorum*) resistance in *Brassica napus* (canola type)

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Identifying the molecular and genetic basis of resistance to Sclerotinia stem rot (*Sclerotinia sclerotiorum*) is critical for developing long-term and cost-effective management of this disease in rapeseed/canola (*Brassica napus*). Current cultural or chemical management options provide, at best, only partial and/or sporadic control. Towards this, a *B. napus* breeding population (Mystic x Rainbow), including the parents, F_1, F_2, BC_1P1 and BC_1P2, was utilised in a field study to determine the inheritance pattern of Sclerotinia stem rot resistance (based on stem lesion length, SLL). Broad sense heritability was 0.58 for SLL and 0.44 for days to flowering (DTF). There was a significant negative correlation between SLL and stem diameter (SD) (r = - 0.39) and between SLL and DTF (r = - 0.28), suggesting co-selection of SD and DTF traits, along with SLL, should assist in improving overall resistance. Non-additive genetic variance was evident for SLL, DTF, and SD. In a genome wide association study (GWAS), a significant quantitative trait locus (QTL) was identified for SLL. Several putative candidate marker trait associations (MTA) were located within this QTL region. Overall, this study has provided valuable new understanding of inheritance of resistance to S. sclerotiorum, and has identified QTL, MTAs and transgressive segregants with high-level resistances. Together, these will foster more rapid selection for multiple traits associated with Sclerotinia stem rot resistance, by enabling breeders to make critical choices towards selecting/developing cultivars with enhanced resistance to this devastating pathogen.