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Genome-wide association mapping of resistance to clubroot in *Brassica napus*

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Clubroot disease, caused by the obligate parasite *Plasmodiophora brassicae* Wor., is a major disease of canola (*Brassica napus* L.) worldwide. Genetic resistance remains the best strategy to manage this disease. The main objective of this study was to identify and map genes in the new sources of resistance to clubroot in *B. napus* using a genome-wide association mapping approach. A world collection of 177 *B. napus* accessions was tested for resistance to four highly virulent pathotypes of *P. brassicae* based on disease severity indices (DSI). This collection was also assessed using genotyping by sequencing (GBS). Genome-wide association analysis using a multi-locus mixed model (MLMM) was performed to detect single nucleotide polymorphisms (SNPs) associated with resistance to each pathotype. The majority of the accessions were highly susceptible, with DSI ranging from 70 to 100%, while 21, 7, 8 and 15 accessions showed high levels of resistance (0 to 20 DSI) to pathotypes 5X (field isolate LG2), 2B, 3A and 3D of *P. brassicae*, respectively. In total, 301,753 high quality SNP sites were identified. Population structure analysis indicated that the accessions belong to two major populations. Genetic association analyses identified 13 significant SNPs: three SNPs for resistance to pathotype 5X-LG2 on chromosomes A08, A09 and C06; three SNPs for pathotype 2B on chromosomes A07, A05 and C01; four SNPs for pathotype 3A on C03, C02, A04 and A05; and three SNPs for pathotype 3D on chromosomes A06 and A09. These SNP markers can be used for marker assisted molecular breeding for clubroot resistance in canola.

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