



# Discovery of clubroot-resistant genes in *Brassica napus* by transcriptome sequencing

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**ABSTRACT.** Clubroot significantly affects plants of the Brassicaceae family and is one of the main diseases causing serious losses in *B. napus* yield. Few studies have investigated the clubroot-resistance mechanism in *B. napus*. Identification of clubroot-resistant genes may be used in clubroot-resistant breeding, as well as to elucidate the molecular mechanism behind *B. napus* clubroot-resistance. We used three *B. napus* transcriptome samples to construct a transcriptome sequencing library by using Illumina HiSeq™ 2000 sequencing and bioinformatic analysis. In total, 171 million high-quality reads were obtained, containing 96,149 unigenes of N50-value. We aligned the obtained unigenes with the Nr, Swiss-Prot, clusters of orthologous groups, and gene ontology databases and annotated their functions. In the Kyoto encyclopedia of

genes and genomes database, 25,033 unigenes (26.04%) were assigned to 124 pathways. Many genes, including broad-spectrum disease-resistance genes, specific clubroot-resistant genes, and genes related to indole-3-acetic acid (IAA) signal transduction, cytokinin synthesis, and myrosinase synthesis in the Huashuang 3 variety of *B. napus* were found to be related to clubroot-resistance. The effective clubroot-resistance observed in this variety may be due to the induced increased expression of these disease-resistant genes and strong inhibition of the IAA signal transduction, cytokinin synthesis, and myrosinase synthesis. The homology observed between unigenes 0048482, 0061770 and the Crr1 gene shared 94% nucleotide similarity. Furthermore, unigene 0061770 could have originated from an inversion of the Crr1 5'-end sequence.

**Key words:** *B. napus*; Clubroot; Transcriptome; Clubroot-resistance genes; Homology