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Identification of candidate genes for resistance to Soybean mosaic virus strain SC3 by using fine mapping and transcriptome analyses

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This study is a continuation of our earlier reports on the identification and mapping of the Soybean mosaic virus (SMV) strain SC3 resistance gene present on chromosome 13 (LG F) of soybean (*Glycine max* (L.) Merr.). We used a combination of fine mapping and transcriptome sequencing to discover the candidate genes for SMV resistance in Qihuang-1. To fine-map the resistance gene, near-isogenic lines (NILs) from a cross between Qihuang-1 (resistant) and Nannong 1138-2 (susceptible) were genotyped with simple sequence repeats (SSR) and insertion and deletion (indel) markers to identify recombination events. Analysis of plants carrying key recombination events placed the resistance gene to a 180-kb region of the 'Williams 82' genome sequence with 17 annotated genes. Transcriptome and quantitative real-time PCR (qRT-PCR) analyses revealed that SMV resistance in Qihuang-1 was probably attributable to the four candidate genes (*Glyma13g25920*, *Glyma13g25950*, *Glyma13g25970* and *Glyma13g26000*). The four candidate genes identified in this study can be used in further studies to investigate the role of resistance genes in conferring SC3 resistance in Qihuang-1.