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Marker-assisted pyramiding of soybean resistance genes  $R_{SC4}$ ,  $R_{SC8}$  and  $R_{SC14Q}$  to soybean mosaic virus

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Soybean mosaic virus (SMV) is one of the major viral pathogens on soybean crops worldwide. Three SMV resistance genes,  $R_{SC4}$ ,  $R_{SC8}$  and  $R_{SC14Q}$  from Dabaima, Kefeng No.1 and Qihuang No.1 cultivars had been identified and mapped on soybean chromosomes 14, 2 and 13, respectively. Soybean cultivar Nannong1138-2 is widely grown in the Yangtze river valley of China. In this study, crosses were made between (Qihuang No.1 × Kefeng No.1) × (Dabaima × Nannong1138-2). Ten simple sequence repeat markers associated with three resistance loci ( $R_{SC4}$ ,  $R_{SC8}$  and  $R_{SC14Q}$ ) were used to assist pyramided breeding. Pyramided families containing three resistance loci ( $R_{SC4}$ ,  $R_{SC8}$  and  $R_{SC14Q}$ ) were evaluated by inoculating with 21 SMV strains from China. Results indicated that the ten markers can be used effectively to assist the selection of resistant individuals containing genes  $R_{SC4}$ ,  $R_{SC8}$  and  $R_{SC14Q}$ . A total of 53 F<sub>6</sub> plants were confirmed to contain three homozygous alleles conferring SMV resistance. Five F<sub>7</sub> homozygous pyramided families exhibited resistance to 21 strains of SMV and showed desirable agronomic traits using dual selection. The resistance-gene-derived pyramided families have practical breeding value by providing broad-spectrum resistance against the existing strains of SMV in China.