

Kinoshita and Shiranui, soybean varieties resistant to Asian soybean rust, have a second resistance gene

Asian soybean rust (ASR) is a major soybean disease that causes early yellowing and defoliation of soybean, resulting in reduced yield. This disease is widespread in soybean production areas around the world, especially in tropical and subtropical regions, and is a serious impediment to the stable supply of soybeans to international markets. In recent years, the susceptibility of the ASR pathogen to fungicides has decreased, resulting in increased control costs and environmental impact. Soybean varieties with resistance genes (*Rpp*) against ASR have since been developed in various regions. The soybean varieties Kinoshita and Shiranui were identified in 2008 as ASR-resistant varieties carrying *Rpp5*. These two varieties have shown resistance to many soybean rusts in various regions and are widely used in Latin America and Asia as parents for resistance variety development. However, their resistance to a wide range of rusts suggested that both varieties may also possess resistance other than *Rpp5*. Therefore, this study was conducted to determine the resistance potential of the Kinoshita and Shiranui varieties in order to appropriately and effectively utilize their resistance to a wide range of ASR pathogens in variety development.

The resistant varieties Kinoshita and Shiranui were crossed with susceptible varieties to produce F₂ populations. Each F₂ population was inoculated with the Japanese ASR strain E1-4-12 and the Brazilian strain BRS-2.5, which differ greatly in virulence, and evaluated for ASR resistance-related traits, respectively. QTL analysis of resistance-related traits was performed to identify resistance loci for each pathogen strain. QTL analysis revealed that Kinoshita and Shiranui possess loci *Rpp3* and *Rpp5*, which exhibit resistance to ASR strains E1-4-12 and BRP-2.5, respectively (Fig. 1). The *Rpp3* carried by both varieties was resistant only to strain E1-4-12 of the two strains used in this study, and the *Rpp5* of both varieties was effective only against strain BRP-2.5. The *Rpp5* and *Rpp3* of the Kinoshita and Shiranui varieties have similar genetic effects as well as genetic loci, suggesting that the two varieties may have the same or very similar resistance-type alleles in *Rpp5* and *Rpp3*, respectively (Table 1).

Because ASR pathogen in the soybean field is known to be diverse, both *Rpp5* and *Rpp3* should be introduced when Kinoshita and Shiranui are used for developing varieties with ASR resistance that have the same levels of resistance as Kinoshita and Shiranui. For the two resistance loci *Rpp3* and *Rpp5*, the use of DNA markers flanking and sandwiching the loci allows for effective and efficient selection for resistant plants in breeding for ASR resistance.

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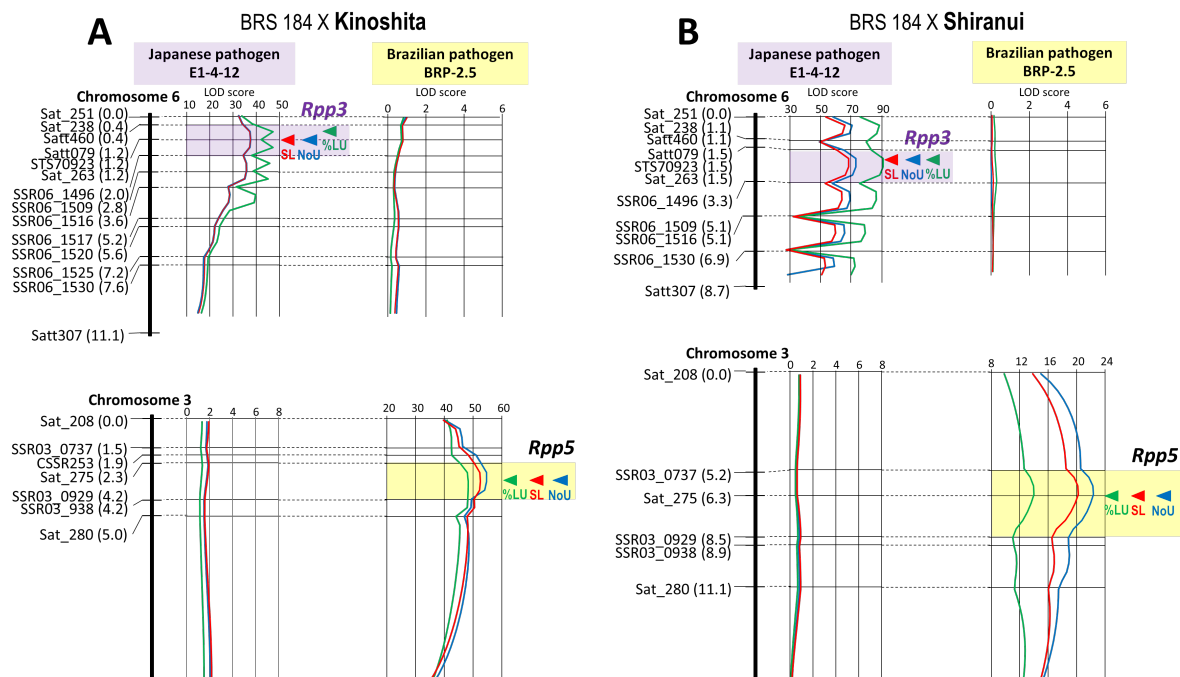


Fig. 1. Genetic maps around resistance loci *Rpp3* and *Rpp5* for Asian soybean rust in Kinoshita (A) and Shiranui (B) mapping populations

Each mapping population was created by crossing with the susceptible variety BRS 184. The DNA marker names and genetic distances from the top marker are shown on the left side of each linkage group, and the LOD values and their peak positions in QTL analysis for resistance-related traits (NoU: numbers of uredinia per lesion; %LU: frequency of lesions with uredinia; SL: Sporulation level) against E1-4-12 and BRP-2.5 strains are shown on the right side of each linkage group.

Table 1. Genetic effects and variance explained (VE) of the resistance genes *Rpp3* and *Rpp5* in the number of uredinia per lesion (NoU)

Parents of population	Resistance gene	Nearest marker	Pathogenic strain	Additive effect ¹⁾	Dominance effect ¹⁾	Variance-explained (%)
BRS 184 × Kinoshita	<i>Rpp5</i>	SSR03_0929	BRP-2.5	-1.15	-0.03	82.60%
	<i>Rpp3</i>	Sat_263	E1-4-12	-0.81	-0.74	51.50%
BRS 184 × Shiranui	<i>Rpp5</i>	Sat_275	BRP-2.5	-0.97	-0.09	52.29%
	<i>Rpp3</i>	Sat_263	E1-4-12	-0.82	-0.81	52.37%

¹⁾ Genetic effects (additive and dominant effects) are relative effects of the resistant (Kinoshita or Shiranui) allele to the susceptible (BRS 184) allele. *Rpp5* of Kinoshita and Shiranui are codominant due to their less dominant effects, while *Rpp3* of both varieties are completely dominant.

Reference: Yamanaka et al. (2023) *Plants* 12: 2263 © The Author(s) 2023

The figure and the table were modified from Yamanaka et al. (2023).