

P-148

Genetic analysis and molecular mapping of resistance gene to *Phakopsora pachyrhizi* in soybean germplasm SX6907

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Soybean rust caused by *Phakopsora pachyrhizi* Sydow has been reported in numerous soybean-growing regions worldwide. The development of rust-resistant varieties is the most economical and environmentally safe method to control the disease. Since 1980s, more than 13000 germplasms have been screened for rust resistance in China. SX6907, a Chinese landrace, is resistant to *P. pachyrhizi* and exhibits immune reaction compared with the known *Rpp* genes. These characteristics suggest that SX6907 may carry at least one novel *Rpp* gene/allele. Three F₂ populations from the crosses of SX6907 (resistant) and Tianlong1, Zhongdou40, and Pudou11 (susceptible) were used to map the *Rpp* gene. Three resistance responses (immune, red-brown, and tan-colored lesion) were observed from the F₂ individuals. The segregation follows a ratio of 1(resistance):2(heterozygous):1(susceptible), indicating that the resistance in SX6907 is controlled by a single incomplete dominant gene (designated as *Rpp6907*). Results showed that *Rpp6907* was mapped on soybean chromosome 18(molecular linkage group G, MLG G) flanked by simple sequence repeat (SSR) markers SSR24 and SSR40 at a distance of 111.9 kb. Among the ten genes marked within this 111.9-kb region between the two markers, three genes (*Glyma18g51930*, *Glyma18g51950*, and *Glyma18g51960*) are nucleotide-binding site and leucine-rich repeat-type genes. These genes may be involved in recognizing the presence of pathogens and ultimately conferring resistance. Based on resistance spectrum analysis and mapping results, we inferred that *Rpp6907* is a novel gene different from *Rpp1* in PI 200492, PI 561356, PI 587880A, PI 587886, and PI 594538A, or a new *Rpp1-b* allele.