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Soybean rust resistance sources and inheritance in the common bean (*Phaseolus vulgaris* L.)

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ABSTRACT. Soybean rust (SBR), caused by the fungus *Phakopsora pachyrhizi*, has been reported in common bean (*Phaseolus vulgaris* L.) cultivars and elite lines that were infected under controlled and natural field conditions in South Africa, the United States, Argentina, and Brazil. Although SBR is currently not a top priority problem for the common bean crop, many bean breeders are concerned about this disease because of the high severity and virulence diversity of *P. pachyrhizi* and its broad host range. In this study, a set of 44 *P. vulgaris* genotypes were tested for resistance to *P. pachyrhizi*; these genotypes included resistance sources to several fungal common bean diseases, carioca-, black- and red-seeded Brazilian cultivars, and elite lines that were developed by the main common bean breeding programs in Brazil. Twenty-four SBR resistance sources were identified. They presented the

reddish-brown (RB) lesion type, characterizing resistance reactions. In addition to the RB lesion type, the PI181996 line presented the lowest disease severity mean score, considering its associated standard error value. For this reason, it was crossed with susceptible lines to study the inheritance of resistance. The results support the hypothesis that resistance to SBR in PI181996 is monogenic and dominant. We propose that this SBR resistance gene, the first to be identified and characterized in common bean, might be designated as *Pkp-1*.

Key words: Disease resistance; Inheritance study; *Phakopsora pachyrhizi*; Plant breeding; Resistance gene

