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Pathogenicity of soybean rust populations in Brazil in 4 cropping seasons of 2007–2011.

(Patogenicidade de populações da ferrugem da soja no Brasil em 4 safras de 2007 a 2011.)

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Soybean rust caused by *Phakopsora pachyrhizi* is one of the most serious threats to soybean production in Brazil. In this study, we evaluated pathogenicity of the 7 rust samples collected in Brazil in the 2010/11 season based on infection types produced on 16 differential varieties, and compared them with those in 3 seasons of 2007/08–2009/10. When the data were classified into 3 categories: susceptible, intermediate, and resistant, none of the 7 samples from the 2010/11 season showed identical pathogenicity profile in the differentials. Cluster analysis and principal coordinate analysis revealed that 31 rust samples from the 4 seasons vary geographically and temporally in pathogenicity. The cluster analysis divided the 31 samples into 2 groups (A and B), and the 7 samples from the 2010/11 season were scattered throughout in both groups. The frequencies of susceptible reaction produced in differentials 3–6, 9, 10, and 12 were significantly higher for group A than for group B. The differentials containing resistance genes *Rpp1*, *Rpp2*, *Rpp3* and *Rpp4*, except for PI 587880A, displayed resistant reaction to only <13%, <39%, 23%, and 38% of Brazilian rust populations, respectively. In contrast, PI 587880A (*Rpp1*), Shiranui (*Rpp5*), and 3 *Rpp*-unknown differentials PI 587855, PI 587905, and PI 594767A, showed resistant reaction to 74%–96% of the populations. This study demonstrated that (i) pathogenicity of *P. pachyrhizi* populations was diverse in Brazil in the 4 seasons, (ii) Brazilian populations of group A were more virulent than those of group B, and (iii) 5 differentials have been effective against recent pathogen populations in the country.