

Characterization of *Phakopsora pachyrhizi* races from a broad geographical and temporal collection

Fernanda Machado Castanho¹; Marcia Kamogae Kuwahara²; Gisely Patricia Fernandes³; Luana Mieko Darben⁴; Alessandra Yokoyama¹; Danielle Cristina Gregório da Silva²; Ricardo Vilela Abdelnoor²; Mauricio Conrado Meyer²; Francismar Corrêa Marcelino-Guimarães²

¹Universidade Estadual de Londrina, Londrina, PR, Brasil. fer.mcastanho@gmail.com; ²Embrapa Soja;

³Universidade do Norte do Paraná - UNOPAR; ⁴Corteva Agriscience.

Abstract

Phakopsora pachyrhizi (Pp) causes the Asian rust soybean, one of the most devastating diseases of the crop. Studies have been revealed a large diversity of pathotypes and efficacy of *Rpp* genes (Resistance to Pp) varying according to the regions of origin of the surveyed. The use of fungicides and adoption of resistant cultivars shown ineffective against all variants of the pathogen. Knowledge of the pathogenic variability existing in populations of pathogens with agronomic importance is very useful for effective control strategies. Here, virulence responses of 38 Pp pure isolates, representing a broad distribution along almost 20-year span and geographic regions (Americas, Africa and Asia), were evaluated against 12 soybean sources of *Rpp* genes. Five quantitative characters were assessed in a total of 90 lesions per genotype under a stereomicroscope: sporulation level (SL); number of uredinia per lesion (NoU); frequency of lesions with uredinia (%LU); lesion color (LC); and frequency of open uredinia (%OU). Phenotypic values were used to rank the level of resistance of each accession. Based on the quantitative data, six qualitative categories were established, varying among susceptible to resistant and immune reactions. Per binary codification, the races were established through a triplet coding system. We identified 16 races distributed among 33 isolates. The major race (11514) grouped 8 isolates showing virulence profile to the *Rpp* 1 (PI 200492), 2, 3, 4, and 5 (PI 200526) and avirulence for *Rpp* from the PI 594766, *Rpp*1(PI 587880A) and 5 (PI 200487). The race 31515 was the most virulent, composes by one Brazilian isolate from Rio Verde, GO in 2014, presenting avirulence only for *Rpp*1b and *Rpp* from PI 594756. Even with a broad pathogenic diversity, the races did not present a temporal and geographical pattern of distribution, once isolates collected in different years and regions, such as from Brazil and Japan, were grouped in a same race. Once the mechanisms of genetic variability, distribution of races and the evolution of the pathogenicity are deciphered, it will contribute to development of novel effective control strategies.

Key-words: Asian soybean rust; virulence; variability