The pathogenicity of Asian soybean rust pathogen in Mexico can be grouped into two broad trends

Asian soybean rust (ASR) caused by *Phakopsora pachyrhizi* is the most important soybean disease in tropical and subtropical soybean cultivation areas. In Mexico, domestic soybean production is increasing each year, and with it, ASR disease has become a major problem. Plant disease control through the introduction of resistant varieties is advantageous in terms of low cost and low environmental impact, but resistance genes must be selected for breeding according to the virulence of the target pathogen. Thus, we analyzed the virulence of *P. pachyrhizi* populations in the major soybean production areas in Mexico.

ASR samples were taken from major soybean production areas in Mexico. Four samples were collected in Tamaulipas and San Luis Potosi states in 2015, and 19 samples were collected in Tamaulipas and Chiapas states from 2016 to 2019. These 23 samples were inoculated onto 12 ASR differential varieties and the reactions were evaluated as resistant, intermediate, or susceptible types. Clustering analysis showed that these ASR samples were classified into two groups (Group 1 and Group 2) that exhibited different virulence characteristics (Fig. 1A). Group 1 consisted of ASR samples collected from Tamaulipas, where soybean varieties carrying the resistance gene *Rpp1-b* were resistant and effective for disease control. However, soybean PI 200492 carrying *Rpp1*, PI 230970 carrying *Rpp2*, and PI 462312 carrying *Rpp3* showed susceptibility to ASR infection in most samples, thus the genes were not effective. (Figs. 1B and 1C). These characteristics were consistent with those exhibited by many of the ASR pathogens in South America. Group 2, on the other hand, consisted mainly of ASR samples collected from Chiapas. Five differential varieties with four resistance genes showed opposite reaction patterns to those from Tamaulipas. The virulence characteristics of this group were consistent with those reported for many ASR fungi in North America. It is rare to observe such clear geographic variation in virulence within a small area of a single country.

The present study found that Mexico has diverse ASR pathogen populations with the virulence characteristics of those reported from both South and North America. We also found a highly virulent ASR sample, MRP-16, which is pathogenic to all seven resistance genes except *Rpp1-b* of PI 587880A. The gene-pyramided line (No6-12-1) carrying the three resistance genes *Rpp2, Rpp4,* and *Rpp5* was resistant to all ASR samples, including MRP-16, and effective in controlling the disease (Fig. 1B). This gene-pyramided line, which is effective against Mexican ASR, is also known to show high resistance, making it a promising breeding material in Mexico. In addition, identifying factors that contribute to the large differences in virulence detected in this study may be helpful in ASR control.

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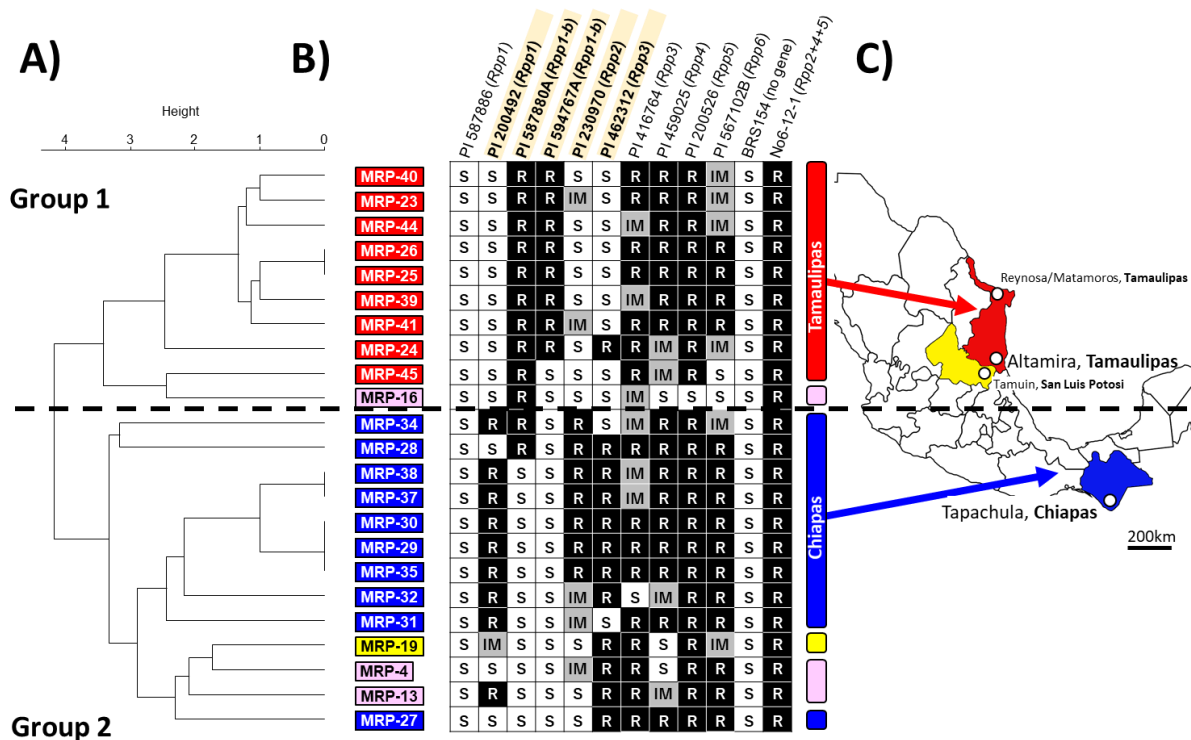
Fig. 1. A dendrogram of Asian soybean rust samples (MRPs) collected in Mexico based on their virulence (A), reaction profiles of the differential varieties (B), and regions where they were collected (C)

Samples obtained in 2016-2019 in Tamaulipas state are shown in red, samples obtained in 2015 in pink, samples obtained in 2015 in San Luis Potosi state in yellow, and samples obtained in 2018 in Chiapas state in blue. The parentheses after the name of the differential varieties indicate the resistance gene (*Rpp*) possessed by R, IM, and S for resistant, intermediate, and susceptible types, respectively.

References: García-Rodríguez et al. (2017) *Mexican Journal of Phytopathology*, 35(2):338–349. https://doi.org/10.18781/r.mex.fit.1701-5, and
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