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Virulence Diversity of Soybean Rust Isolates from Africa

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Abstract

Soybean rust caused by the biotrophic pathogen *Phakopsora pachyrhizi* is a highly destructive disease that occurs worldwide causing substantial yield losses. The disease has so far spread across most soybean growing areas in Africa threatening the growing soybean sector. Breeding for resistance is so far the best management strategy for soybean rust. Knowledge about *P. pachyrhizi* virulence is therefore needed to guide development and deployment of soybean germplasm with durable resistance against all pathogen populations. To assess the virulence diversity of *P. pachyrhizi*, 17 isolates from four different African countries were characterised on 11 soybean host differentials with known resistance genes. All the isolates induced tan lesions with abundant sporulation on genotypes without any known resistance genes and on those with resistance genes Rpp4 and Rpp5b. The most durable gene was Rpp2 as 96 % of the isolates induced reddish brown lesions with little or no sporulation. The South African isolate was the most virulent with virulence on six of the host differentials, whereas those from Malawi and some of the isolates from Tanzania had the lowest virulence. Four distinct pathotypes were identified in this study, one each in Kenya, Malawi and South Africa and two in Tanzania representing considerable *P. pachyrhizi* virulence. The three isolates from Malawi and 50 % of the Tanzania isolates were grouped into one common pathotype, suggesting the presence of an identical *P. pachyrhizi* population in those countries. Soybean genotypes carrying Rpp1b, Rpp2, Rpp3, and Rpp5a resistance genes and cultivars Hyuuga and UG 5 were found to be resistant against most of the African isolates and therefore may be useful for soybean-breeding programs in Africa or elsewhere.

Keywords: Differentials, *Phakopsora pachyrhizi*, resistance