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Virulence diversity of *Phakopsora pachyrhizi* isolates from East Africa compared to a geographically diverse collection

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Soybean rust caused by the biotrophic pathogen *Phakopsora pachyrhizi* is a highly destructive disease that occurs worldwide causing substantial yield losses. Knowledge about *P. pachyrhizi* virulence is needed to guide development and deployment of soybean germplasm with durable resistance against all pathogen populations. To assess the virulence diversity of *P. pachyrhizi*, 25 isolates from eight different countries including 17 isolates from Africa were characterized on 11 soybean genotypes. 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. Of the African isolates tested, the South African isolate was the most virulent, whereas those from Kenya, Malawi and some of the isolates from Tanzania had the lowest virulence. An Argentinian isolate was virulent on most host differentials, including two cultivars carrying multiple resistance genes. Ten distinct pathotypes were identified in this study, four of which comprised the African isolates representing considerable *P. pachyrhizi* virulence. 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.