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INVESTIGATIONS INTO GENETIC DIVERSITY OF *PUCCINIA KUEHNII* SUPPORT THE INTRODUCTION OF THE SUGARCANE ORANGE RUST PATHOGEN FROM AFRICA TO THE AMERICAS

J. DIJOUX^{1.5}, L. BLONDIN^{2.3}, P. ROUMAGNAC^{2.3}, D. CARDENAS⁷, L.M. CANO⁷, S. SOOD⁸, J. H. DAUGROIS^{2.3}, J.-Y. HOARAU^{1.5,6}, AND P. ROTT^{2.3}

¹eRcane, La Réunion, France; ²CIRAD, UMR PHIM, Montpellier, France; ³PHIM, Plant Health Institute, Univ. Montpellier, CIRAD, INRAE, Institut Agro, IRD, Montpellier France; ⁴CIRAD, UMR AGAP Institut, Montpellier, France; ⁵UMR AGAP Institut, Univ Montpellier, CIRAD, INRAE, Institut Agro, Montpellier, France; ⁶CIRAD, UMR AGAP Institut, Sainte-Clotilde, La Réunion, France; ⁷University of Florida, Institute of Food and Agricultural Sciences IFAS, Department of Plant Pathology, Indian River Research and Education Center IRREC, Fort Pierce, USA; ⁸USDA-ARS, Sugarcane Field Station, Canal Point, USA

e-mail: philippe.rott@cirad.fr

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Orange rust caused by *Puccinia kuehnii* poses a significant threat to sugarcane cultivation in countries affected by this disease. Orange rust disease was limited to the Eastern Hemisphere for over a century before it was first reported from the Western Hemisphere (Florida) in 2007. Since then, P. kuehnii spread all over the Americas where several sugarcane varieties grown commercially showed severe disease symptoms. These susceptible varieties needed to be progressively replaced by tolerant or resistant ones. Understanding the genetic diversity and variation in virulence of P. kuehnii is crucial for developing effective control strategies. However, the complexity of working with an obligate biotrophic fungus, like P. kuehnii, which cannot be grown on artificial media, creates challenges for genetic studies. Additionally, rust fungi are dikaryotic organisms possessing two highly heterozygous haploid nuclei in each urediniospore and a reference genome is not available yet for the orange rust pathogen. In this study, we investigated the genetic diversity of P. kuehnii using a collection of fungal isolates from 20 geographical locations. No significant diversity was found using 19 microsatellite markers previously used in Brazil to demonstrate the occurrence of different genotypes of the pathogen in this country [Urashima et al., 2020. J. Phytopathol. 168(10):581-590]. However, we confirmed that the isolates of P. kuehnii from the Western Hemisphere can be differentiated from those of the Eastern Hemisphere (including Africa) using the single nucleotide polymorphism (SNP) PkITS1-183A>G initially discovered by Glynn et al. [2010. Plant Pathol. 59(4):703-711]. Additional genetic diversity among these isolates was demonstrated based on the partial sequencing of three effector-coding regions of *P. kuehnii*. All these data support the hypothesis that the sugarcane orange rust isolates in the Americas diverged from isolates of the pathogen that previously spread in Africa.