



Genetic diversity among *Puccinia melanocephala* isolates from Brazil assessed using simple sequence repeat markers

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ABSTRACT. Brown rust (causal agent *Puccinia melanocephala*) is an important sugarcane disease that is responsible for large losses in yield worldwide. Despite its importance, little is known regarding the genetic diversity of this pathogen in the main Brazilian sugarcane cultivation areas. In this study, we characterized the genetic diversity of 34 *P. melanocephala* isolates from 4 Brazilian states using loci identified from an enriched simple sequence repeat (SSR) library. The aggressiveness of 3 isolates from major sugarcane cultivation areas was evaluated by inoculating an intermediately resistant and a susceptible cultivar. From the enriched library, 16 SSR-specific primers were developed, which produced scorable alleles. Of these, 4 loci were polymorphic and 12 were monomorphic for all isolates evaluated. The molecular

characterization of the 34 isolates of *P. melanocephala* conducted using 16 SSR loci revealed the existence of low genetic variability among the isolates. The average estimated genetic distance was 0.12. Phenetic analysis based on Nei's genetic distance clustered the isolates into 2 major groups. Groups I and II included 18 and 14 isolates, respectively, and both groups contained isolates from all 4 geographic regions studied. Two isolates did not cluster with these groups. It was not possible to obtain clusters according to location or state of origin. Analysis of disease severity data revealed that the isolates did not show significant differences in aggressiveness between regions.

Key words: Brown rust; Genetic diversity; Microsatellite; Sugarcane; *Puccinia melanocephala*; Simple sequence repeat