GENETIC DIVERSITY OF ISOLATES OF *Crinipellis perniciosa* FROM *Theobroma* spp USING ISSR MARKERS

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Witches broom disease caused by the basidiomycete fungus *Crinipellis perniciosa* (Stahel) Singer reduce yield significantly in cupuassu tree (Theobroma grandiflorum) in Amazon region. The variability of the *C. perniciosa* pathogen, as well as the absence of a suitable screening method for the precocious evaluation of the resistance to have been limiting the identification of source of resistance against *C. perniciosa* and, consequently, the incorporation of new genotypes of interest in breeding programs of the cupuassu tree. The objective of this work went to characterize the genetic diversity of nineteen *C. perniciosa* isolates from vegetative brooms of *T. grandiflorum* collected in the Amazon region (Amazon, Pará, Roraima and Amapá) and of *Theobroma* spp. collected in the State of the Amazon. After the optimization of the technique of ISSR for *C. perniciosa*, 100 UBC oligonucleotídeos (primers 801-900) were evaluated to select a set of primers that could be useful for genetic variability study. Preliminarily were selected four primers that yielded clear and polymorphic bands: 811 (GA) 8C, 844 (CT) 8TRC, 884 HBH (AG) 7 and 885 BHB (GA) 7. The polymorphism analysis used the coefficient of Jaccard and UPGMA method. Although a small *primers* number was used, the results showed that it was more difficult to distinguish isolates obtained from the different hosts than those from different States. In general, isolates from different host plant (*T. grandiflorum* and *Theobroma* spp.) were clustered together by State. However was observed that MC17 and MC18 isolates showed exclusive bands. These results indicated that the importance of knowing the variability of *C. perniciosa* for incorporating durable resistance in the cupuassu breeding programs.