01.014 - GENOTYPE CHARACTERIZATION OF THE *Haematobia irritans* (DIPTERA: MUSCIDAE) FROM BRAZIL, DOMINICAN REPUBLIC AND COLOMBIA BASED ON RANDOMLY AMPLIFIED POLYMORPHIC DNA (RAPD) ANALYSIS

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Haematobia irritans is an economically important obligate blood feeding ectoparasite of cattle. Parasitism of cattle by an economic level of horn flies can result in reduced weight gain as a result of decreased feed efficiency, and decreased milk production. In addition, diminished leather quality can result from intense horn fly feeding. The abundance of genotypes within and among populations involves two different, but related components: demographic and genetic structure. Demographic structure refers to processes influencing the number and distribution of phenotypical classes of individuals. The genetic structure which can be described as the genetic variation distribution resulting from the action of factors such as migration, selection, mutation and genetic derive. In this study, the randomly amplified polymorphic DNA (RAPD) technique was used to analyze genetic variability of populations of horn fly from Brazil, Dominican Republic and Colombia, to evaluate the genotypic similarity of the populations studied and also to get a RAPD marker able to identifying the geographical origin of each of those populations. The hierarchical group analysis shows that Colombia population was more distant from the others, presenting zero similarity with the others, while the closest populations were Brazil and Dominican Republic with 0.250 similarity. This value leads to the conclusion that Brazil and Dominican Republic populations share approximately 25% of nucleotide sequences complementary to the selected primers, which promotes the genotype distinction among Brazilian, Colombia and Dominican Republic population from different geographical origins. The primer that best characterized the different American's populations of *H. irritans* was OpH19, once it generated a single genotype pattern for each one of the populations studied, being the best molecular weight marker to distinct the geographic origin of the samples. * luciana@cpafro.embrapa.br Apoio Financeiro: CAPES