



Genotyping in the Brazilian Criollo Horse Stud Book: resources and perspectives

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ABSTRACT. The goal of this research was to evaluate the ability of the genotyping information available in the Brazilian Criollo Horse Stud Book to describe the genetic variability of the breed and the exclusion probability determined in comparative tests. Altogether, two softwares were used in the analyses of the available genotypes: Cervus 3.0.3 and Genepop 4.0. Eight microsatellite markers totaled 109 alleles,

with an average of 13.6 ± 0.6 alleles per locus. Large differences between expected and observed heterozygosity were ubiquitous (0.821 ± 0.07 and 0.470 ± 0.17 , respectively). Although the estimated null allele frequency caused initial concern (0.284 ± 0.199), it is likely that it was a reflection of the inbreeding coefficients found (0.432 ± 0.184). All loci showed significant deviation from Hardy-Weinberg equilibrium, with heterozygote deficit ($P < 0.0001$) and genotypic linkage disequilibrium with at least one marker. The high polymorphic information content (0.798 ± 0.088) could not warrant exclusion power for three loci (HMS7, HMS6 and HTG4) above 50% (0.491 ± 0.158). However, combined exclusion probability reached 99.61%, a level close to ideal. The results demonstrate the excellent performance of the markers assessed in describing the genetic status of the breed and suggest the considerable ability to establish parentage.

Key words: SSR; Parentage testing; Genetic monitoring