

## Genetic diversity in the Pantaneiro horse breed assessed using microsatellite DNA markers

E.H. Giacomoni<sup>1</sup>, G.P. Fernández-Stolz<sup>1</sup> and T.R.O. Freitas<sup>1,2</sup>

<sup>1</sup>Programa de Pós-Graduação em Genética e Biologia Molecular, Universidade Federal do Rio Grande do Sul, Instituto de Biociências, Porto Alegre, RS, Brasil

<sup>2</sup>Departamento de Genética, Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brasil

Corresponding author: E.H. Giacomoni  
E-mail: elise.giacomoni@ufrgs.br

Genet. Mol. Res. 7 (1): 261-270 (2008)

Received July 18, 2007

Accepted January 24, 2008

Published March 18, 2008

**ABSTRACT.** The genetic variability for a sample of 227 animals from three populations of Pantaneiro horses was estimated using data from 10 microsatellite loci. The number of alleles and the proportion of heterozygosity indicated high variability. A total of 91 alleles were found, with a significantly high mean number of alleles. The mean polymorphic information content was 0.7 and the paternity exclusion probability was 99.3%. The inbreeding coefficient ( $F_{IS}$ ) was low for the three populations: Ipiranga ( $F_{IS} = 0.147$ ), Nova Esperança ( $F_{IS} = 0.094$ ) and Promissão ( $F_{IS} = 0.108$ ). Genetic differentiation among all three populations was low ( $F_{ST} = 0.008$  to  $0.064$ ). Three methods were used to test for a recent bottleneck effect. The graphical method and the Wilcoxon test using the stepwise mutation model showed no bottleneck pattern for any of the populations. The test by two-phase mutation model showed genetic signatures of bottleneck for Ipiranga and Promissão. When we consider standard deviation value for Nova Esperança, the  $M$ -statistic detected a bottleneck pattern, but this result could be explained by a sample size effect. Therefore, there is no immediate cause for concern regarding loss of variation within the breed.

**Key words:** Genetic variability; Horse; Pantaneiro horses; Microsatellites