Genetic diversity and population structure in Brazilian Mangalarga Marchador horses

J.B. DeAssis[1], D.M. DeLaat[1], M.G.C.D. Peixoto[2], J.A.G. Bergmann[3], C.G. Fonseca[1] and M.R.S. Carvalho[1]

[1]Departamento de Biologia Geral, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brasil
[2]EMBRAPA Gado de Leite, Juiz de Fora, MG, Brasil
[3]Departamento de Zootecnia, Escola de Medicina Veterinária, Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brasil

Corresponding author: M.R.S. Carvalho
E-mail: mraquel@icb.ufmg.br

ABSTRACT. One hundred and fifteen unrelated Mangalarga Marchador horses were sampled from three geographically distinct regions of Minas Gerais State, Brazil (South, Southeast, and Northeast) and tested for 10 microsatellite loci. Genetic diversity and population structure parameters were estimated with ARLEQUIN 3.0, CERVUS 2.0, POPGENE 1.31, GENEPOP on the web, STRUCTURE 2.0, and SPAGEDI 1.2 software packages. Under Hardy-Weinberg assumptions, seven markers were at equilibrium (LEX014, LEX017, LEX019, SGCV23, TKY321, VHL20, and VIASH39), while two (ASB3 and LEX031) presented significant homozygote excess. Seventy-four alleles were identified in these nine markers, with a mean of 8.22 alleles. Mean heterozygosity was 0.637 and polymorphism information content was 0.662. Markers ASB3, LEX019, SGCV23, TKY321, and VHL20 were highly informative (PIC >0.7) and may be useful for eventual expansion of parentage test panels. The F_{ST} value (0.0562) indicated relatively little geographical structure. However, based on a Bayesian-based cluster analysis under a three-cluster model, 94% of the 115 individuals were correctly assigned to the subpopulations from where they were sampled. Mean

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pairwise f was relatively high (0.11), and in spite of the efforts towards non-consanguineous sampling, 1% of the pairs of individuals shared over 50% of the alleles. These results strongly suggest that the population is genetically structured. Under a conservation genetics approach, two strategies are recommended: avoidance of crosses between highly endogamic individuals and stimulation of crosses between individuals from those regions for which low genetic flow was identified.

Key words: Mangalarga Marchador horse; Genetic diversity; Population genetic structure