Genetic diversity and population structure of different varieties of Morada Nova hair sheep from Brazil

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ABSTRACT. The aim of this study was to analyze genetic diversity and population structure among varieties of White (N = 40), Red (N = 32), and Black (N = 31) Morada Nova hair sheep from flocks in the northeastern Brazilian semiarid region. Fifteen nuclear microsatellite markers and two regions of mitochondrial DNA were used. The intra-population analysis demonstrated that the White variety had higher diversity, while the Red variety had the lowest values. The Bayesian analysis to assess the genetic population structure allowed differentiation between White, Red, and
Black varieties, and revealed a tendency towards sub-structuring in the White variety flocks from the States of Ceará and Paraíba. The results of analyses of molecular variance showed that the greatest genetic structure was found when comparing flocks rather than varieties (8.59 vs 6.64% of the total variation, P < 0.001). Based on genetic distance, Dtl, both the dendrogram analysis and the principal coordinate analysis showed the formation of two main groups: one composed of White and another of Black and Red individuals. Five and two haplotypes were found for the D-loop region and the ND5 gene, respectively. A haplotype unique to the Red variety was found in the D-loop region and a variety haplotype unique to the Black variety was found in the ND5 gene; however, these frequencies were low and therefore require further validation. These results support the existence of substantial differences between the Red and White varieties and should be used as separate genetic resources and to improve conservation programs.

**Key words:** *Ovis aries*; mtDNA; Animal genetic resources; Microsatellites; Genetic management