

## Short Communication

## Analysis of polymorphisms in the mitochondrial *ND5* gene in Pantaneira and Creole breeds of sheep

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**The aim of this study was to assess genetic variation between a population of Pantaneira sheep in the Brazilian state of Mato Grosso do Sul, and Creole sheep from the south of the country by molecular analysis of the *ND5* gene in mitochondrial DNA. The analysis revealed the presence of 16 haplotypes with all Pantaneira sheep grouped together carrying a single haplotype, and there was no grouping with any of the Creole sheep. The  $F_{ST}$  value was 0.44, indicating that there is a genetic difference between the two breeds, which may indicate that both breeds underwent differentiation.**

**Key words:** *Ovis aries*, *ND5* gene, genetic diversity, phylogeny, breed differentiation.

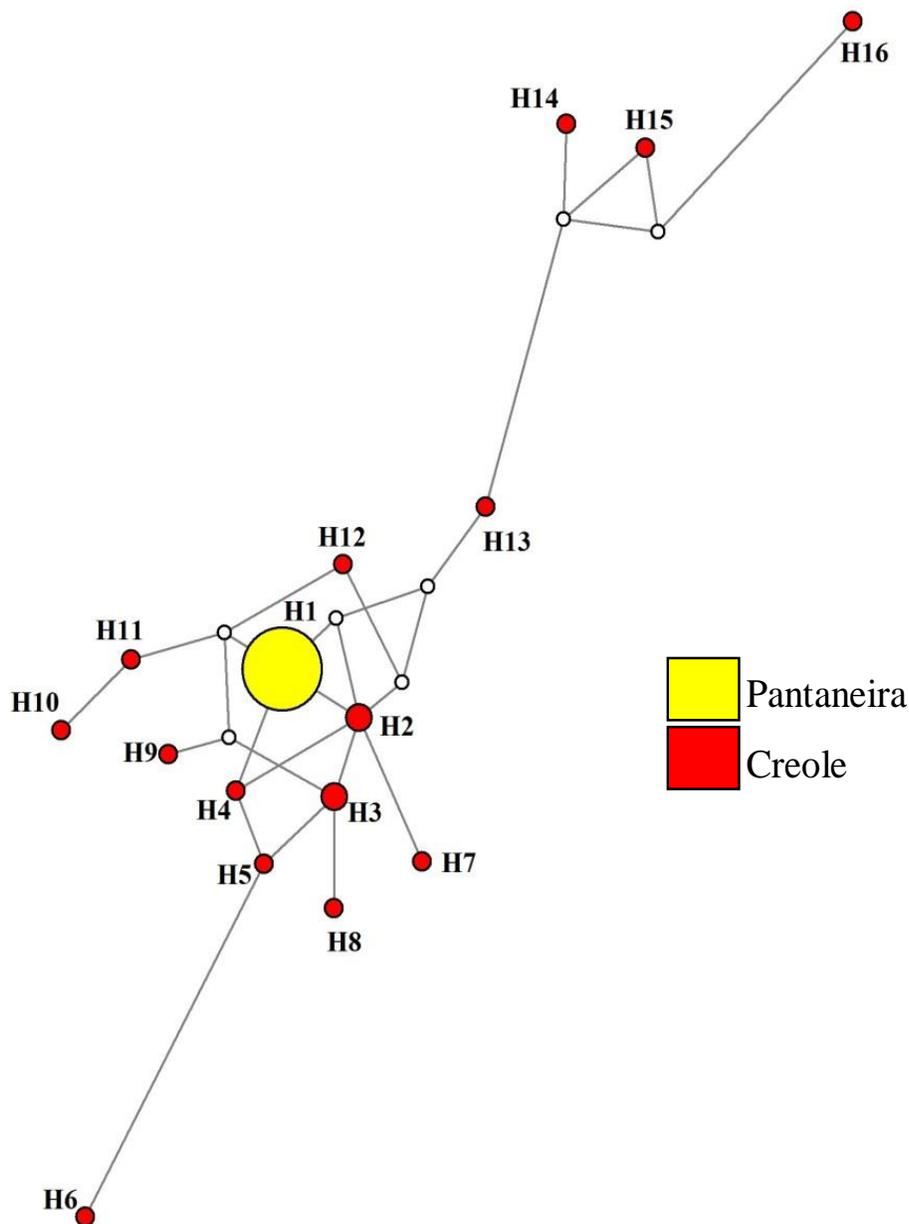
### INTRODUCTION

Brazil has many types of domestic animals, including sheep, which originated from breeds brought by colonisers after the discovery. The first steps towards obtaining funding for the improvement, management and conservation of Brazilian naturalised sheep are characterising the diversity of naturalised races, the genetic relationship between them and understanding their origins (Mariane and Cavalcante, 2006). The Creole sheep has been reared for centuries in the Brazilian states of Rio Grande do Sul and Santa Catarina, where there are two known varieties, Fronteira and Serrana (Gonçalves et al., 2010). Considering the geographic distribution of sheep in Brazil and phenotypic similarities between the animals, it is

thought that Pantaneira sheep originated from the Creole sheep, and research has been carried out to determine whether the difference between the groups is sufficient for the Pantaneira sheep to be recognised as a separate breed (Paiva et al., 2008). NADH dehydrogenase is one of the main enzymes found in respiratory complexes in mammals. It has 42 polypeptide chains, seven of which are encoded by the mitochondrial genome. The subunit five (*ND5*) was used by Tserenbataa et al. (2004) and by Gonçalves et al. (2010) to study sheep diversity. The former study searched for subspecies of *Ovis ammon* in Mongolia by sequencing this region, and the results suggested the existence of two subspecies (*O. ammon*

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**Figure 1.** Network constructed by the median-joining method (Bandelt et al., 1999) showing the 16 haplotypes found using the mtDNA *ND5* gene for individuals from the Pantaneira and Creole sheep. The area of the circles for each haplotype is proportional to its frequency. The lengths of the lines are proportional to the mutational steps that separate each haplotype. The white dots are median vectors that represent hypothetical haplotypes introduced by the algorithm used.

the Pantaneira breed and in two varieties of Creole sheep, with the distance between breeds being 0.44, according to the distance method pairwise difference based on  $F_{ST}$  values calculated with AMOVA. Figure 1 shows that the haplotype networks constructed for Pantaneira and Creole sheep, based on mutation points present in the sequences, demonstrate the relationship between the different haplotypes. Table 2 shows the haplotype and nucleotide diversities calculated with Arlequin 3.5 for the *ND5* gene.

## DISCUSSION

The  $F_{ST}$  value found in this study with the *ND5* gene, calculated with AMOVA, was 0.44 and according to Hartl and Clark (2010),  $F_{ST}$  values above 0.25 indicate a genetic difference. Therefore, we may say that there was differentiation between Pantaneira and Creole breeds when analyzed with this marker. In addition, Holsinger and Weir (2009) say that if the  $F_{ST}$  value is high the allele

**Table 2.** Haplotype (H) and nucleotide ( $\pi$ ) diversities for Pantaneira and Creole sheep.

Breed	H	$\pi$
Pantaneira	1.000±0.017	0.000±0.000
Creole	1.000±0.020	0.010±0.006

frequency is different indicating difference between populations, which once again shows that there could be differentiation between the populations studied. The network (Figure 1) revealed that Creole sheep have a different haplotype than Pantaneira sheep since they did not group together, suggesting that differentiation has occurred between these groups, therefore more research would be necessary to know if this would be enough so that the Pantaneira sheep could be acknowledged as a different breed, a suggestion also made by Paiva et al. (2008). Furthermore, several haplotypes in the Creole sheep were close to the one formed by the Pantaneira breed animals which may indicate that, although these animals do not share the same haplotype, they belong to the same haplogroup. The fact that all animals of the Pantaneira breed grouped together in one single haplotype explains the values found for haplotype and nucleotide diversity (Table 2). The geographical region where these animals are found today belonged previously to Paraguay, so it is possible that the Pantaneira breed has been influenced by Paraguayan breeds and the analysis of its mitochondrial genome might confirm this assumption, by showing their genetic distance from the Creole. Thus, the significant differences identified for the mtDNA *ND5* gene between Pantaneira and Creole sheep may indicate that differentiation has occurred in both races; however, further research using other markers is required to investigate this further.

### Conflict of interest

The authors have no conflict of interests to declare.

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