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Detection of selection signatures for ear carriage in Maltese goat breed

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Abstract

Selection and breeding practices in goats have led to the fixation of several traits. This is probably due to the standardization of several peculiar morphological characteristics that have always been one of the major exclusion criteria of individuals from selection. Among these, ear carriage is one of the most ancient and considered a signature of domestication in several species, such as the dog, pig, sheep and goat (Boyko *et al.*, 2010). The availability of improved genomic analyses tools for goats may provide useful information on genes involved in this trait. By studying, for example, the homozygosity decay of haplotypes (contiguous length of alleles) such information can be detected. In the current study, we focused on the Maltese goat, a breed showing floppy ears, in comparison with other Italian breeds using a goat medium density SNP chip (Nicoloso *et al.*, 2015). A total 48,767 SNP markers for 369 animals belonging to 16 breeds or populations were analyzed. Genotypes were imputed within population excluding markers without known position on the current genome assembly (ARS1, Bickhart *et al.*, 2017). Population analysis using MDS, ADMIXTURE and fastSTRUCTURE confirmed the good differentiation among the populations. Integrated Haplotype Score (iHS, Sabeti *et al.*, 2007) was performed for each population, comparing the regions detected on the Maltese breed with the others considered to detect genes that may be involved into shaping ear morphology. These results may provide new insights into ear carriage phenotype by detecting genes that play a pivotal role in shaping the goat phenotypic diversity.

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