

CONSTRUINDO SABERES, FORMANDO PESSOAS E TRANSFORMANDO A PRODUÇÃO ANIMAL

## GENETIC DIVERSITY AND POPULATION STRUCTURE STUDY IN GOATS

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This study was carried out to validate the Illumina Goat SNP50 BeadChip, and to study the genetic diversity and population structure in goats from the Embrapa Goats and Sheep, Sobral, Ceará, Brazil. A total of 127 goats were genotyped (30 Anglo Nubiano-AN, 30 Canindé-CA, 36 Moxotó-MO and 32 Saanen-SA). Genotypes were edited to remove markers located on sex and mitochondrial chromosomes, monomorphic, unknown map position, call rate < 0.98, minor allele frequency < 0.05, and deviation from HW proportions ( $p < 10^{-6}$ ), resulting on 39,726 (AN), 36,532 (CA), 38,431 (MO) and 44,025 (SA) SNPs retained for further analyses. The SNP markers in high linkage disequilibrium ( $r^2 > 0.90$ ) were also removed, remaining 25,493 (AN), 23,493 (CA), 26,511 (MO) and 31,875 (SA). Population structure and genetic diversity study was based on observed heterozygosity ( $H_o$ ), expected Heterozygosity ( $H_s$ ), inbreeding coefficient ( $F_{is}$ ) and principal component (PC) analysis. The Illumina Goat SNP50 BeadChip has been shown to be informative due to its wide sample in genome, which is important to study genetic diversity, population structure, and to perform Genome-wide Association and genomic selection. Although 14% to 18% of SNP were removed due to high LD, estimates of MAF, HWE and HZ before and after pruning were similar. The expected and observed heterozygosity ( $H_e$  and  $H_o$ ) were lower for the native breeds: CA (0.31 and 0.33) and MO (0.34 and 0.34), when compared to the specialized breeds: SA (0.39 and 0.40) and AN (0.34 and 0.34). This indicates that there is greater genetic diversity in specialized breeds. The PCA results showed that the first two PC explained 82.02% of the observed variation, indicating that most variation of the data can be summarized with only two vectors. The PCA analysis grouped samples as follows: the first PC split native breeds (MO and CA) and specialized breeds into two distinct groups; the second PC separated the specialized SA and AN breed. Overall, the Goat SNP50 panel can be used satisfactorily for genetics studies with Brazilian native goat breeds.

**Palavras-chave:** *capra hircus*, genotyping, goat snp50

Promoção e Realização:



Apoio Institucional:



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