

CONSTRUINDO SABERES, FORMANDO PESSOAS E TRANSFORMANDO A PRODUÇÃO ANIMAL

## CHARACTERIZATION OF RUNS OF HOMOZYGOSITY IN SANTA INÊS SHEEP

Aurino de Araujo REGO NETO<sup>\*1</sup>, José Lindenberg Rocha SARMENTO<sup>2</sup>, Natanael Pereira da Silva SANTOS<sup>1</sup>, Gleyson Vieira dos SANTOS<sup>2</sup>, Luciano Silva SENA<sup>2</sup>, Daniel BIAGIOTTI<sup>3</sup>, Bruna Lima BARBOSA<sup>2</sup>, Maria Ivamara Soares MACEDO<sup>2</sup>

\*corresponding author: aurinorego@hotmail.com

<sup>1</sup>Universidade Federal do Piauí, Bom Jesus, Piauí, Brasil

<sup>2</sup>Universidade Federal do Piauí, Teresina, Piauí, Brasil

<sup>3</sup>Colégio Técnico de Bom Jesus, Bom Jesus, Piauí, Brasil

Runs of homozygosity (ROH) are continuous homozygous segments that are present in genomes of individuals and populations. Identification and characterization of ROHs may clarify genetic events of populations. The purpose of this study was to evaluate the autozygosity of Santa Inês sheep in order to identify and characterize the occurrence of ROHs, as well as to investigate ROH islands for gene content in segments shared by more than 50% of the animals in study. Data from 428 Santa Inês sheep raised in the states of Piauí and Maranhão (Brazil) were used. From those animals, 271 were genotyped using the high density Illumina Ovine SNP50K BeadChip. After quality control 51,874 SNPs were used for genomic analysis. The pedigree-based relationship matrix (A) and the genomic relationship matrix (G) were used to calculate relationships among individuals. Pedigree information (FPED), runs of homozygosity (FROH), observed versus expected number of homozygous genotypes (FHOM), and the genomic relationship matrix (FGRM) approaches were used in order to estimate inbreeding coefficients. To estimate the extent of linkage disequilibrium between all adjacent pairs of SNPs present on autosomal chromosomes we calculated the squared correlation coefficient between two loci ( $r^2$ ). For identification of runs of homozygosity in autosomal chromosomes, segments of at least 50 homozygous SNPs with a minimum length of 1,000 Kb by animal were considered. The linkage disequilibrium measured by  $r^2$  was 0.4443. The average inbreeding coefficients calculated from FPED, FROH, FHOM and FGRM were 0.0004, 0.035, 0.025, and 0.552, respectively. The estimates of average relationship were 0.02 and 0.255, based on A and G, respectively. A total of 4,022 runs of homozygosity were identified throughout the genome. Three regions on chromosome 16 (OAR16) stand out, because they were shared by more than 50% of the animals used in this study. This is probably an indicative that intensive selection is occurring for traits whose expression is controlled by genes located on OAR16. No genes were observed in chromosomal regions shared by more than 50% of the animals in study. The inbreeding calculated based on pedigree data was underestimated in comparison to the inbreeding estimated using ROHs.

**Keywords:** hair sheep, homozygous regions, inbreeding, pedigree, realized kinship

Promoção e Realização:



Apoio Institucional:



Organização:

