## GENÉTICA Y MEJORAMIENTO

## Inbreeding and runs of homozygosity in creole sheep breeds

Endogamia y series de homocigosidad en razas criollas de ovinos

Johanna Ramírez-Díaz<sup>1\*</sup>, Arianna Manunza<sup>1\*</sup>, Filippo Biscarini<sup>1</sup>; Paolo Cozzi<sup>1</sup>, Luz A Álvarez<sup>2</sup>, Gerson Barreto Mourao<sup>3</sup>, Gabriel Ciappesoni<sup>4</sup>, Pablo Peraza<sup>4</sup>, José Arranz<sup>5</sup>, Fernando Freire<sup>5</sup>, Juan C Rincón<sup>2</sup> and Alessandra Stella<sup>1</sup>

<sup>1</sup>Institute of Agricultural Biology and Biotechnology – Italian National Research Council – CNR, Milan, Italy, ORCID 0009-0006-4995-7665, ORCID 0000-0001-8812-8962, ORCID 0000-0002-3901-2354, ORCID 0000-0003-0388-6874, ORCID 0000-0003-2850-3964. <sup>2</sup>Universidad Nacional de Colombia sede Palmira. Departamento de Ciencia Animal, Palmira, Colombia, ORCID 0000-0001-9483-3158, ORCID 0000-0002-6769-6407. <sup>3</sup>Universidade de Sao Paulo. Animal Science Departament, ESALQ - Piracicaba, Sao Paulo, Brazil, ORCID 0000-0002-0990-4108. <sup>4</sup>Instituto Nacional de Investigación Agropecuaria. Canelones, Uruguay, ORCID 0000-0002-0091-3956, ORCID 0000-0001-6822-0307. <sup>5</sup>Universidad de Leon. Department of Animal Production, Leon, Spain, ORCID 0000-0001-9058-131X.

\*Corresponding author: johanna.ramirezdiaz@ibba.cnr.it; arianna. manunza@ibba.cnr.it

Introduction: In livestock, the advancement of genotyping technology has introduced new methods for assessing inbreeding based on single nucleotide polymorphism. Homozygosity runs (ROH) provide a more accurate method for estimating past and recent inbreeding rates at the individual/population level compared to traditional pedigree-based estimations or in the absence of pedigree records. Furthermore, ROH metrics can be used for the identification of regions under strong selection and provide insights into evolutionary trends over time. **Objective:** 

This work aimed to estimate the genomic inbreeding coefficient (FROH) and ROH patterns in fifteen local sheep breeds from Africa (NQA: Namagua, RMA: Red Maasai, RDA: Ronderib) Barbados (BBB: Barbados BlackBerry), Brazil (STI: Santa Ines: BMN: Morada Nova), Colombia (OPCE: Ethiopian, OPCP: Peliguey, OPCS: Sudan, OPCW: Wayúu); Ecuador (ECU: Creole), Spain (CAS: Castellana, LXT: Latxa, CHU: Churra) and Uruguay (CRL: Creole). Methods: SNPs on the sheep autosomes from the OvineSNP50 BeadChip (Illumina Inc) were used. After quality control (MAF<0.01, sample and SNP callrate >0.95), 359 sheep and 36,613 SNPs were used for further analysis. The Consecutive Runs method within the R package detectRUNS was used to detect ROH and estimate FROH, ROH descriptive statistics per breed, chromosome, SNP, and length classes were calculated. **Results and Discussion:** The average FROH ranged from 0.08 (CAS) to 0.44 (BBB). BMN, RDA, CRL, and STI showed FROH values above 0.33, while in the Colombian and Ecuadorian populations, FROH was lower than 0.26. The total number of ROH varied among populations. BBB, BMN, and CRL showed a large number of homozygous segments compared to the other breeds; the lowest number of ROH was found in CAS. In contrast, the longest ROH in CHU, and the shortest ROH were found in ECU, OPCE, OPCP, OPCS, and OPCW. The majority of ROH were detected in lengthier size classes (>6Mbp) across almost all breeds. Conclusion: Our findings indicate high genomic inbreeding in most populations, which could be related to their breeding history, demographic changes, or husbandry practices, and also underline the importance of developing more sustainable breeding programs that take into account the conservation of local sheep breeds.

**Keywords:** AGnR, autozygosity, genomic relationships, local breeds, ROH

Palabras clave: AGnR, autocigosis, genómicas, relaciones, razas locales, ROH