Provisional Book of Abstract

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Uncovering the architecture of production-driven introgression in Cinisara cattle

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Local livestock breeds play a pivotal role in maintaining agricultural sustainability, biodiversity conservation, and cultural heritage. They often possess unique genetic traits tailored to local environments including rusticity, heat tolerance, and digestive efficiency. Cinisara is a dual-purpose local cattle breed of Podolian ancestry mostly farmed in western Sicily, Italy, and is an integral part of Sicilian agriculture. However, spurious crossbreeding with cosmopolitan breeds aimed at improving meat or milk yield has been reported. To better understand the conservation status and ongoing selection of this unique breed, we investigated and detailed the current depth of cosmopolitan breeds introgression in Cinisara through local ancestry inference (LAI). We genotyped 71 unrelated Cinisara cattle at 65k SNPs, subsequently merging the dataset with genotype data of publicly available cosmopolitan cattle breeds, such as Holstein, Brown Swiss, Limousine, Modicana and Podolica. After quality checks, Cinisara recorded moderate levels of heterozygosity (0.359) and low levels of inbreeding (0.040). Global ancestry analysis confirmed the Podolian origin of the breed while highlighting significant introgression from Holstein and Brown Swiss, contributing 27% and 15%, respectively, to the ancestry composition of the Cinisara population. The Treemix analysis confirmed the migration events from Holstein and Brown Swiss. Local genomic ancestry was inferred using three reference populations: Podolica cattle, representing the ancestral origin of the Cinisara, and the two sources of cosmopolitan introgression: Holstein and Brown Swiss. Among the SNPs identified as highly introgressed (top 1%), 258 and 257 were associated with the Holstein and Brown Swiss reference populations, respectively. Gene-annotation enrichment analysis revealed 52 and 48 candidate genes within the regions defined by the Holstein and Brown Swiss references, respectively. These genomic regions exhibited high to complete substitution by the genomes of the two cosmopolitan breeds, predominantly overlapping with known QTLs associated with milk production traits. These findings align with the historical use of cosmopolitan breeds to enhance the production performance of local breeds. However, they also raise significant concerns regarding the preservation of traditional breeds, livestock biodiversity, and their cultural and economic value. The results underscore the importance of developing informed breeding strategies to balance production improvements with the conservation of genetic heritage.