adequately muscled but without heaviness. We can hypothesise that selection for such hunting behaviour, for which particular anatomical features are required, could have shaped, at least in part, the genetic background of this breed and, consequently, the frequency/presence of the detected CNVRs in these genes.

P024

Genome-wide analysis identifies a new potential candidate marker associated with the coat colour sidedness in Cinisara cattle breed

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Coat colour is one of the most important phenotypic features in livestock breeds. Cinisara is a local cattle breed generally of uniform black colour which occasionally presents a particular phenotype, with animals typically displaying a white band along their spine, from the head to the tail, and on the ventral line (colour sidedness). Therefore, this breed provides an ideal model to study the genetic components underlying phenotypic variation in coat colour. In order to identify the potential causative markers affecting the phenotypic variability, we compared the two groups of Cinisara via a case-control genome-wide association study (GWAS) and a genome-wide F_{ST} analysis. A total of 63 animals, ten with sidedness phenotype and 53 with uniform black colour were genotyped with Illumina Bovine 50 K. After filtering for quality, the final number of markers retained for the analysis was 45,246. In the GWAS, at the $p<.05$ Bonferroni corrected, we identified a single strongly associated marker. An average inflation factor (λ) of 1.08 indicated that the GWAS was not inflated by population structure. To further support the association, a genome-wide F_{ST} case-control analysis was also performed. The marker with the highest F_{ST} value (F_{ST}=0.559) that differentiated between the groups overlapped with the significant SNP identify in the GWAS. Therefore, the comparison among GWAS and F_{ST} analysis revealed a single nucleotide polymorphism (SNP), *ARS-BFGL-NGS-55928*, at the position 21,048,672 bp on bovine chromosome (BTA) 20, significantly associated with the trait. Only one gene (*PLK2*) was annotated near the associated SNP in a window of ±200 kb. The protein encoded by this gene is a member of the polo-like kinase, the same family of several known coat-colour candidate genes. Based on the reported results, we draw the possible conclusion that the identified marker is potentially associated with the coat colour sidedness in Cinisara. Once again, the local breeds with their genetic variability represent an important resource and model to study the genetic basis affecting peculiar traits. Moreover, these results should be of value for future studies, and constitute a preliminary report to further genomic research on coat colour sidedness. Future studies would be particularly relevant to refine these results and to better understand the genetic basis for this phenotype.

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P025

Genome-wide characterisation of runs of homozygosity and estimation of genomic inbreeding in Sicilian goat breeds

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The availability of single nucleotide polymorphism (SNP) assays allows for the determination of autozygous segments based on runs of consecutive homozygous genotypes (ROH). ROH are widely used as predictors of whole-genome inbreeding levels in livestock species. In this study, we computed several ROH parameters to investigate different scenarios of contemporary goat breeding in five Sicilian breeds. Individuals of Argentata dell'Etna (ARG, $n=48$), Derivata di Siria (DDS, $n=32$), Girgentana (GIR, $n=59$), Maltese (MAL, $n=16$) and Messinese (MES, $n=22$) were genotyped with the Illumina Goat SNP50 BeadChip. After filtering, the final number of animals and SNPs retained for analyses were 174 and 48,348, respectively. A total of 3687 ROH segments >2 Mb were detected. The ROH parameters revealed well-defined differences between breeds. The mean number of ROH per breed ranged from 3.02 (ARG) to 38.81 (MAL). The average length of ROH ranged from 4.98 Mb (ARG) to 9.61 Mb (DDS). MAL breed showed the highest value of inbreeding (F_{ROH}=0.125), followed by GIR (F_{ROH}=0.108), whereas ARG showed the lowest one (F_{ROH}=0.009). ARG also showed the highest number of samples for which no ROH were detected ($n=7$). Each ROH segment was categorised based on its physical length in five categories, and the mean sum of ROH per breed was calculated. The results showed that, for all breeds, the majority of ROH segments were <8 Mb in length. DDS and MAL had a larger mean portion of their genome (98.97 Mb and 89.12 Mb, respectively) covered in longer ROH (>20 Mb). High ROH coverage within the short category