

discriminant analysis significantly separated LRCI from HRCI. Then the Bayesian GWAS (B-GWAS) was developed by using the BayesR software and, at the end of the procedure, markers were ranked according to their posterior inclusion probability and the first 698 SNPs were selected. Only markers simultaneously selected in the two procedures (11) were considered associated with RCI. The subsequent gene discovery analysis highlighted 50 genes in the neighborhood (250 kb downstream and upstream) of the 11 SNPs with 17 genes directly associated with RFI and average daily gain.

## P100

### Application of single-step GBLUP in Italian Comisana sheep

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Comisana is a dairy sheep breed reared in central and southern Italian regions used to produce PDO cheeses. Since 2000 a nucleus flock has been established at the breeders association experimental station aiming at improving both milk yield and composition using pedigree-based EBVs and fitting a lactation model. Recently, within the national CHEESR project, ewes of the experimental station were genotyped (Illumina OvineSNP50 Beadchip) and a repeated test-day model was implemented using both pedigree-based (TD-PBLUP) or single-step genomic best linear unbiased prediction (TD-ssGBLUP). The main objective of this study was to compare results from TD-PBLUP and TD-ssGBLUP. Data consisted of daily milk production and weekly fat and protein contents for 1138 Comisana sheep, 50K SNP genotypes for 309 animals and 2062 animals in the pedigree. Overall, a total of 169 individual – dam pairs were available. After a quality check 45,343 SNPs were retained. A multiple-trait repeatability test-day model was fitted including year of birth, month of calving, class of days in milk as fixed effects, and flock-test-date, permanent environmental and additive genetic as random effects. Phenotypes of 100 ewes (50 with genotypes) were masked to create a validation group. Heritability ranged from 0.09 (fat content) to 0.33 (daily milk yield). The average accuracy of TD-PBLUP and TD-ssGBLUP EBVs for the validation group was 0.43 and 0.45 for milk yield, 0.48 for fat content and 0.62 for protein content. When considering only ewes with genotypes the average accuracy

of TD-ssGBLUP was higher than that of TD-PBLUP only for milk yield (0.40 vs. 0.45) while for protein and fat content did not change being 0.60 and 0.48, respectively. Results from the current research confirm the usefulness of a single-step approach but they depend on the trait and its heritability, the percentage of genotyped individuals and the population structure. The upcoming inclusion of ram genotypes is expected to increase the accuracy of the TD-ssGBLUP EBVs.

## P101

### Genetic structure at CSN1S1, CSN2 and CSN1S2 loci of four autochthonous goat breed reared in Lazio and Campania regions

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One main aspect of safeguard plans for livestock Autochthonous Genetic Types (AGTs) is to ensure economic sustainability of their farming. This encourages farmers to contribute to the preservation of AGTs. The aim of this study was to characterize the genetic structure of four AGTs of endangered goats at the  $\alpha$ S1,  $\beta$  and  $\alpha$ S2 calcium sensitive caseins encoding genes CSN1S1, CSN2 and CSN1S2, respectively. The peculiar polymorphisms detected at these loci are associated with milk qualitative characteristics and have been largely investigated in widespread dairy goat breeds. On the contrary, there are very few studies carried out in AGTs goats. This study was performed on 50 Neapolitan goats, typical of the Campania region, and on 61 goats which included the three breeds Monticellana, Capestrina and Grigia Ciociara, reared in Lazio region (Lazio AGTs goat). Genotyping of quantitative alleles at CSN1S1, CSN2 and CSN1S2 loci was performed according to previous studies. At the CSN1S1 locus a high variability was observed in all four AGTs. In particular, a higher frequency of the null allele N was observed in Neapolitan goats than Lazio AGTs goats (0.420 vs. 0.008). On the contrary a higher frequency of F allele, associated with a low  $\alpha$ S1 casein content in milk, was observed in Lazio AGTs goat (0.442) than Neapolitan goat (0.120). All four AGTs do not carry the null alleles CSN1S1 01, CSN2 01 and CSN1S2 0 and the alleles associated with an intermediate content of  $\alpha$ S1 (CSN1S1 E) and  $\alpha$ S2