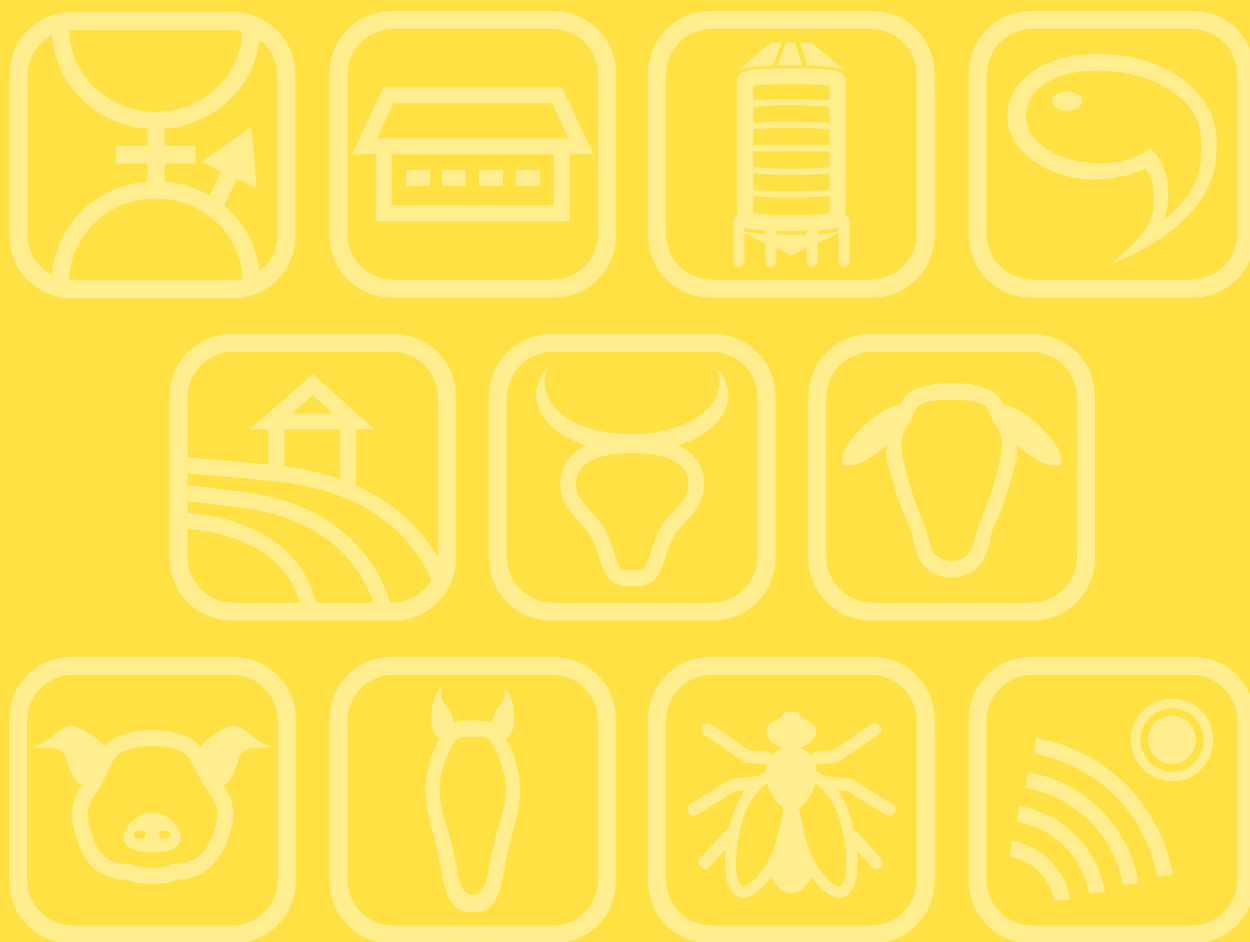


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Effects of nonsynonymous SNPs at GH2-N and GHR genes on coagulation properties of Assaf ewes' milk

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Sheep milk coagulation properties are of interest as potential selection criteria once milk is mainly used for cheese yield. The effects of nonsynonymous substitution at the growth hormone (GH2-N copy) and growth hormone receptor (GHR) genes and their haplotypes on milk production, milk composition (fat, protein, lactose, total solids and fat free total solids content), pH, and coagulation properties assessed by Optigraph [clotting time (R), gel firmness after 20 minutes (A20), and after a 2R (AR) period and rate of firming (OK20)] were studied in Assaf ewes. Milk production and composition were evaluated monthly until the sixth month of lactation (184 ewes), and pH and coagulation properties were evaluated at the first and third month of lactation (92 ewes). Data were analysed using a mixed-model procedure with fixed effects of SNP and month of lactation, considering the linear and quadratic effect of ewe' lambing age covariate. In the GH2-N copy gene, two substitutions (X12546 g.597T>C and g.1024T>C, three haplotypes) were studied. GH2-N genotypes and haplotypes had no effect on milk production and composition, however, they affected significantly AR throughout lactation ($P<0.01$). In the GHR copy gene, SNPs rs1086611503, rs595567866 and rs597181420 and seven haplotypes were studied. GHR genotypes and haplotypes had no effect on milk production and composition, except for SNP rs1086611503, who tended to affect protein and total solids content ($P<0.10$). Regarding milk coagulation properties, rs597181420 genotypes influenced pH and R, with CC ewes having lower values than TT ewes ($P<0.01$). The GHR haplotypes influenced significantly R and A20 ($P<0.05$), and AR ($P<0.01$) throughout lactation. Effects observed upon gel firmness parameters highlight the usefulness of those SNPs in gene-assisted selection programs for milk coagulation properties. Funding: Project financed by European Fund for Regional Development (ERDF) [ALT20-03-0145- FEDER-000019]

Genetic variability following selection for scrapie resistance in six native Italian sheep breeds

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Scrapie is a neurodegenerative disease of sheep belonging to the group of transmissible spongiform encephalopathies. Susceptibility to scrapie is associated with polymorphisms in the prion protein (PrP) gene. Genetic selection is currently the most effective mean for eradication of the susceptible VRQ allele in favour of resistant ARR allele. The aim of our study was to determine changes of genetic variability in 6 native sheep breeds from autonomous province of Bolzano (northern Italy), following simulation of scrapie selection scenarios. DNA samples from 684 rams were analysed for PrP polymorphisms and for 10 ISAG microsatellite loci to estimate genetic variability (GenAlEx software). The PrP predominant allele was ARQ (51.8%), while the ARR and VRQ allele frequencies were 23.5 and 9.7%, respectively. The ARR/ARR, ARR/ARQ and ARQ/ARQ genotypes represented 6.8%, 23 and 28.6% of all population respectively. Across all microsatellite loci a total of 163 alleles were detected with a mean of 10.4 alleles per locus, and 35 private alleles were found with a frequency below 9%. Average observed (H_o) and expected (H_e) heterozygosity values overall loci were 0.74 and 0.78 respectively, showing a statistically significant deviation from HWE in all breeds. This heterozygosity deficit is confirmed by positive Fis value, determining a moderate inbreeding rate in each breed. Simulating a mild selection, where only rams having at least a VRQ allele should be excluded from reproduction, H_o , H_e and Fis remained almost unchanged in each breed, indicating that genetic variability should not be affected by the removal of these individuals. With a moderate selection scenario, considering only rams with at least one ARR allele, we observed a decrease in the mean alleles per breed (8.9) and the maintenance of heterozygosity deficiency except for 2 breeds, where HWE deviation was no longer significant. These results showed that selection strategies, considering only PrP resistant rams, should not dramatically affect genetic variability of these autochthonous breeds.