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Effects of allele variants at the E-Locus on production, fertility and conformation traits in Holstein dairy cattle

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At the Extension (E) locus, the E^D (dominant black), the E⁺ (combination of black and red), and the e (recessive red) alleles are segregating. *Bos Primigenius*, the archetype of dairy cattle, is supposed to be of genotype E^D/E⁺, i.e. changing the red coat colour at birth into black later in life. This could be due to natural selection for environmental adaption and suggests the hypothesis that bulls carrying the E⁺ allele are characterized by improved fertility, persistency, longevity, or functional type traits as well. In total, 299 sons of 4 heterozygous E^D/E⁺ bull sires were genotyped. 53.2% of sons were of genotype E^D/E^D and 46.8% of genotype E^D/E⁺ indicating that all bull dams were homozygous E^D/E^D. National EBVs of bulls were de-regressed and then analyzed with the GLM procedure including the fixed effect of the bull sire, the regression coefficient for the number of E⁺ alleles representing half of the gene substitution effect, and the random residual effect consisting of polygenic and environmental effects. The E⁺ variant was associated ($p < 0.01$) with improved maternal non-return rate and maternal calving ease, and highly significant for rump angle ($p < 0.001$), i.e. favouring animals with low pin bones. For all other traits, no significant impact of the different allele variants was found.

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Genetic characterization of two sheep breeds from Southern Italy by STR markers

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Altamura and Leccese are triple-purpose sheep breeds from Southern Italy that suffered in recent years a marked population size reduction. Aim of this work was to evaluate the level of within and among-breed genetic variability, as a contribution in conservation decisions. In the whole, 182 animals were typed for 19 STR markers. Data analysis was carried out by the software Arlequin. The mean number of alleles per marker was 11.3 (range 4 to 17). Several "private" alleles were observed, mainly in Leccese. Significant ($P < 0.01$) deviation from Hardy-Weinberg proportions was present for some markers, with excess of homozygous genotypes. More than 50% of all pairwise marker comparisons showed gametic unbalance in both breeds. Allele-sharing similarities were 0.369 and 0.317 within Altamura and Leccese, respectively, whereas it was 0.298 between breeds, indicating a significant level of genetic differentiation; the mean value of F_{ST} was 0.044. The breed assignment test allocated all individuals to their true breed of origin, except for one Altamura and one Leccese individual. The present results may contribute to design a more appropriate management of these genetic resources.



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Amiata donkey local breed: genetic and morphological characterization

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The genetic and morphological characterization of the local Amiata donkey breed has been considered. The genetic structure was investigated using information from pedigrees (608 subjects) and using STR markers (18 microsatellite loci were analysed in 50 unrelated individuals), while the morphological structure was investigated through the data reported in the Anagraphic Register (10 scores, evaluated by certificated experts of the breed and measurements of withers height, chest and cannon circumference). Genealogical analysis reveal that the inbreeding level seems to be rather acceptable, contrary to the expectation for a population that has suffered a severe bottleneck in recent years. However, the lack of genealogical records for a substantial number of individuals may have caused a possible underestimation of the inbreeding coefficient. In fact, a substantial increase in the average inbreeding coefficient is observed in those subjects with the maximum number of traced generations. On the contrary molecular data evidenced an elevated genetic homogeneity. From the point of view of the morphological analysis the presence of two well separate morphological groups and the clean uniformity is evident inside the breedings.

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The influence of milk protein polymorphisms on morphometric characteristics of milk fat globules in Italian Friesian dairy cow

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The influence of b-casein (b-CN), k-casein (k-CN) and b-lactoglobulin (b-LG) genotype on morphometric characteristics of milk fat globules was evaluated on 89 milk samples from Italian Friesian pluriparous cows reared in the same herd in a medium-temperate climatic zone in the province of Pisa. Individual milk samples were collected and analyzed in a triplicate. Milk protein genotypes were determined by isoelectric focusing analysis of individual milk samples. The morphometrical analysis of fat globules (number of milk fat globules/ml and diameter) was performed. The frequency distribution of total measured milk fat globules was evaluated according to their size. Fat globule diameters were divided into nine classes of 1.5 micron width: from class 1 (1.5-3) to class 9 (>13.5). The analysis of variance was carried out to evaluate the effect of b-CN, k-CN, and b-LG genotype on all the evaluated parameters with simultaneous adjustment for sampling season, parity, and days from calving as a covariate. Significant effects were observed mainly for b-LG genotype, with AA genotype associated with a higher proportion of fat globules greater than 6 micron than AB and BB.