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CSN1S1 gene: allele frequency, and the relationship with milk production traits in three Iranian indigenous cattle and Holstein breeds of Iran

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CSN1S1 is one of the major proteins in milk of mammals. Milk protein genes are supposed to influence on milk yield and its compositions. In this study we aimed to determine allele frequencies of CSN1S1- 5` and B variants and their effect on milk traits in three indigenous (two Bos indicus and one Bos taurus) and Holstein breeds in Iran. DNA samples were gathered from 400 animals. ALF, SSCP and PCR-SSCP were used for genotyping of promoter and coding region of exon 17. CSN1S1*B variant was nearly fixed in Holstein but it was intermediate in indigenous breeds. All four alleles of promoter were found in breeds but in different frequencies. Allele B was found in combination with all four promoter alleles. Allele '4' promoter was not found in any cow having the allele 'C' in all breeds. Statistical analysis performed for Holstein and one of indigenous breed (Golpaygani). BC/23 genotype yielded the highest fat percentage ($P<0.05$) in Holstein but it had no significant effect on Golpaygani. There was not any homozygous CC for CSN1S1 in Holstein to show whether C variant would be advantageous for fat percentage. BC/22 genotype had no significant effect on milk production of Golpaygani but they tended to produce higher milk than the other genotypes. Differences of allelic frequencies and milk production traits between these breeds might be due to differences in origin of breeds or selection breeding programs.

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Detection and correction of outliers for fatty acid contents measured by mid-infrared spectrometry using random regression test-day models

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Calibration equations were developed to quantify fatty acids (FA) in milk using mid-infrared spectrometry. Belgian equations used showed a good ability to predict the contents of saturated (SAT) monounsaturated FA (MONO). Cross-validation coefficient of determination were 99.54% and 98.23% for SAT and MONO, respectively. Some outliers can appear and have impact on the estimation of breeding values. The aim of this study was to develop methods of outlier detection. The first method determined limitations based on individual examinations of extreme values. The second model was based on the residue estimated from random regression test-day models. The dataset contained 58,443 test-day records collected from 16,470 first parity Luxembourg Holstein cows in 699 herds. Models included as fixed effects: herd*test date, days in milk, and age. Random effects were regressed using Legendre polynomials of order 2 and were: herd*year of calving, permanent environment, and animal effect. The residual effect was assumed to be constant through the lactation. Detection by a random regression approach gave better results. The replacement of outlier values by the corresponded expected values was the better approach to calculate reliable breeding values.