

Genetic parameters for major milk proteins in three French dairy cattle breeds

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Genetic parameters of the major milk protein contents were estimated in the three main French dairy cattle breeds i.e. Montbéliarde, Normande and Holstein in the framework of the PhénoFinLait programme. Protein composition was estimated from Mid-Infrared (MIR) spectrometry on 266,508 test-day milk samples from 57,477 cows in first lactation. Lactation means, expressed in percentage of milk or protein, were analyzed with an animal mixed model including fixed environmental effects (test-day x herd, month x year of calving and spectrometer) and a random genetic effect. Genetic parameter estimates were very consistent across breeds. In milk or in protein, heritability estimates (h^2) were moderate to high for α s1, α s2, β and κ -caseins and for α -lactalbumin ($0.21 < h^2 < 0.58$). In each population, β -lactoglobulin was the most heritable trait ($0.57 < h^2 < 0.75$). Genetic coefficients of variation ranged from 1 to 10%. Genetic correlations (r) were very sensitive to the expression unit. Protein fractions were generally in opposition when they were expressed in protein, except between whey proteins and α s2-casein ($0.39 < r < 0.60$) and between β and κ -caseins ($0.55 < r < 0.64$). In milk, r estimates were close to zero or positive, with highest r values found between different caseins ($0.45 < r < 0.92$). In the three populations, β -lactoglobulin was positively correlated with α s1-casein ($0.21 < r < 0.42$) and α s2-casein ($0.46 < r < 0.62$) whereas the correlations were close to zero with β and κ -casein ($-0.15 < r < 0.21$). These results, obtained from a large panel of cows, show that routinely collected MIR could be used to modify milk protein composition by selection. However, antagonisms between proteins will have to be considered.

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