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Comparison of definitions for lactation persistency in Polish Holstein-Friesian cattle

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Persistency of lactation is defined as an ability to maintain a stable milk production during lactation. It is not only related to milk yield but also to health and reproduction of cows and the profitability of production. The aim of this study was to analyse the properties of three definitions of lactation persistency in the Polish Holstein-Friesian cows. The following definitions were used: second principal component of additive genetic covariance matrix for a particular lactation (Pers1), second regression coefficient of random regression sub-model used to model the additive genetic effect (Pers2), and the difference in breeding values at DIM 280 and at the peak of lactation (DIM 30 to 50) (Pers3). The data consisted of test-day milk yield records from lactations 1 to 3 collected on 1,759,084 Polish Holstein-Friesian cows. Variance components were estimated using the Gibbs-sampling approach based on a three-lactation random regression model with the third order of Legendre polynomials. Estimates of heritability for persistency ranged from 0.07 (Pers3 in lactation 1) to 0.20 (Pers2 in lactation 2). The lowest correlation between EBVs for 305-day milk yield and persistency was found for Pers1 (0.10, 0.03 and 0.06 for first, second and third lactation, respectively). Lactation curves of high and low Pers1 EBV bull daughters differed in shape. The genetic curves of sires with high Pers1 EBVs had a clearly increasing trend with DIM. The daily EBVs of sires with high lactation persistency were about +4 kg of milk higher between the beginning and the end of lactation, compared to sires with low lactation persistency (the difference of -3 kg of milk). Pers1 seems to be the most suitable definition of lactation persistency for Polish Holstein Friesians and it is therefore recommended for routine genetic evaluations.

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Quantile regression mixed model at different milk production levels of Iranian Holsteins

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The objective of this study was to estimate the effects of environmental factors such as herd, year and season of calving, Holstein gene percentage, age at first calving as fixed effects, and random animal effects on milk yield using quantile regression (QR) mixed model. An animal model was used to compare and discuss the results. Data comprised of 64,530 primiparous cows from 754 herds calved between 1996 and 2010. Mixed QR model was carried out using LQMM package of R software. The results showed that the effects of age at first calving and Holstein gene percentage across different quantiles were not similar. The spearman correlation between predicted breeding values from QR analyses at different quantiles with ones from animal model were high (0.88). It shows the ranking of animals based on EBV from different models is almost identical, while, the fixed effects differ across quantiles. The genetic trends estimated with QR at different quantiles were different, such that the genetic progress was highest among high producing cows (0.75th quantile).