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Fixed and random regression models for South African Holstein under two production systems

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In fixed regression models (FRM), the shape of the lactation curve is determined by fixed (non-genetic) effects only, while the additive genetic effect is assumed to be constant within lactation. Random regression models (RRM) allow this shape to also vary with the additive genetic and permanent environment effects of the cow. Test-day records from South African Holstein (SAHST) herds were analysed using restricted maximum likelihood under different multitrait (milk production for each of the first three lactations) FRM, including the current FRM officially used for SAHST genetic evaluations. Two separate datasets were considered including herds using either a pasture (PAST) or a total mixed ration (TMR) production system. Results of the various FRM were compared to the current SAHST genetic evaluation model which clusters most of the fixed effects together and considers them as constant over the lactation. An alternative FRM cumulating different lactation curves for different fixed effects was retained based on the results of the analyses of the PAST dataset. This model was also compared to the current SAHST model using the TMR dataset. The alternative FRM was then extended to a RRM combining for each lactation an average production effect and a persistency effect and this model was compared with the current SAHST model for both production systems. Both the RRM for PAST and TMR had a better goodness of fit as well as a lower MSE than the current SAHST model. Overall, RRM had higher heritability estimates for both production systems, especially at the beginning and at the end of each lactation. Estimates of between lactation genetic correlations were also higher for RRM. Results from RRM analyses showed that the genetic correlations between average production and persistency within parity were stronger (and negative) for TMR than for PAST systems. The extra source of information from RRM enables a genetic prediction of persistency and are expected to increase the accuracy of genetic predictions.