Genetic evaluation of persistency in extended lactations

***L. Polman*[1]*, S. Rensing*[1]*, Z. Liu*[1]*, E. Tholen*[2] *and J. Heise*[1]**

[1] IT Solutions for Animal Production (vit), Heinrich-Schröder-Weg 1, 27283 Verden, Germany

[2] Institute of Animal Science, University of Bonn, Endenicher Allee 15, 53115 Bonn, Germany

Abstract

In April 2023, a new breeding value for milk yield persistency was introduced for German Holsteins, Jerseys, Red Dairy Cattle, German black-and-white dual purpose, and red-and-white dual-purpose breeds. The aim is to allow selection of animals that are genetically suited for voluntarily extended lactations. The new breeding value was derived from the Random-Regression-Test-Day-Model (3 yield traits: protein-kg, fat-kg, milk-kg; 3 lactations each; 2nd order legendre polynomials in the genetic effect) that is used for routine genetic evaluations. The new trait is defined as the slope of the genetic Legendre polynomial between DIM 150 and 305 for each yield trait in each lactation. EBVs for fat and protein persistency are then combined according to their economic impact, using the same weights as for the overall yield index RZM: fat-kg:protein-kg weighted 1:2. The newly defined persistency index has a cumulative heritability of 0.34. Correlations of genomic breeding values to the traits that are included in the total merit index RZG are close to zero, except for RZM (0.24) and longevity RZN (0.18). Reliabilities for youngest genotyped animals without performance observations are approx. 0.60, which is lower than for the RZM. We observe a small positive genetic trend in the newly defined persistency trait in German Holsteins, which is expected, given the small but positive correlation to RZG that stems from the correlations to RZM and RZN.

Key words: milk yield, persistency, Holstein, extended lactations, Germany

Introduction

In recent years, the interest of farmers to extend the lactations of their cows has increased. Main reasons are: 1) low calf prizes; 2) each calving exposes cows to severe risks in their health and even survival; 3) reduce the portion of dry periods, where cows are not productive; 4) expectation of higher successful insemination rates (Römer et al. 2021, Van Knegsel 2022). This voluntary increase of lactation lengths puts new focus on the persistency of milk production and promises benefits in contact to animal health, economics and management (Lehmann et al. 2014; Do et al. 2017; Sehested et al. 2019). Common definitions of persistency consider a fixed period from lactation peak up to a certain day in milk (DIM) in the second half of the lactatation (Van Doormaal 2007, Biassus et al. 2010, Fürst et al. 2021, Aamand 2022). Our interest is persistency in extended lactations that go well beyond 305 days (Sehested et al. 2019). The aim is therefore to provide farmers with a breeding value that allows for the selection of animals that are genetically suited to maintain their production in extended lactations: the RZPersistenz.

Materials and Methods

Data was taken from the German routine genetic evaluation system of milk production traits for Holsteins in August 2022:

- EBVs for the Legendre coefficients from the conventional pedigree-based Random-Regression Test-Day Model (RRTDM).
- Genotype data used in the German Holstein genomic evaluations.
- Raw phenotypic data to validate the results.

The EBV data set from the RRTDM, which is described in Liu et al. (2000), consisted of about 17 million females and 200 000 bulls. The raw phenotypic test-day-data included about 19 million lactations and was used to assess the impact of the selection on the new EBV for persistency on the phenotypic scale in extended lactations. For this purpose, the following selections were applied:

- Data from black-and-white Holsteins only
- lactations from 2012 onward
- minimum calving interval of 550 days
- only use days in milk (DIM) up to 400

These filters were applied to achieve a best-possible representative data set of long lactations without an impact of gestation to the shape, which was described in previous works (Grossman and Koops 2003; Muir et al. 2004). After this step, approx. 7% of phenotypic data were used for validation.

The genetic deviation curve of the RRTDM for German dairy cattle is modelled using 2nd order Legendre polynomials, which gives the following function 1:

$$f(dim) = \frac{\sqrt{5}(3(\frac{dim-155}{150})^2-1)}{2} \quad a_2 + \sqrt{3}(\frac{dim-155}{150}) \quad a_1 + a_0 \qquad [1]$$

Where a_0, a_1, a_2 are the EBVs for the Legendre regression coefficients (index denotes the order), and *dim* is the time, measured as days in milk.

Legendre polynomials in the RRTDM are defined from DIM 5 to DIM 305. We defined lactation persistency as the slope of the curve between DIM 150 and DIM 305. The first point was chosen, because we do not want to affect the lactation peak region and the latter is simply the end of the parameter range. The weights for the EBVs of the Legendre coefficients can then be computed from the following formula 2, where the subscripts *1* (earlier) and *2* (later) of *dim* represent the start and end DIM during lactation.

$$\frac{f(dim_2)-f(dim_1)}{dim_2-dim_1} = \frac{3\sqrt{5}}{2}(\frac{dim_2^2-dim_1^2}{150^2} - \frac{310(dim_2-dim_1)}{150^2}) \quad a_2 + \frac{\sqrt{3}}{150}(dim_2-dim_1) \quad a_1 \qquad [2]$$

From this calculation, we get for each trait and lactation a persistency breeding value. These were then combined in the same way as the milk production index RZM is combined: weighting the first three lactations equally and afterwards combine fat-kg and protein-kg with a ratio of 1:2, which represents their economic weights. This results in the RZPersistenz.

To compute the h^2 of the RZPersistenz, we used the estimated variants component Tables per trait for genetic (G), permanent environment (PE) and residual (R) effects used in RRTDM with the resulting weights (w) for a_1 and a_2, while a_0 get zero weight. The formula is: $h^2 = w'Gw/\ (w'Gw + w'Pew + w'Rw)$. For the cumulative h^2 of RZPersistenz, the same weighting as for the EBV between lactations and traits are applied.

The aim of the new breeding value is to identify the genetic ability of animals to maintain their production level in extended lactations that go well beyond DIM 305. Therefore, we conducted a validation with phenotypic data up to DIM 400 to assess that our definition, which goes only to DIM 305, also works well for extended lactations. For this, approx. 1000 black-and-white Holstein AI-bulls born from 2013 to 2016 were grouped into 25%-quantiles based on their EBVs for persistency. Mean phenotypic daughter performance was then compared between daughters of top and bottom bulls.

Genomic breeding values were estimated with the same method as described in Liu et. al. (2011). Deregressed EBVs of RZPersistenz were used as phenotypes for the reference population. The training set based on German animals with a minimum of 8 phenotypic test day records (for bulls, at least 10 daughters were required that fulfilled this requirement) to cover enough phenotypic information in the relevant interval of the lactation.

Results & Discussion

In Figure 1 and 2, we see the mean phenotypic lactation curves in milk-kg from daughters of AI bulls in different lactations. These results for milk-kg are also largely valid for fat- and protein-kg. In general, we observe differences between the first and higher lactations, with a lower absolute level, but flatter course from primiparous cows. These findings were expected and are also described in Schutz et al. (1990) and López et al. (2015). The daughters of the top 25% bulls with regard to RZPersistenz show the same mean phenotypic curve in early lactation as the daughters of the bottom 25% bulls. The curves start to differentiate in the second half of the first lactation and after the first third of higher lactations. The difference is a flatter slope of the top 25% bulls' daughters.

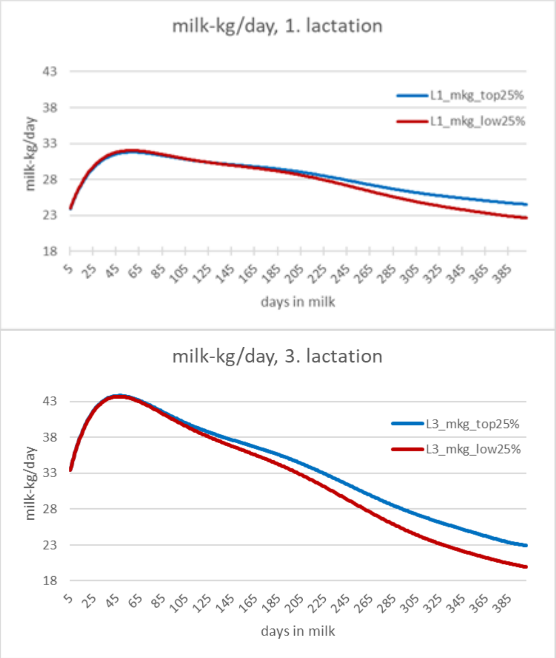

Figure 1 and 2. Phenotypic lactation curves for milk-kg from daughters of AI-bulls divided in best and worst 25% for RZPersistenz.

In the mean phenotypic curves of third lactation, the yield of 23kg is reached approx. 70 days later in for daughters of top bulls compared to bottom ones. In first lactation the difference on 25kg is approx. 60 days. These results show that the RZPersistenz extrapolates well up to DIM 400, although the lactation curve information used in RZPersistenz includes only DIM up to 305.

With a cumulative heritability of 0.34 for RZPersistenz we observe that this is lower than the h^2 of RZM. One reason most likely is the definition of the RZPersistenz that includes also less information than in RZM (only 2 of 3 regression coefficients). The mean genomic reliability of young, genotyped animals is 0.6. This is less than for gRZM (0.74), which results from the lower h^2 on the one hand and a smaller training set for the genomic evaluation on the other hand. Reasons for the latter are:

- We only include bulls with a minimum of 10 daughters with at least 8 test-day records (compared to 6 test-day records for RZM), in order to have enough phenotypic information in the relevant second half of the lactation.
- Only German information can be used in RZPersistenz. For RZM, we can use MACE results to also get foreign information. This does not work for RZPersistenz, because MACE gives only single-trait results and no information on single regression coefficients.

gEBV correlations calculated from 105 557 young female black-and-white Holsteins from herd genotyping to most other EBVs in RZG (total merit index) are close to zero. RZM (0.24) and RZN (0.18) show a small positive correlation. We observe also a small positive genetic trend also for recent years in the newly defined RZPersistenz in German Holsteins, which is likely caused by these small but positive correlations. In contrast to previous studies for persistency like Harder et al. (2006a) or Appuhamy et al. (2007), who report undesired genetic and phenotypic connections to metabolic diseases or udder health, we do not observe such negative correlations. The reason might be that our definition does not include the lactation peak period. This point may also explain why we found only few and small positive correlations and close-to-zero correlations to, e.g., reproduction traits.

Different studies on lactation persistency expect benefits in reproduction traits or less metabolic challenges early in lactation. Among others because of a decrease of peak yield (Jakobsen et al. 2002, Muir et al. 2004, Harder et al. 2006a, Harder et al. 2006b, Van Knegsel 2022). With our consideration of the period after peak, we increase the focus on extend lactations, without an impact to peak yield (Figure 1 and 2). In herds with voluntarily extended lactations, a positive effect on conception rates might be expected, because at a later insemination time point, the energy balance of the animals is more favorable, which aids conception (Van Knegsel 2022). Therefore, in the context of extended lactations, fertility traits need some re-consideration, e.g., the interval from calving to first insemination is no longer as relevant as it is currently in the RZR, the over-all fertility index (Vit 2023).

Future developments will include the extension of the RRTDM beyond DIM 305, which will give the opportunity to directly use information on genetic curves from longer lactations to further increase the accuracy of RZPersistenz.

Conclusions

The RZPersistenz provides breeders with information to support the effective selection of animals that are genetically suited to perform lactations with flatter curves, without an influence on the peak period. This can be used in extended lactations. Based on gEBV correlations no negative side-effects on other traits are expected from selection on the RZPersistenz.

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