Comparison of milk yield based resilience indicators across dairy cattle breeds

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Abstract

Resilience is increasingly recognized as an important trait for dairy cattle to improve their functioning and welfare. The log transformed variance (LnVar) and autocorrelation (r_{auto}) of daily milk yield deviations from an expected lactation curve have been studied as potential resilience indicators, so far only using data of Holstein Friesian cattle. The aim of this research was to compare the resilience indicators between different breeds present at Dutch dairy farms and to estimate the effect of crossbreeding on these indicators. Significant differences in LnVar and r_{auto} were found across twelve breeds, with the breed effects on LnVar different from the effects on r_{auto}. We estimated negligible heterosis effects for r_{auto} and LnVar. This study suggests that different breeds respond differently to environmental disturbances and that different breeds might have different levels or types of resilience.

Introduction

Recent local and global developments of the dairy farming industry, such as up-scaling of farm size, have created a demand for healthy and easy-to-manage cows (Elgersma et al., 2018). At the same time, future aspirations towards more circular and agroecological dairy farming, might lead to more environmental challenges for animals due to variable feed quality or exposure to weather extremes. To improve animal functioning and welfare, a more resilient cow is desired (Berghof et al., 2019). A resilient cow is minimally affected by a disturbance or rapidly returns to its former state upon exposure (Colditz and Hine, 2016; Berghof et al., 2019).

Increasing cow resilience through genetic selection requires large-scale quantification of this trait (Berghof et al., 2019). Scheffer et al. (2018) proposed to quantify resilience using automatically recorded high-frequency data of traits that are affected by disturbances. For dairy cows, such trait could be milk yield. Milk production drops when cows perceive a disturbance or when they have a disease (Elgersma et al., 2018). In the past, fluctuations in daily milk yield (DMY) have been proposed to create indicators for resilience of individual cows (Colditz and Hine, 2016; Elgersma et al., 2018; Poppe et al., 2020; Adriaens et al., 2020). Poppe et al. (2020) calculated resilience indicators from the deviations of DMY records from an expected lactation curve. In the data set of Poppe et al. (2020), consisting of purebred Holstein Friesian (HF) cows only, a low variance and autocorrelation were shown to indicate a high level of resilience.

Health, fertility, longevity and production level differ between breeds. For example, Bieber et al. (2019) showed that local breeds from Sweden, Austria, Switzerland and Poland tended to live longer, have a better health and fertility, but produced less than the commercial breeds HF or Brown Swiss. They described the local breeds to be more robust and therefore more suitable for locally adapted organic or agroecological dairy production systems. However, large scale analyses of resilience traits based on DMY of non-HF breeds have not been performed. In this study, we compared the resilience indicators proposed by Poppe et al. (2020) across breeds and estimated the effect of crossbreeding on these indicators.

Material & Methods
The dataset consisted of 2,763,357,043 milk yield records from farms with an automatic or conventional milking system provided by breeding company CRV (Arnhem, the Netherlands). These records included animal ID, milk yield and the date and start and end time of the milking of in total 1,528,030 dairy cows. Additionally, pedigree data of each animal were available. Data editing steps and calculation of resilience indicators were similar to Poppe et al. (2020). In the current study, purebred animals (at least 87.5% of one breed) and crossbred animals (50% HF and 50% of another breed) were selected. The resilience indicators were calculated only for first parities of cows that were milked by an automatic milking system and whose age at first calving was more than 640 days. For these animals, DMY was calculated. All DMY records made after 350 days in milk were removed from the dataset. Animals that had their first DMY record later than 14 days after calving, that had less than 50 DMY records or that had more than 5% missing records per lactation were removed from the dataset.

Calculation of resilience indicators. The resilience indicators used in this study were based on deviations of DMY records from an expected lactation curve that corrects for the lactation shape in absence of disturbances. For the calculation of this expected lactation curve, a polynomial quantile regression (Equation 1) was fitted on the DMY records of each cow:

$$DMY_t = \beta_0 + \beta_1 t + \beta_2 t^2 + \beta_3 t^3 + \beta_4 t^4 + \varepsilon \qquad (1)$$

where DMY_t was the observed DMY on lactation day t and ε was a random error term.

Next, variance and autocorrelation were calculated from the daily deviations of DMY from the expected lactation curve. The variance of those deviations had a right-skewed distribution. To create a normally distributed variable a log-transformation was applied to the variance trait (LnVar). The autocorrelation was calculated with a time lag of 1 day (r_{auto}).

Statistical analysis. Breed and heterosis effects on average daily milk yield (ADMY) and on the resilience indicators LnVar and r_{auto} were estimated using linear regression models. For ADMY and autocorrelation the following model was used:

$$y = \mu + FLV + MON + BS + ZRB + NRB + MRY + BBL + JER + G + FH + AYS + cross + \varepsilon \qquad (2)$$

Where y was the observed ADMY or r_{auto}, the HF breed was taken as intercept, the other fixed effects represent the individual breed proportions, with respectively FLV as Fleckvieh, *MON* as Montbéliarde, *BS* as Brown Swiss, *ZRB* as Swedish Red, *NRB* as Norwegian Red, *MRY* as Meuse-Rhine-Yssel, *BBL* as Belgium Blue, *JER* as Jersey, *G* as Groninger Whiteheaded, *FH* as Dutch Friesian and *AYS* the proportion of Ayrshire. $cross$ was the fixed effect of an animal being a cross (1) or purebred (0) cow to estimate the heterosis effect, and ε was a random error term. Additional to the fixed effects of Equation 2, the model for LnVar included the ADMY as a covariate to correct for the scale effect of milk yield level across breeds. This was done based on the knowledge that an increase in the mean of a trait typically leads to a (proportional) increase of its variance (Falconer and Mackey, 1996).

Results
The final dataset included 450,642 pure and crossbred animals of twelve different breeds (Table 1). The breeds Meuse-Rhine-Yssel, Jersey and Dutch Friesian were mostly present as purebreds, while other breeds were more frequently used for crossbreeding. The individual fixed breed effects showed that ADMY of all breeds was significantly lower than that of the Holstein Friesian. The heterosis effect on ADMY was significant and was estimated at +0.9 kg.

Table 1. Number of pure- and crossbreds and the breed effects on the average daily milk yield (ADMY) for the breeds in the final dataset.

| Breed[1]	HF	MRY	FLE	JER	MON	FH	BS	G	ZRB	NRB	BB	AYS
Purebreds	426,335	1818	1010	757	663	282	137	33				
Crossbreds		879	7338	411	3456	62	3133	149	2196	1470	472	41
ADMY (kg)	27.2	20.0	22.1	17.9	22.8	20.9	21.5	13.6	20.0	23.3	20.6	19.4

[1] HF=Holstein Friesian, MRY=Meuse-Rhine-Yssel, FLE=Fleckvieh, JER=Jersey, MON= Montbéliarde, FH=Dutch Friesian, BS=Brown Swiss, G=Groninger Whiteheaded, ZRB= Swedish Red, NRB=Norwegian Red, BB=Belgium Blue, AYS=Ayrshire

The r_{auto} differed slightly between breeds (Figure 1). The r_{auto} of Fleckvieh, Montbéliarde, Brown Swiss, Belgium Blue and Jersey was significantly lower than HF, suggesting that their recovery rates are higher. In contrast, Swedish and Norwegian Red and Dutch Friesian had a significantly higher r_{auto} than HF, suggesting that their recovery rate was lower. The heterosis effect on r_{auto} was estimated at -0.007, which is negligible compared to the breed effects.

The LnVar increased with 0.021 per kg ADMY. Breed effects of Montbéliarde and Swedish Red showed a significantly higher LnVar than HF (Figure 2), which is associated with a more variable milk yield. Fleckvieh, Norwegian Red, Jersey, Dutch Friesian and especially the Groninger Whiteheaded and Meuse-Rhine-Yssel breeds showed a significant lower LnVar than HF, suggesting that those breeds have a more stable milk yield in presence of common disturbances. The heterosis effect was estimated at +0.028, which is negligible.
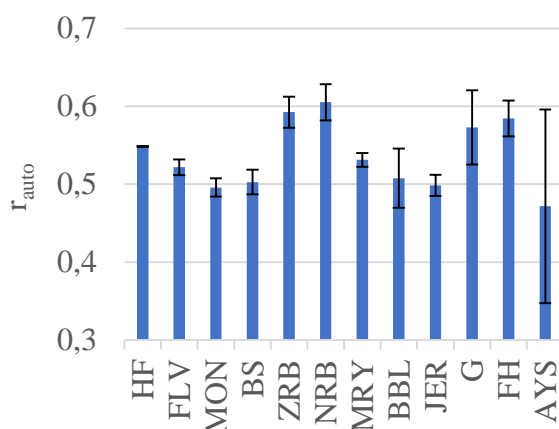
Figure 1. Breed effects on the r_{auto}. Error bars represent the 95% confidence interval.
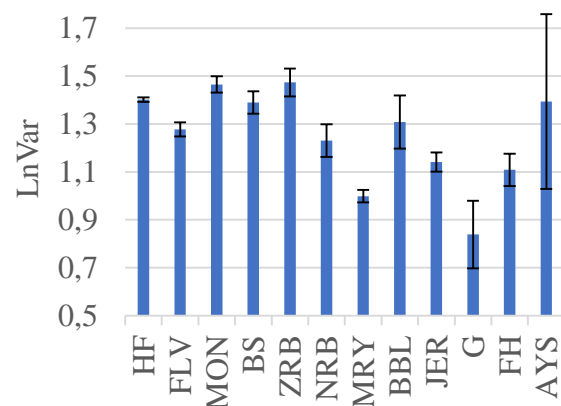
Figure 2. Breed effects on the LnVar, using daily milk yield as covariate. Error bars represent the 95% confidence interval.

Discussion

The aim of this study was to compare breeds present at Dutch dairy farms for the resilience indicators LnVar and r_{auto}. Differences in LnVar and r_{auto} were found across breeds, demonstrating cattle breeds differ in milk yield variability and recovery rate. This suggests that the level and type of resilience varies between breeds. Some breeds score better for LnVar and others score better for r_{auto}, this suggests that different breeds respond differently to environmental disturbances.

In this study, heterosis effects for the resilience indicators were negligible. That was against our expectations because heterosis effects are strongest for health and functional traits (Sørensen et

al., 2008). Still, crossbreeding could improve LnVar and r_{auto} of the offspring because some breeds score better than HF. The effect of ADMY as a covariate in the model of LnVar was of considerable strength, taking into account the difference in ADMY between breeds. This is largely explained by a statistical effect, but there might be underlying biological reasons too (Poppe et al. 2021). More research is needed to understand that relationship better.

There is no proof in this study that breeds with more favourable LnVar and r_{auto} are indeed more resilient because we have no information on the environmental challenges or on an animal's vulnerabilities that are causing drops in milk yield. The type of production system that the animals are kept in, and thus the type or level of environmental challenges, might be different for the different breeds. In addition, different breeds might be specifically more susceptible to different health issues. So, drops in milk yield might be caused more by mastitis in one breed but more by claw problems in the other. Further research is needed to explore this.

This study suggests that different breeds respond differently to environmental challenges and that different breeds might have different levels or types of resilience (Friggens et al., 2021). This study, however, involved only two resilience indicators, that were both based on milk yield. For a deeper understanding of the resilience of different cattle breeds, more indicators derived from fluctuations in DMY and/or more sources of information, such as animal activity, could be explored (Adriaens et al. 2020).

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References

Adriaens, I., Friggens, N.C., Ouweltjes, W., Scott, H., Aernouts, B. et al. (2020). J. Dairy Sci. 103:7155-7171. https://doi.org/10.3168/jds.2019-17826

Berghof, T.V.L., Poppe, M. and Mulder, H.A. (2019). Front. Genet. 9:692. https://doi.org/10.3389/fgene.2018.00692

Bieber, A., Wallenbeck, A., Leiber, F., Fuerst-Waltl, B., Winckler, C. et al. (2019). J. Dairy Sci. 102(6):5330-5341. https://doi.org/10.3168/jds.2018-16147

Colditz, I.G., and Hine, B.C. (2016). Anim. Prod. Sci. 56(12):1961–1983. https://doi.org/10.1071/AN15297

Elgersma, G.G., de Jong, G., van der Linde, R., and Mulder, H.A. (2018). J. Dairy Sci. 101(2):1240–1250. https://doi.org/10.3168/jds.2017-13270

Falconer, D.S. and Mackay, T.F.C. (1996). Introduction to Quantitative Genetics. 4th ed, Pearson Education Limited, Essex, UK.

Friggens, N.C., Adriaens, I., Boré, R., Cozzi, G., Jurquet, J. et al. (2021). 10.5281/zenodo.5473794

Poppe, M., Veerkamp, R.F., van Pelt, M.L., and Mulder, H.A. (2020). J. Dairy Sci. 103(2):1667–1684. https://doi.org/10.3168/jds.2019-17290.

Poppe, M., Mulder, H.A., Kamphuis, C., and Veerkamp, R.F. (2021). J. Dairy Sci. 104:616-627. https://doi.org/10.3168/jds.2020-18525

Scheffer, M., Bolhuis, J.E., Borsboom, D., Buchman, T.G., Gijzel, S.M.W. *et al.*. (2018). Proc. Natl. Acad. Sci. U. S. A. 115(47):11883–11890. https://doi.org/10.1073/pnas.1810630115

Sørensen, M.K., Norberg, E., Pedersen, J., and Christensen, L.G. (2008). J. Dairy Sci. 91(11), 4116-4128. https://doi.org/10.3168/jds.2008-1273