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M. van Niekerk[1,2*], F.W.C. Neser[1], J.B. van Wyk[1] and V. Ducrocq[1,2]

[1] Department of Animal, Wildlife and Grassland Sciences, University of the Free State, 205 Nelson Mandela Drive, Park West, Bloemfontein 9301; [2] Université Paris-Saclay, INRAE, AgroParisTech, UMR GABI, 78350, Jouy-en-Josas, France; [*]michiel@ganna.co.za

Abstract

Genetic improvement for persistency of milk production in South African Holstein cattle in a total mixed ration or pasture production system will be impeded because of the existence of genotype by environment interaction between the production systems. Previous studies where herds' production system were known (unlike reality) showed that rainfall level indicate the production system preferred by producers. The study aimed to determine the effect of including average rainfall in a random regression model as a possible proxy for production system used. The animal-additive-genetic effect due to annual rainfall (class) was added to the existing additive-genetic-average-production and -persistency effect. Heritability estimates of rainfall class 1 ("low" rainfall) coincided with total mixed ration estimates while rainfall class 5 ("high" rainfall) coincided with pasture estimates in later lactations. Results suggest that genetic background responsible for average production level and persistency over the lactations are not consistent over different rainfall areas.

Introduction

Genotype by environment interaction has been shown to exist in South African (SA) Holstein dairy cattle in previous studies by Ducrocq et al. (unpublished data) and Van Niekerk et al. (2019, 2021). In the latter two studies, clear differences in genetic parameters between herds using a total mixed ration (TMR) or pasture (PSTR) production system were shown. Specifically, genotype by environment interaction for persistency of production between the two production systems were indicated with genetic correlations for the first three lactations being below 0.64 throughout (Van Niekerk et al., 2021). This mean that animals whose progeny perform well in TMR will not necessary perform well under PSTR conditions with regards to milk production (MilkPr) traits. Selecting sires whose progeny will perform satisfactory or superior in both or one of the production systems will thus not be accurate, as the production system used by herds are not known and thus ignored in genetic evaluations of SA Holsteins. Ducrocq et al. (2015) showed that the production system used by herds are dependent on the rainfall (long term annual average) of the herd's location (nearest town) in SA. They also showed that rainfall had the largest effect on the genetic variability of MilkPr using a reaction norm model. The aim of this study was to investigate the effects of including average rainfall of the towns nearest to the applicable herds as a proxy for the production system used, utilising a previously developed alternative random regression model (aRRM; Van Niekerk et al., 2019).

Materials & Methods

Full access to the complete pedigree and milk recording data that were used in this study were given by the SA Holstein Cattle Breeders' Society.

Data. Test-day (TD) records of MilkPr (kg) from 1988 to 2016 were used for the analysis. The dataset consisted of the first three lactations of cows from 37 herds, of which 26 utilize a TMR and 11 a PSTR production system. Cows with seven or more TD records per lactation and who completed their first lactation were used in the study. Sires with less than 10 daughters and contemporary groups with less than five cows were excluded from the dataset.

Statistical analyses. Restricted maximum likelihood was used to analyse the data, making use of the Wombat software (Meyer, 2007). MilkPr was analysed using multi-lactation records and the aRRM (Van Niekerk et al. (2019). This model was created as a better substitute to the fixed regression model used for genetic evaluations of SA Holsteins (Interbull, 2022). In the aRRM the animal-additive-genetic random effects were defined as separate for each lactation and expressed as a function of days in milk, containing a constant plus a regression slope multiplied by current days in milk. Consequently, each lactation is a combination of an (additive) genetic-average-production (GPr) and -persistency (GPe) effects (first and second eigenvector per lactation, respectively). In the analysis for this study, a third term (regression) over each day in milk was added for the animal-additive-genetic effect (third eigenvector). This term represents the genetic effect due to rainfall (GR), as a proxy to dominant production system. Rainfall level (long term annual average) was categorised in five classes as follow: Class 1: 413 to 492 mm; Class 2: 493 to 597 mm; Class 3: 598 to 672 mm; Class 4: 673 to 787 mm; Class 5: 788 to 1008 mm. Classes were defined according to a relative balanced distribution of herds over rainfall level. The permanent environmental effect was included in the same way as the animal-additive-genetic effect. Residual variance was considered heterogeneous over and between lactations and partitioned in 10 classes per lactation. This aRRM, TD and multi-lactation model that included the GR effect (GR model) for MilkPr can be described as follows:

$$\mathbf{y} = \mathbf{Tt} + \mathbf{Ss} + \mathbf{Hh} + \mathbf{Ll} + \mathbf{Mm} + \mathbf{Aa} + \mathbf{Cc} + \mathbf{Qu} + \mathbf{Zp} + \mathbf{e} \quad (1),$$

where **y** is a vector of 24-h test-day MilkPr observations for the lactations; **t** is a vector of fixed Herd x Test-day x Number of milkings interaction (contemporary group) effects; **s** is a vector of fixed Herd x Calving year x Calving season x Lactation number interaction effects. The following vectors of fixed regression coefficients are included in equation (1): **h** for Herd effects; **l** for Calving year x Lactation number interaction effects; **m** for Calving month effects; **a** for Calving age class effects (8 classes); **c** for previous calving interval class effects (8 classes). The random regression coefficients for the animal additive genetic and permanent environmental effects were **u** and **p**, respectively and **e** is a vector of residual effects. The matrices **T**, **S**, **H**, **L**, **M**, **A**, **C**, **Q** and **Z** are incidence matrices that relate observations to their respective effects.

Results and Discussion

The model that included the GR effect in this study did not have a better Bayesian Information criterion (increase of 27,316.38) compared to results from Van Niekerk et al. (2021), where the TD records from TMR and PSTR were treated as different traits (i.e., multi-trait analyses) and without the GR effect (TMR-PSTR model). However, there was an improvement of the Bayesian information criterion (decrease of 2,879.55) compared to results from Van Niekerk et al. (2021), where TD records from TMR and PSTR were treated as the same trait, also without the GR effect. This model can be seen as a 'national SA Holstein genetic evaluation' (nGE model). The addition of the GR effect in the current model explained 7.8% of the animal-additive-genetic effect for MilkPr in lactation 1 and decreased to 0.9% and 0.0% for lactation 2 and 3, respectively.

In lactation 1 (Figure 1), heritability estimates from the GR model were similar between ("low") rainfall classes 1, ("medium) 3 and ("high") 5, and in close agreement to TMR and nGE estimates. In lactation 2 the rainfall class 1 and 3 estimates were still close to each other and to TMR and nGE estimates. However, rainfall class 5 estimates were higher during early- to midlactation and closer to heritability estimates from the PSTR production system. In lactation 3 the differences between the heritability estimates of rainfall class 1, 3 and 5 are more pronounced during mid- to late-lactation with estimates from rainfall class 5 being closest to PSTR estimates, and rainfall class 1 estimates still being closest to TMR estimates (as in lactation 1 and 2). (Van Niekerk et al., 2021).

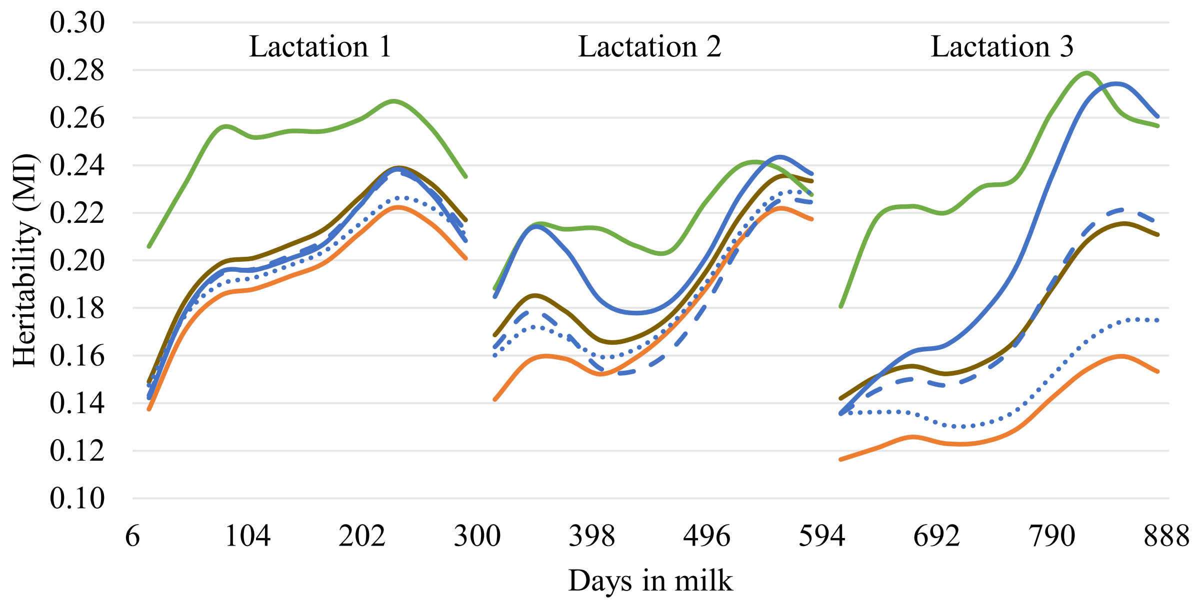

Figure 1. Heritability estimates for milk production over the first three lactations using the model including the genetic effect due to rainfall (class 1: blue dotted; class 3: blue dashed; class 5: blue solid; GR model), compared to a previous model where the two production systems were defined as different traits (total mixed ration: orange; pasture: green; TMR-PSTR model), as well as a 'national SA Holstein genetic evaluation' model excluding the genetic effect due to rainfall and TD records undefined for production system (brown; nGE model).

The nGE heritability estimates are similar to the TMR estimates as most records analysed with the nGE model came from herds using a TMR production system (Van Niekerk et al., 2021). Rainfall class 1 heritability estimates being close to previous TMR heritability estimates make sense as 100% of herds in this class use a TMR production system. This also make sense to a lesser degree, for rainfall class 3 estimates as 78% of herds utilise a TMR production system. 75% of herds employing a PSTR production system in rainfall class 5 explains the similarity of these estimates with previous PSTR estimates. Rainfall classes 3 and 5 heritability estimates seem to follow nGE and PSTR estimates more precisely in later lactations, specifically lactation 3. (Van Niekerk et al., 2021).

Genetic correlations (Table 1) between the GR and GPr effects were positive but weak, ranging from 0.43 to 0.32 for lactation 1 and 2, and 0.19 for lactation 3. The genetic correlation between the GR and GPe effects were negative and also weak for lactation 1 and 2 (-0.28 and -0.30, respectively), but positive and close to zero for lactation 3 (0.10).

The GPr and GPe components are made up of the average-additive-genetic level and persistency respectively, of performance of animals and their progeny, irrespective of the rainfall area(s) in which they produce and are measured in, over each of the lactations. When the additive-genetic performance of animals and their progeny are further regressed for average rainfall, the genetic correlations mentioned suggest that the genes involved in MilkPr are not consistent and reliable over different rainfall areas.

Table 1. Genetic correlations between the different animal-additive-genetic effects for milk production (MilkPr) over the first three lactations.

MilkPr		Lac1[1]			Lac2[1]			Lac3[1]		
		GPr[2]	GPe[3]	GR[4]	GPr[2]	GPe[3]	GR[4]	GPr[2]	GPe[3]	GR[4]
Lac1[1]	GPr[2]	1.00								
	GPe[3]	-0.29	1.00							
	GR[4]	0.43	-0.28	1.00						
Lac2[1]	GPr[2]	0.90	-0.41	0.43	1.00					
	GPe[3]	-0.07	0.12	-0.03	-0.15	1.00				
	GR[4]	0.20	-0.41	0.88	0.32	-0.30	1.00			
Lac3[1]	GPr[2]	0.88	-0.35	0.32	0.98	-0.24	0.25	1.00		
	GPe[3]	-0.08	0.03	-0.07	-0.14	0.95	-0.26	-0.22	1.00	
	GR[4]	0.26	-0.15	0.52	0.27	0.03	0.38	0.19	0.10	1.00

[1]Lac_i – Lactation 1, 2 or 3; [2]GPr – (additive) genetic-average-production effect; [3]GPe – (additive) genetic-average-persistency effect; [4]GR – (additive) genetic effect due to long-term-annual, average rainfall.

Conclusions

Considering the heritability estimates in this study and supported by previous research, including rainfall level as an important climatic variable in the proposed aRRM for MilkPr seem to be a good proxy for production system used by Holstein herds in SA, especially for later lactations. The way in which the rainfall classes are constructed may have an important effect on the heritability estimates. More herds in high rainfall areas that utilise a PSTR production system should be identified and incorporated in the study to increase accuracy of genetic parameters.

References

Ducrocq, V., Cadet, A., Patry, C., Pienaar, L., Van Wyk, J.B. *et al*. (2015) Interbull Meeting, Orlando, Florida, United States of America. https://interbull.org/static/web/Ducrocq_GxE2015.pdf

Interbull. (2022) https://interbull.org/ib/geforms

Meyer, K. (2007) WOMBAT – A tool for mixed model analyses in quantitative genetics by REML. J. Zhejiang Uni. SCIENCE B 8:815-821. [doi:10.1631/jzus.2007.B0815]

Van Niekerk, M., Neser, F.W.C., and Ducrocq, V. (2019) 51st South African Society for Animal Science (SASAS) congress, University of the Free State, Bloemfontein, South Africa. http://dx.doi.org/10.13140/RG.2.2.17663.15520

Van Niekerk, M., Neser, F.W.C., Van Wyk, J. B., and Ducrocq, V. (2021) Proc. of the 72nd Annual Meeting of the European Federation of Animal Science, Davos, Switzerland. http://dx.doi.org/10.13140/RG.2.2.17981.38883