

## An investigation into the possibility of a Genotype by Environmental interaction for milk production in the South African Jersey population

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### Abstract

The possibility of a genotype by environment interaction for milk production in the South African Jersey population was investigated by grouping 37687 first lactation records completed between 1985 and 1999 into different production or environmental levels. The dataset consisted of 301 herds and 884 sires. Three different sets of criteria were used to group the animals. Firstly a cluster analysis was applied using different management, climatic and genetic factors. This analysis resulted into four different clusters. Secondly the herds were divided into four categories according to feeding systems and geographic location. All herds using a Total Mixed Ration (TMR) were placed in one group while the pasture herds form a second group. Herds that were situated in the warmer northern areas of South Africa (Limpopo and Northern KwaZulu-Natal) were placed into a third group and the herds in the Overberg area that did not have access to irrigation water formed a fourth group. Lastly the herds were divided into four groups according to production levels. A bivariate animal model was used to determine genetic correlation estimates for milk production between each group in the different scenarios. The correlations varied between 78% and 99%. The lowest correlation was between the warmer Northern areas and the Overberg area. The highest correlation was between Cluster 3 and Cluster 4 as well as between the low production group and the medium-low production group. The high genetic correlations indicate that no G x E existed for the different scenarios.

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### Introduction

Dairy production in South Africa is conducted under a wide variety of production systems. These systems vary from highly intensive zero grazing to pasture based milking with the minimum use of supplementation of concentrates. Climatic conditions vary from a winter rainfall area in the south to a sub-tropical summer rainfall area in the north. The western part of the country is a semi-desert while the eastern part is classified as a sub-tropical area. It therefore stands to reason that a possible genotype-environment interaction (G x E) could exist among the different production systems or climatic regions. Genotype x environment interaction can be defined as different sets of genes that determine varying levels of expression in different environments (Bertrand *et al.*, 1987). If such a G x E exists it can reduce the accuracy of the genetic analysis (Naser *et al.*, 1996) and the reliability of such evaluations is overestimated (Ibi *et al.*, 2005).

In dairy cattle cluster analysis over different ecological regions and countries is used to overcome this problem. The herd-cluster model is appealing because an animal's genetic merit is predicted for each unique environment or management system, regardless of country borders (Weigel & Rekaya, 2000). A number of studies were done to investigate G x E by using cluster analyses (Lin & Lin, 1994; Weigel & Rekaya, 2000; Fiske *et al.*, 2001; Zwald *et al.*, 2003a; b). These were mostly done on dairy cattle investigating borderless international genetic evaluations. The purpose of this study was to investigate the possibility that a G x E exists among the different production systems and/or climatic regions in South Africa using different methods to classify herds into either groups or clusters.

### Materials and Methods

The data consisted of 37687 first lactation records of Jersey cows born between 1985 and 1999 the progeny of 520 sires in 264 herds. Three different sets of criteria were used in the analysis.

The herds were first divided into four different groups. These groups were based on the following criteria:

- Group 1: Herds that were on a Total Mixed Ration (TMR), irrespective of farm location.
- Group 2: Herds that were on a pasture system with concentrate supplementation.
- Group 3: Herds in the Overberg and Southern Cape region that did not have access to irrigation.
- Group 4: Herds that were in the sub-tropical areas of South Africa.

Secondly, a cluster analysis was used to group herds according to the following factors: SAINET (van Niekerk, 2004), percentage pasture, times milked per day, herd size, mid-winter temperature, sire's percentage USA genes, latitude, mid-summer rainfall, age at first calving and kilograms milk produced per lactation. Cluster analysis is an exploratory technique designed to classify data into subgroups which share similar characteristics (Lin & Lin, 1994). The Fastclus clustering procedure in SAS (1992) was used for herd clustering. This procedure performs a disjoint cluster analysis based on Euclidean distances. This iterative method guarantees that the distances between all observations in the same cluster will be less than the distances between observations in different clusters (Zwald *et al.*, 2003a). Four clusters were formed. The different factors and their mean values that were used in the clustering process are presented in Table 1.

**Table 1** The mean values for dairy herds grouped according to the cluster analysis based on differences in herd genetic levels, management practices, herd size and environmental factors

Cluster	SAINET	Pas- ture (%)	Times milk	Herd size	Mid- winter temp (°C)	Sire's USA genes (%)	Lati- tude	Mid- summer rainfall (mm)	Age first calving (months)	Milk (lact) (kg)
1	94.97	37.34	2.00	63.84	18.56	32.51	30.55	71.95	27.85	3600
2	99.93	25.85	2.02	97.82	18.92	48.66	30.28	81.97	27.03	5457
3	102.55	9.83	2.17	102.52	19.00	57.90	29.05	93.31	25.72	6812
4	97.91	37.08	2.02	90.59	19.67	42.03	31.48	70.84	27.18	4570

The last grouping of herds was done according to the following criteria:

- P1: All herds with an average production less than 4000 kg per lactation;
- P2: All herds with an average production  $\geq$  4000 kg and  $<$  5000 kg per lactation;
- P3: All herds with an average production  $\geq$  5000 kg and  $<$  6000 kg per lactation;
- P4: All herds with an average production  $\geq$  6000 kg per lactation (National Dairy Cattle Performance testing scheme: South Africa)

Once the clusters were established, a stepwise regression was done to determine the fixed effects that were to be included in the models to be used for the genetic (co)variance estimates. Milk production in each group or cluster was considered as a separate, but possible related trait, across clusters. Estimates of the (co)variance components were obtained using ASREML (Gilmore *et al.*, 2002). The following model was used in the analysis:

$$y = X\beta + Za + e$$

Where  $y$  is an  $n \times 1$  vector of records,  $X$  is a  $n \times p$  incidence matrix that relates data to the unknown vector of location parameters  $\beta$ . The vector  $\beta$  contained the fixed effects. The incidence matrices  $Z$  relate the unknown random vectors of the direct breeding value ( $a$ ) to  $y$ . The unknown vector  $e$  contains the random residuals due to environmental effects peculiar to individual records.

Animal was included as a random effect, herd-birth year-calving season (hyys) was used as a fixed effect and days in milk and age at first calving were used as co-variates. Bivariate animal models were used to obtain correlation estimates between the groups or clusters, as the data set was too large to include all clusters or groups in one analysis.

## Results and Discussion

The genetic correlations between the different groups according to feeding and geographical location are presented in Table 2. All correlations were highly significant. The highest correlation (97.8) was estimated between the TMR herds and the herds in warmer sub-tropical areas of the country. A possible reason for this high correlation is that all the herds in the sub-tropical areas parts are on a TMR system. The bulk of these herds have also put certain measurements in place to try to control the effect of the extreme heat.

The lowest correlation (78.2) was estimated between the Overberg herds and the herds in the sub-tropical areas of the country. The Overberg region is a winter rainfall area that allows the use of dry land pastures in winter. However, in summer cows are kept in small camps and fed a TMR. Production in the Overberg region also had the lowest correlation with the other two regions. The circumstances in the Overberg require a cow that can utilise pastures just as effectively as TMR.

**Table 2** Genetic correlation estimates (%) for milk yield between the different groups of herds

	Pasture system	Overberg region	Sub-tropical areas
TMR	95.5	89.2	97.8
Pasture system		86.8	96.6
Overberg region			78.2

Robertson (1959) indicated that the genetic correlation gives a measure of the practical rather than statistical significance of the traits, and suggested that an estimated genetic correlation appreciably lower than one (<0.80) would indicate changes in the ranking of genotypes in the two environments. In the study where herds were divided into different groups according to feeding and geographical location only the correlation between herds in the Overberg region and those in the sub-tropical areas of the country indicate a possible G x E.

Herds in Cluster 3 (Table 1) had the lowest dependence on pastures (9.83%), the highest percentage USA genetics (57.90%), the highest average milk production, lowest age at first calving and the highest genetic level. The bulk of these herds was run on TMR and was located in the northern parts of the country. Herds with the highest dependence on pastures were allocated to Clusters 1 and 4. The difference between these two clusters was the percentage USA genetics (32.5% vs. 42.0%), the average herd size (63.8 vs. 90.6) and average milk production (3600 kg vs. 4570 kg). The majority of the herds in both of these clusters were situated in the southern part of the country. Cluster 2 was the cluster with the second highest percentage USA genetics in the herd. The biggest difference between Cluster 2 and Cluster 3 was the average pasture content in the animal's diet (25.9% vs. 9.8%) and the average milk production (5457 kg vs. 6812 kg). The majority of the herds in Cluster 2 was also situated in the southern part of the country.

**Table 3** Genetic correlation estimates (%) for milk yield between the different clusters constructed according to genetic levels, management practices, herd size, environmental influences and geographical location

	Cluster 2	Cluster 3	Cluster 4
Cluster 1	88.6	88.2	97.7
Cluster 2		99.2	95.1
Cluster 3			92.4

The highest correlation estimate (Table 3) was obtained between Clusters 2 & 3 while the lowest correlation was obtained between Clusters 1 and 3. Although all correlations were highly significant, none of these estimates indicated a significant G x E.

The low producing group (P1 < 4000-Table 4) had the lowest correlation with all the other groups in the analysis where production was used as criteria. The lowest correlation estimate was obtained between the low producing herds (P1) and high producing herds (P3 and P4), while the highest correlation estimate was obtained between the herds grouped in the two high producing groups. The main difference is that all the low producing herds were pasture based and that feeding in the other three groups varied between TMR and pastures, with a combination between the two in some instances. Again all correlations were significant.

**Table 4** Genetic correlation estimates (%) for milk yield between herds grouped according to their milk production (kg)

	P2	P3	P4
P1	87.5	82.8	85.3
P2		96.9	98.8
P3			99.3

## Conclusion

The high genetic correlation estimates indicate that no G x E for milk yield existed between the different production systems or -environments. However, more research is needed to investigate the possibility of such an interaction for fertility and longevity in dairy cattle.

## References

- Bertrand, J.K., Hough, J.D. & Benyshek, L.L., 1987. Sire x environment interactions and genetic correlations of sire progeny performance across regions in Dam-Adjusted Field Data. *J. Anim. Sci.* 64, 77-82.
- Lin, C.Y. & Lin, C.S., 1994. Investigation of genotype-environment interaction by cluster analysis in animal experiments. *Can. J. Anim. Sci.* 74, 607-612.
- Fikse, F., Rekaya, R. & Weigel, K.A., 2001. Genotype by environment interaction for milk production traits in Guernsey cattle. *Proc. Interbull Bull.* 27, 9-12.
- Ibi, T., Hirooka, H., Kahi, A.K., Sasae, Y. & Sasaki, Y., 2005. Genotype x environment interaction effects on carcass traits in Japanese Black cattle. *J. Anim. Sci.* 83, 1503-1510.
- Gilmour, A.R., Cullis, B.R., Welham, S.J. & Thompson, R., 2002. ASREML Reference manual. NSW, Agriculture Biometric No.3 NSW Department of Agriculture, Orange. 210 pp.
- Neser, F.W.C., Konstantinov, K.V. & Erasmus, G.J., 1996. The inclusion of herd-year-season by sire interaction in the estimation of genetic parameters in Bonsmara cattle. *S. Afr. J. Anim. Sci.* 26, 75-78.
- Robertson, A., 1959. The sample variance of the genetic correlation coefficient. *Biometrics* 15, 469-475.
- SAS, 1992. Statistical Analysis Systems user's guide: Stat. version 6.03. SAS Institute Inc. Cary, N.C., USA.
- Van Niekerk, D.J., 2004. SAINET – 'n Nuwe begin. *SA Jersey Journal* 53 (1) 22-24.
- Van Niekerk, D.J. & Neser, F.W.C., 2004. Application of a multiple-trait herd cluster model for genetic evaluation of Jersey sires in South Africa. *Proc. 40<sup>th</sup> SASAS Congr.*, Goudini Spa. p. 43.
- Weigel, K.A. & Rekaya, R., 2000. A multiple-trait herd cluster model for international dairy sire evaluation. *J. Dairy Sci.* 83, 815-821.
- Zwald, N.R., Weigel, K.A., Fikse, W.F. & Rekaya, R., 2003a. Application of a multiple trait herd cluster model for genetic evaluation of dairy sires from seventeen countries. *J. Dairy Sci.* 86, 376-382.
- Zwald, N.R., Weigel, K.A., Fikse, W.F. & Rekaya, R., 2003b. Identification of factors that cause genotype by environment interaction between herds of Holstein cattle in seventeen countries. *J. Dairy Sci.* 86, 1009-1018.